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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 469)
S Edwards, J.B.D.M., Jobert.S. and Giordano, J.E.
EST and encoded human protein
L Patent: JP 2002010789-A 1356 15-JAN-2002;
GENSET CORP
OS Homo sapiens (human)
PN JP 2002010789-A/1356
PD 15-JAN-2002
PF 07-AUG-2000 JP 2002080989
PR 05-AUG-1999 US 60/147499
PR 05-AUG-1999 US 60/147499
PI JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI
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AC133135 Papio anu
AC163368 Bos tauru
AE016801 Vibrio vu
AE000823 Methanoba
CS072276 Sequence
AX588689 Sequence
AX588689 Sequence
BD107959 EST and e
AX412406 Sequence
BD110503 EST and e
AX414950 Sequence
BD10503 EST and e
AX91784 Sequence
BD108278 EST and e
AX917784 Sequence
AX97559 Sequence
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AX574405 Sequence
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AX60204 Sequence
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AX60211 Homo sapi
BC036256 Homo sapi
BC036256 Homo sapi
BC046121 Homo sapi
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BC099498 Mus muscu
AC126036 Mus muscu
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AX984897 Sequence
AC1913557 Mus muscu
AC157365 Mus muscu
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AP000622 Homo sapi
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AC01309498
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AC127289
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JP 2002010789-A/1356.
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C12N1/21,
PC C12N5
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   DEFINITION
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-G=Abss/ABSWBEs spool/US10664025/runat 08052006 173641 29351/app query.fasta_1
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-UNITS=bits -START=1 -EMD=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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AR413726 Sequence
AX970560 Sequence
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3163.483 Million cell updates/sec
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                                                                                                                       9, 2006, 13:15:42 ; Search time 458.2 Seconds
                                     Ltd
                  GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration
                                                                                - nucleic search using frame plus p2n model
                                                                                                                                                                                                                                                                                                                                                                              5883141 segs, 28421725653 residues
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Maximum Match 100%
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Maximum DB seq length: 200000000
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9: gb_pr:*

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9: gb_hr:*

9b_un:*

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Ygapop 10.0 , Y
Fgapop 6.0 , F
Delop 6.0 , D
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Best Local Similarity:
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Edwards, J.-B.D.M., Jobert, S. and Giordano, J.-Y.
EST's and encoded human proteins
Patent: US 6639063-A 1363 28-OCT-2003;
Genset S.A.;;
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seq VLMLLAVLIWTGA/EN
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Location/Qualifiers
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Conservative:
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CS072276
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                                                                                                                                                                                          1. .469 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
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52. 1102
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/22. 122
/note="Von Heijne matrix score 10.699998092651 seq VLMLLAVLIWTGA/EN"
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Giordano,J.Y.
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72. .500
/note="unnamed protein product"
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Sequence 563 from Patent WO02083898.
AX588688.
AX588688.1 GI:27900344
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
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Full-length human cdnas encoding potentially secreted proteins
Patent: WO 02083898-A 564 24-OCT-2002;
                                                                                                                                                                                         MetalaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAla 17
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PE Corporation (NY) (US)
Location/Qualifiers
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Sequence 23358 from Patent WO02068579.
CQ737424
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AX588689
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla; Eutheria, Euterchini, Eutheria, Euterchini, Hominidae, Homo.

1 (bases 1 to 512)

Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.

EST and encoded human protein

Patent: JP 2002010789-A 36 15-JAN-2002;
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//organism='Homo sapiens"
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AR412406.1 GI:40167516
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07-AUG-2000 JP 2000280989
05-AUG-1999 US 60/14745
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JP 2002010789-A/36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAT 15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarxhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53. .103
hote="Von Heijne matrix score 10.699998092651 seq
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                                                                                                                                                                                                                                                                                                                                                                               Dumas Milne Edwards, J.B., Jobert, S. and Giordano, J.Y. ESTs and encoded human proteins
Patent: EP 1104808-A 43 06-JUN-2001;
Genset (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
1 (bases 1 to 512)
Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
EST's and encoded human proteins
Patent: US 6639063-A 43 28-OCT-2003;
WOX;
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                                                                                                                                                                                                                           Length:
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                        Dumas Milne Edwards, J.B., Jobert, S. and Giordano, J.Y. BSTs and encoded human proteins
Patent: EP 1104808-A 2587 06-JUN-2001;
Genset (FR)
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AX971784
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EST and encoded human pro
BD109278.1
BD109278.1
GI:23204096
JP 2002010789-A/1355.
Homo sapiens (human)
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Homo sapiens
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BD109278
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ON EST and encoded human protein.

N BD110503

BD110503

BD110503

BD110503.1 GI:23205321

JP 2002010789-A/2580.

Homo sapiens (human)

SM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Hominidae; Homo.

Hominidae; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo.

E Gewards, J. B. D. M., Jobert, S. and Giordano, J. E.

E ST and encoded human protein

E ST and encoded human protein

E GENSET CORP
                                                                                PAT 18-SEP-2002
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JP 2002010789-A/2580
IS-JAN-2002
07-AUG-2000 JP 2000280989
05-AUG-1999 US 60/147499
USAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI
                                                                                                                                                                                                                                                                                                                                                                                C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
                                                                                                                                                                                                                                                                                                                                                                                                          C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC
linear
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1 (bases 1 to 560)

Edwards, J.-B.D.W., Jobert, S. and Giordano, J.-Y.
BST's and encoded human proteins
Patent: US 6639063-A 2587 28-OCT-2003;
Genset S.A.;;
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Matches:
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Mismatches:
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Key Joseph 272. 539.
Location/Qualifiers
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Sequence 2587 from patent US 6639063.
AR414950.
AR414950.1 GI:40170060
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PN JP 200
PD 15-JAM
PF 07-AIA
PR 05-AIG
PI GIORDANO
PC C12N15
C12N15/00
C12N15/00
CC EST at
FF CDS
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BD110503
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53 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT 103
                                                                             1 MetAlaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAla 17
                                              US-10-664-025-3903_COPY_1_17 (1-17) x AR413725 (1-642)
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PN JP 2002010789-A/1355

PN JP 2002010789-A/1355

PN JP 2002010789-A/1355

PR 15-JAN-2002

PP 07-AUG-2000 JP 2000280989

PR 05-AUG-1999 US 60/147499

PI JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI GIORDANO

PC C12N1/21,

PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N1/19, PC C12N1/5/00

CC VON Hedjne matrix

CC Score 10.6599998092651

CC Score 10.6599998092651

CC Seq VLMLAVLWTGA/EN

FH Key

FT CDS

FT Sig_peptide 533 .103.
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Clans/10,ClaP21/02,ClaP21/08,ClaQ1/68,ClaN15/00,Clans/00, PC
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 642)
Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
EST's and encoded human proteins
EST's and encoded human proteins
Genset S.A.;;
WOX;
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                                Hominidae; Homo.

1 (bases 1 to 642)

Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.
EST and encoded human protein
GENETH: JP 2002010789-A 1355 15-JAN-2002;
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Sequence 1362 from patent US 6639063.
AR413725.1 GI:40168835
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Ab690052 Human GSS
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Adr62236 Cotton cD
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Abg117617 Drosophil
Abg1845 Bifidobac
Ab17616 Drosophil
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Abg8177 Pseudomon
Ach85891 Human sec
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Adg5341 Human sec
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Aas34722 Human DNA
Ab192353 Human sec
Aah32256 Human olf
Abd05379 Pseudomon
Abd05292 Pseudomon
Add03085 P. aerugin
                        Adb63550 Human cDN
Aac69528 Human sec
Acc50642 Human sec
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ABQ19336
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ADQ53491
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AAS34722
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ADU58490
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WO200142451-A2.
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Abz36690 Human GEN
Ab4743 Human sec
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          GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Ygapop 10.0 , Y
Fgapop 6.0 , F
Delop 6.0 , D
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No.
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WPI; 2003-075548/07

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The invention relates to full length GENSET human nucleic acids encoding potentially secreted proteins. The nucleic acids and the polypeptides they encode may be used in the prevention, treatment and diagnosts of diseases associated with inappropriate GENSET gene expression. For example, they be used to treat disorders associated with decreased GENSET gene expression by rectifying mutations or deletions in a patient's genome that affect the activity of GENSET or by supplementing the patients own production of GENSET polypeptides. Conversely, antisense nucleic acid molecules may be administered to down regulate GENSET expression by binding with the cells' own genes and preventing their expression. The sense and antisense nucleic acids may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence to determine which patients may be in need of restorative therapy. The GENSET polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of GENSET nucleic acid of expression and activity. The present sequence is a GENSET nucleic acid of
                                                                              Full length GENSET human nucleic acids encoding potentially secreted proteins, useful in gene therapy and vaccination against a variety of diseases, and for diagnosis of those diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 470 BP; 137 A; 87 C; 107 G; 139 T; 0 U; 0 Other;
                                                                                                                                                                                                Claim 7; Page 583; 921pp; English
  2001-367870/38
                             P-PSDB; AAG89145
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470
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     Length:
Matches:
Conservative:
Mismatches:
Indels:
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Alignment Scores:
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US-10-664-025-3903_COPY_1_17 (1-17) x AAH64748 (1-470)

ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT 187 MetAlaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAla 17

ABZ36691 standard; cDNA; 497 RESULT 2 ABZ36691

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BP.

ABZ36691;

(first entry) 21-FEB-2003 Human GENSET coding sequence SEQ ID 564.

Cytostatic; antiinflammatory; nootropic; neuroprotective; cardiant; gastrointestinal; gene therapy; GENSET; heavy metal toxicity; cancer; inflammatory disease; immune disorder; neuromuscular; toxicity; central nervous system; cardiovascular; gastrointestinal; gene; ss.

Ношо варіепв

WO200283898-A1

24-OCT-2002

18-APR-2001; 2001WO-IB000914.

18-APR-2001; 2001WO-IB000914

GEST) GENSET

Giordano J; Dumas Milne Edwards J, Jobert S, Tanaka H, Bejanin S,

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The present invention relates to novel GENSET polynucleotides (ABZ36404-ABZ36511) encoding polypeptides (ABP75953-ABP76368). The polynucleotides and polypeptides are useful in screening and diagnostic assays for abnormal GENSET expression and/or biological activity. They are also useful for screening of compounds for treating or preventing GENSET-related disorders, such as heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, central nervous system (CNS), cardiovascular or gastrointestinal effects of the toxicity. The polynucleotides are useful for constructing or expanding chromosome maps
                                                New GENSET polynucleotides and polypeptides, useful for treating heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, CNS, cardiovascular or gastrointestinal effects of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 497 BP; 127 A; 99 C; 117 G; 154 T; 0 U; 0 Other;
                                                                                                                                                                                      Claim 12; Page 579; 735pp; English.
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497 117 0 0 0 US-10-664-025-3903_COPY_1_17 (1-17) x ABZ36691 (1-497) Indels: Gaps: 81.00 100.0% 100.0% 100.0% Query Match:

Length: Matches: Conservative: Mismatches:

0.00016

Alignment Scores:

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Percent Similarity: Best Local Similarity:

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ABZ36690 RESULT

ABZ36690;

BP.

ABZ36690 standard; cDNA; 500

(first entry) 21-FEB-2003 Human GENSET coding sequence SEQ ID 563.

Cytostatic; antiinflammatory; nootropic; neuroprotective; cardiant; gastrointestinal; gene therapy; GRNBET; heavy metal toxicity; cancer; inflammatory disease; immune disorder; neuromuscular; toxicity; central nervous system; cardiovascular; gastrointestinal; gene; ss.

Homo sapiens

WO200283898-A1.

24-OCT-2002.

18-APR-2001; 2001WO-IB000914.

18-APR-2001; 2001WO-IB000914

(GEST) GENSET.

Giordano Jobert S, Dumas Milne Edwards J, Bejanin S, Tanaka H,

WPI; 2003-075548/07

New GENSET polynucleotides and polypeptides, useful for treating heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, CNS, cardiovascular or gastrointestinal effects of the toxicity

Claim 12; Page 578; 735pp; English

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The present invention relates to novel GENSET polynucleotides (ABZ36404-ABZ3641) encoding polypeptides (ABP75963-ABP76368). The polynucleotides and bolypeptides are useful in screening and diagnostic assays for abnormal GENSET expression and/or biological activity. They are also useful for screening of compounds for treating or preventing GENSET-related disorders, such as heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, central nervous system (CNS), cardiovascular or gastrointestinal effects of the toxicity. The polynucleotides are useful for constructing or expanding chromosome maps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to full length GENSET human nucleic acids encoding potentially secreted proteins. The nucleic acids and the polypeptides they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GENSET gene expression. For example, they be used to treat disorders associated with decreased GENSET gene expression by rectifying mutations or deletions in a patient's genome that affect the activity of GENSET or by supplementing the patients own production of GENSET polypeptides. Conversely, antisense nucleic acid molecules may be administered to down regulate GENSET expression by binding with the cells' own genes and preventing their
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                                                                                                                                                                                                                                                                                                                                                                                                                      ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT 122
                                                                                                                                                                                                                                                                                                                                                                                                 1 MetAlaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAla 17
                                                                                                                                                                                  Sequence 500 BP; 129 A; 100 C; 113 G; 155 T; 0 U; 3 Other;
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Matches:
Conservative:
Mismatches:
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P-PSDB; AAG89140.
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expression. The sense and antisense nucleic acids may also be used as DNA pobbes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence to determine which patients may be in need of restorative therapy. The GENSET polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of GENSET polypeptide expression and activity. The present sequence is a GENSET nucleic acid of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; GSSP3; circulating blood glucose level; insulin sensitivity; body mass; serum glucose regulation; body weight loss; obesity; metabolic-related disorder; impaired glucose tolerance; stroke; insulin resistance; hyperlipidaemia; atherosclerosis; heart disease; hypertension; syndrome C; type I diabetes; type II diabetes; microangiopathy; retinopathy; neuropathy; nephropathy; coular lesion; polycystic ovarian syndrome; acanthosis nigrican; leprechaunism; lipoatrophy; physical performance; exercise; dyslexia; schizophrenia; attention-deficit disorder; hyperactivity disorder; psychiatric disorder;
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                                                                                                                                                                                 Matches:
Conservative:
Mismatches:
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                                                                                                                                                                      Length:
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P-PSDB; ABG31324.
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Bihain B;
                                                                                                invention
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                                                                                                                                                      Alignment Scores:
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23-FEB-2001; 2001US-0271175P. 08-MAR-2001; 2001US-0274503P. 09-MAR-2001; 2001US-0274552P.

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The present invention relates to the isolation of human GSSP3
polypeptide, and polynucleotide sequences that encode it. The GSSP3
polypeptide reduces circulating blood glucose levels, increases insulin
sensitivity, and/or reduces body mass. The GSSP3 polypeptide and
polynucleotide sequences are useful in serum glucose regulation, fatty
acid metabolism, body weight loss, and prevention of body weight gain.
Compositions comprising GSSP3 polypeptides are useful for controlling
blood glucose levels, for treating metabolic-related diseases or
disorders (e.g. obesity, impaired glucose tolerance, insulin resistance,
chyperlipidaemias, atheroselerosis, heart disease, hypertension, stroke,
syndrome C. type I or II diabetes, diabetes related complications,
microangiopathy, retinopathy, neuropathy, nephropathy, polycystic ovarian
syndrome, ocular lesions, microangiopathic lesions, or syndromes such as
are also useful to improve physical performance during work or exercise,
and to treat dyslexia, attention-deficit disorder, attention-
                                                              useful for reducing body mass or preventing body weight gain, comprises administering composition comprising GSSP3 polypeptide.
Reducing circulating glucose levels or increasing insulin sensitivity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                schizophrenia. The present sequence encodes human GSSP3 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  deficit/hyperactivity disorder, and psychiatric disorders such as
                                                                                                                                                                                                                                        Disclosure; Page 95-96; 97pp; English.
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Sequence 1337 BP; 457 A; 214 C; 240 G; 426 T; 0 U; 0 Other;

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1337
17
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               Matches:
Conservative:
Mismatches:
Indels:
       0.000524
              81.00
100.0%
100.0%
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Best Local Similari
Alignment Scores:
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US-10-664-025-3903_COPY_1_17 (1-17) x ABK90053 (1-1337)

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53 Aregeerragaagrerrgargereereergererragarrregaeeggeer 103
1 MetAlaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAla 17
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Human cDNA encoding, CGDD4, INCYTE 5284076CB1
       ABS78646 standard; cDNA; 1480 BP.
                    16-DEC-2002 (first entry)
RESULT 6
ABS78646
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Human; 88; gene; cell growth; differentiation; death; CGDD; cancer; cell proliferative disorder; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; paroxysmal nocturnal haemoglobinuia; psoriasis; polycythaemia vera; primary thromobocytopaenia; developmental disorder; renal tubular acidosis; anaemia; mental retardation; epilepsy; AIDS; neurological disorder; Alzheimer disease; Parkinson's disease; asthma; reproductive disorder; infertility; autoimmune disorder; gout; allergy; inflammatory disorder; acquired immunodeficiency syndrome; uveitis; autoimmune thyroiditis; contact dermatitis; Crohn's disease; infection; diabetes mellitus; glomerulonephritis; irritable bowel syndrome; multiple sclerosis; osteoarthritis; osteoporosis; pancreatitis; rheumatoid arthritis.

11 79

ADB63550 standard; cDNA; 1492 BP.

ADB63550 RESULT 7

04-DEC-2003 (first entry)

ADB63550;

US-10-664-025-3903_COPY_1_17 (1-17) x ABS78646 (1-1480)

Conservative: Mismatches: Matches: Length:

Percent Similarity: Best Local Similarity:

Query Match:

0.000591 81.00 100.0% 100.0% 100.0%

Alignment Scores: Pred. No.:

Indels:

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38-FEB-2002; 2002WO-US003715.
Homo sapiens
                                                                         19-SEP-2002
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09-FEB-2001; 2001US-0268111P.

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The invention relates to an isolated polypeptide comprising CGDD1-12 (cell growth, differentiation and death), a naturally occurring amino coll growth, differentiation and death), a naturally occurring amino caid sequence at least 90% identical to CGDD, a biologically active fragment or an immunogenic fragment. Also included are the polymucleotides encoding CGDD1-12, a recombinant polymucleotide comprising a promoter sequence operably linked to the CGDD comprising a promoter sequence operably linked to the CGDD polymucleotides, a cell transformed with the recombinant polymucleotide, an anti-cGDD antibody, screening for compounds which bind to/modulate or are ant/agonists of CGDD or alter the expression of CGDD polymucleotide and accordance of CGDD polymucleotide microarray. The polypeptides, polymucleotide and a gonists and antagonists are useful for diagnosing, treating or cGDD polymucleotide microarray. The polypeptides, polymucleotide and a preventing disorders associated with aberrant expression of CGDD, particularly cell proliferative (e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia ccirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia ccirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia ccirrhosis, aporiasis, primary thromobocytopaemia or cancer), developmental cycle), or autoimmune/inflammatory disorders (e.g. renal tubular aciders (e.g. infertility or a disruption in the menstrual cycle), or autoimmune/inflammatory disorders (e.g. Alzheimer disease, Parkinson's disease or cplepsy), reproductive disorders (e.g. infertility or a disruption in the hyproditis, contact dermatitis, crohn's disease, diabetes mellitus, coteoporosis, pancreatis, theumatoid arthritis, osteoporosis, pancreatis, rheumatoid arthritis, osteoporosis, pancreatis, rheumatoid arthritis, cupencedices of protein associated with CGDD. The present sequence encodes cc accorders (e.g. accorders (e.g. accorders (e.g. accorders (e.g. acco
                                                                                                                                                   Baughn MR;
Burford N;
                                                                                                                                                                                                                                                                                                                                   and
or
                                                                                                                                                                                                                                                                                                                            New human proteins associated with cell growth, differentiation death, useful for diagnosing, treating or preventing autoimmune inflammatory disorders (e.g. AIDS, allergy or anemia), cancer, atherosclerosis or hepatitis.
                                                                                                                                                Elliott VS,
, Duggan BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1480 BP; 463 A; 244 C; 265 G; 508 T; 0 U; 0 Other;
                                                                                                                                                   Warren BA, Elliott '
TY, Lal PG, Duggan
Khare R, Walia NK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 169; 181pp; English.
                                                                                                                                                   Yao MG, Ison CH, Lu Y,
Xu Y, Gietzen KJ, Tang
Richardson TW, Tran UK,
                                                                                                    (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                       WPI; 2002-723356/78.
                                                                                                                                                                                                                                                                                 P-PSDB; ABG97353
                                                                                                                                                                                Ding L,
Lu DAM,
                                                                                                                                                      Yue H,
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Human cDNA encoding clone TESTI20282420.
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Human; ss; gene; pharmaceutical; diagnostic; gene therapy; tissue regeneration; cell regeneration; membrane protein; signal transduction-related protein; transcription-related protein; osteoporosis; neurological disease; cancer; tumour.

Homo sapiens

Location/Qualifiers

/*tag= a /product= "Clone TESTI20282420 protein"

EP1308459-A2

07-MAY-2003

28-MAR-2002; 2002EP-00007401.

05-NOV-2001; 2001JP-00379298. 25-JAN-2002; 2002US-00350978.

(HELI-) HELIX RES INST. (REAS-) RES ASSOC BIOTECHNOLOGY.

Sato H, Ishii S; (, Irie R, Tamechika I; Otsuki T, Wakamatsu A, Sato H, Hio Y, Otsuka K, Nagai K, Irie Otsuka M, Nagahari K, Masuho Y; Isogai T, Sugiyama T, Yamamoto J, Isono Y, Seki N, Yoshikawa T,

WPI; 2003-450961/43.

P-PSDB; ADB65520

polynucleotides and polypeptides, useful for developing a diagnostic cer or medicines for regulation of their expression and activity, or targets of gene therapy marker 88

Claim 1; Page; 222pp; English

The invention discloses a polynuclectide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel polypeptides. Also claimed is a polypeptide encoded by the polynuclectide or its partial peptide, an antibody binding to the polypeptide or peptide of the polynuclectide, immunologically assaying the polypeptide or peptide of the polynuclectide by contacting the polypeptide or peptide of the polynuclectide by contacting the polypeptide or peptide of the polynuclectide by contacting the polypuclectide in an expressible manner and an antisense polynuclectide. The oligomuclectide is useful as a primer for synthesising the polynuclectide in an expression and an antisense polynuclectides and encoded for detecting the polynuclectide. The polynuclectides and encoded proteins are useful as pharmaceutical agents and many disease-related proteins are useful as pharmaceutical agents and many disease-related genes may be included in them, for developing a diagnostic marker or mediciones for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell regenteration. Membrane proteins, signal transduction-related proteins, disease-related proteins and genes curviculation-related proteins, disease-related proteins and genes concoing them can be used as indicators for diseases (e.g. osteoporosis, the activity or expression of the encoded protein to treat diseases. The copy and activity or expression of the encoded protein to treat diseases. The copy and activity or expression of the encoded protein to treat diseases. The copy and activity or expression of the encoded protein to treat diseases. sequence presented is a cDNA of the invention. Note: Some of the sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office.

Sequence 1492 BP; 452 A; 250 C; 272 G; 518 T; 0 U; 0 Other;

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1492
17
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      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
        0.000597
              81.00
100.0%
100.0%
                               Best Local Similarity:
                       Percent Similarity:
Alignment Scores:
Pred. No.:
                                      Query Match:
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US-10-664-025-3903_COPY_1_17 (1-17) x ADB63550 (1-1492)

17 MetAlaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAla 22 용

AAC69528 RESULT

AAC69528 standard; DNA; 1898 BP

AAC69528;

31-JAN-2001

(first entry)

Human secreted protein gene 17 clone HTELS08.

Immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective; nootropic; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; gene therapy; infection; human; secreted protein; ss.

Homo sapiens.

WO200061623-A1.

19-OCT-2000

06-APR-2000; 2000WO-US008979.

09-APR-1999;

99US-0128693P. 99US-0130991P. 26-APR-1999;

HUMA-) HUMAN GENOME SCI INC

Shi Y; Birse CE; Rosen CA, Soppet DR, Florence KA, Moore PA, Komatsoulis GA, 1 HS, Ebner R, J, Komats
 Olsen HS, Ruben SM, Na foung PE;

WPI; 2000-647418/62.

New nucleic acid molecules encoding 62 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.

Claim 1; Page 543-544; 716pp; English.

The invention relates to the isolation of genes (AAC69512-C69587)

checoding 62 human secreted proteins (AAB38321-B38396). The genes can be used to generate fusion proteins by linking to the gene for the human immosphobulin G FC portion (AAC69503) for increasing the stability of the fusion protein as compared to the human protein only. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic a range of human tissues disclosed in the specification. The nucleic diagnosis, proteins, antibodies and (ant)agonists are useful in the city proteins, antibodies and (ant)agonists are useful in the city fundation of: (a) autoimmune diseases e.g. rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms of the breast or liver; (c) cardiovascular disorders e.g. cardiac arrest; (d) cerebrovascular disorders e.g. Alzheiner's disease; (g) infections (f) nervous system disorders e.g. Alzheiner's disease; (g) infections caused by bacteria, viruses and fungi; and (h) ocular disorders e.g. cardiac carrest corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, for expense skin aging due to sunburn, conting and epithelial cell proliferation, to prevent skin aging cell culture of conting and epithelial cell proliferation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis

Sequence 1898 BP; 595 A; 315 C; 332 G; 654 T; 0 U; 2 Other;

0.000796

Length: Matches: Conservative:

1898 17 0

81.00 100.0% Percent Similarity:

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The present invention relates to novel human secreted proteins (ABR49633-ABR496145) and their coding sequences (ACC50344-ACC50856). The proteins and their coding sequences are useful for the preparation of a diagnostic or pharmaceutical composition for diagnosing or treating a cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary arteriosclerosis and myocardial ischaemia), neural disorders, immune system disorders, muscular disorders, pulmonary disorders, renal disorders, immune cartoriferative disorders and/or cancerous diseases and conditions, for proliferative disorders and/or cancerous diseases and conditions, for conventing neural damage which occurs in neuronal disorders or infection, for treating thrombosis and arteriosclerosis, for treating or preventing neural damage which occurs in neuronal disorders or enurodegenerative conditions such as Alzheimer's diseases and Parkinson's disease, to enhance bone and periodontal regeneration and aid in tissue transplants or bone grafts, to prevent skin aging or hair loss, to companie the market growth and differentiation of haematopoletic cells and bone marrow cells when used in combination with other cytokines, to maintain organs before transplantation or for supporting cell culture of primary tissues, to increase or decrease differentiation or proliferation of embryonic stem cells, or to modulate mammalian characteristics or metabolism. Note: The sequence data for this patent was published in continual and continual continual and continual conti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic; vulnerary; antiinflammatory; nootropic; neuroprotective; antiparkinsonian; gene therapy; human; cardiovascular disorder; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human secreted proteins, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating cardiovascular disorders such as arrhythmia.
                                                                                                                                            Sequence 1898 BP; 595 A; 315 C; 332 G; 654 T; 0 U; 2 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted protein coding sequence, SEQ ID 309.
                                                                                                US-10-664-025-3903_COPY_1_17 (1-17) x AAC69528 (1-1898)
  Mismatches:
                         Indels:
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                                                Gaps:
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                                                                                                                                                                                                                                                                                                ACC50642 standard; cDNA; 1898
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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100.0%
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Best Local Similarity:
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                    Query Match:
DB:
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protein genes, and ABP00011-ABP00299 represent the proteins they encode.

Drotein genes, and ABP00011-ABP00299 represent the proteins they encode.

ABZ71479-ABZ71540 represent human secreted protein genomic fragments. The invention also encompasses antibodies specific for the secreted proteins, the use of the secreted proteins in drug screening, and recombinant vectors and host cells comprising a nucleic acid of the invention. The secreted proteins, nucleic acids encoding them, antibodies or antibody fragments specific for the secreted proteins, and modulators of protein activity are useful for diagnosing, treating, ameliorating or preventing digestive disorders. Such conditions include disorders of the mouth, cesophagus, stomach, small intestine, large intestine, liver, biliary tract and pancreas, and include cancers of these organs and tissues. The secreted proteins and their nucleic acids may also be used in the treatment of immune disorders, inflammation, infection, treatment of immune disorders, and to promote wound healing. Nucleic acids by the invention may be used for chromosome identification, chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; secreted protein; digestive disorder; gastrointestinal disorder; mouth; oesophagus; stomach; small intestine; large intestine; liver; biliary tract; pancreas; cancer; tumour; hyperproliferative disorder; immune disorder; inflammation; infection; wound healing; drug screening; chromosome identification; chromosome mapping; cytostatic; antiinflammatory; immunosuppressive; vulnerary; gene therapy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human secreted proteins and nucleic acids, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating e.g. gastrointestinal diseases and disorders, or cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Secreted protein-encoding gene 165 cDNA clone HTELS08, SEQ ID NO:175.
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                                                                                                                                                                                                  1 MetalaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAla
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              1898
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                       ABZ71354 standard; cDNA; 1898 BP
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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P-PSDB; ABR00175.
                                                                             Best Local Similarity:
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                                                        Percent Similarity:
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Alignment Scores:
Pred. No.:
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                                                                                                  Query Match
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595 A; 315 C; 332 G; 654 T; 0 U; 2 Other;

Sequence 1898 BP;

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The invention relates to isolated nucleic acid molecules ADB91065-ADB91448 and ADB91835-ADB91911 encoding human secreted proteins ADB91449-ADB91448 and ADB91835-ADB91911 encoding human secreted proteins ADB91449-ADB9144
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mapping, in gene therapy, for identifying individuals from minute biological samples, as hybridisation probes, and as molecular weight markers. The present sequence represents a human secreted protein-encoding cDNA Clone of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Secreted protein; gene therapy; antidiabetic; diabetes; human; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1898 BP; 595 A; 315 C; 332 G; 654 T; 0 U; 2 Other;
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                                                                                                                                                                                                                 Length:
Matches:
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Mismatches:
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                                                                                                                                                                                                                                                                                              Best Local Similarity:
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                                                                                                                                                                                                                                                                     Percent Similarity:
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The invention relates to a novel human secreted polypeptide comprising a defined sequence given in the specification. The polypeptide, nucleic acid molecule, antibody, agonist or antagonist of the invention may be useful for preparing a composition for diagnosing or treating a haemopoietic or haematologic disorder such as ansemia, autoimmune disorders such as rheumatoid arthritis, inflammation, Grave's disease, diabetes, systemic lupus erythematosus or glomerulonephritis, neurodegenerative disorders including Parkinson's disease and Alzheimer's disease, wounds and hyperproliferative disorders including atherosclerosis or cancer, as well as bacterial, viral, fungal or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                antianaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                             antidiabetic; immunosuppressive; dermatological; nephrotropic; antidate antiparkinsonian; neuroprotective; nootropic; antibacterial; virucide; fungicide; antiparasitic; antiarteriosclertic; vulnerary; cytostatic; haemopoietic; haematologic; anaemia; autoimmune disordar; rheumatoid arthritis; inflammation; Grave's disease; diabetes; systemic lupus erythematosus; glomerulonephritis; neurodegenerative; Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis; cancer; bacterial; viral; fungal; parasitic infection; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human secreted polypeptide for diagnosing, preventing or treating hematopoietic or hematologic disorders (e.g. anemia), autoimmune disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer
                                                                                                                                                                  1898
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                                                                                                                                    US-10-664-025-3903_COPY_1_17 (1-17) x ADB91291 (1-1898)
                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein-related DNA - SEQ ID 356.
                                                Conservative:
Mismatches:
              Length:
Matches:
                                                                                    Indel8:
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                                                                                                                                                                                                                                                                          BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
                                                                                                                                                                                                                                                                        ADC73723 standard; DNA; 1898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-MAR-2002; 2002WO-US008277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                           01-JAN-2004 (first entry)
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P-PSDB; ADC74338.
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                                                                  Similarity:
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                                                Percent Similarity:
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Alignment Scores:
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                                                                                                                                                                                                                                                                                                          ADC73723;
                                                                                  Query Match:
                                                                  Best Local
                                                                                                                                                                                                                                          RESULT 12
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parasitic infections. The polypeptide may also be used during gene therapy procedures and for identifying a binding partner by contacting the polypeptide with a binding partner and determining whether the binding partner increases or decreases the activity of the polypeptide. The current sequence is that of the human secreted protein-related DNA the invention.
     888888888
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Sequence 1898 BP; 595 A; 315 C; 332 G; 654 T; 0 U; 2 Other;

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Human; GSSP3; circulating blood glucose level; insulin sensitivity; body mass; serum glucose regulation; body weight loss; obesity; metabolic-related disorder; impaired glucose tolerance; stroke; insulin resistance; hyperlipidaemia; atherosclerosis; heart disease; hypertension; syndrome C; type I diabetes; type II diabetes; microangiopathy; retinopathy; neuropathy; nephropathy; ocular lesion; polycystic ovarian syndrome; acanthosis nigrican; leprechaunism; lipoatrophy; physical performance; exercise; dyslexia; schizophrenia; attention-deficit disorder; hyperactivity disorder; psychiatric disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reducing circulating glucose levels or increasing insulin sensitivity, useful for reducing body mass or preventing body weight gain, comprises administering composition comprising GSSP3 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chicca J, Yen-Potin F;
                                                                                                                                                                65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to the isolation of human GSSP3
                                                                                                                                      1 MetAlaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAla
                                                                                                                                                       ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT
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Matches:
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                                                                                  Gaps:
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                                                                                                                                                                                                                        BP
                                                                                                         US-10-664-025-3903_COPY_1_17 (1-17)
                                                                                                                                                                                                                      ABK90052 standard; DNA; 10115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ebbets-Reed D,
                                                                                                                                                                                                                                                                                                         genomic sequence.
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                                    Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
Alignment Scores:
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                                                                                                                                                                                                                                                                                                         Human GSSP3
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                                                                                                                                                                                                                                                  ABK90052;
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                                                               Query Match
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No.:
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polypeptide, and polynucleotide sequences that encode it. The GSSP3 polypeptide reduces circulating blood glucose levels, increases insulin sensitivity, and/or reduces body mass. The GSSP3 polypeptide and polynucleotide sequences are useful in serum glucose regulation, fatty acid metabolism, body weight loss, and prevention of body weight gain.

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Compositions comprising GSSP3 polypeptides are useful for controlling blood glucose levels, for treating metabolic-related diseases or disorders (e.g. obesity, impaired glucose tolerance, insulin resistance, hyperlipidaemias, atherosclerosis, heart disease, hypertension, stroke, syndrome C, type I or II diabetes, diabetes related complications, microangiopathy, neuropathy, nephropathy, polycystic ovarian syndrome, ocular lessions, microangiopathic lesions, or syndromes such as acanthosis nigricans, leprechaunism and lipoatrophy). The polypeptides are also useful to improve physical performance during work or exercise, and to treat dyslexia, attention-deficit disorders such as schizophrenia. The present sequence encodes human GSSP3 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           murine; mouse; valproate; ss; multi-parameter high throughput screening; whyfis; disease signature; neuropsychiatric; neurodegenerative; schizophrenia; bipolar affective disoder; BAD; autism; Parkinson's; Alzheimer's disease; neuroleptic; nootropic; antimanic; antidepressa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murine cDNA differentially expressed in the presence of valproate Seq62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying a compound that can treat disease or disorders, such as, neuropsychiatric disorder e.g., schizophrenia, or autism, comprises determining the expression of one or more efficacy genes in a cell contacted with the test compound.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGCCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT
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                                                                                                                                                                                                                              Sequence 10115 BP; 2860 A; 1941 C; 1815 G; 3475 T; 0 U;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PSYC-) PSYCHIATRIC GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADV34986 standard; cDNA; 185548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUN-2001; 2001US-0299151P.
07-SEP-2001; 2001US-0317828P.
25-SEP-2001; 2001US-0325150P.
14-NOV-2001; 2001US-033947P.
18-JAN-2002; 2002US-0349936P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUN-2002; 2002US-00175523.
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Palfreyman M, Rajan P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-118903/12
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This invention relates to a novel screening method identified as a multiparameter high throughput screening (MPHTS) assay. Specifically, it refers to an assay that utilises the disease signature of a plurality of specific genes associated with a particular disease, and identifies differential expression between those cells taken from individuals differential expression between those cells taken from individuals affected by that disease and those that are not affected. The present invention then describes the screening of candidate pharmaceutical compounds to identify those that have a potential therapeutic benefit for the treatment of neuropsychiatric and neurodegenerative disorders including schizophrenia, bipolar affective disorder (BAD) and autism, as well as Parkinson's and Alzheimer's disease. Accordingly, the compounds well as Parkinson's and Alzheimer's disease. Accordingly, the compounds not contropic, antimanic and antidepressant. Furthermore, the screening method used in MPHTS will be automated, such that a large number of test compounds may be rapidly screened with a minimal amount of labour and differentially expressed in mice in the presence of a gene that is differentially expressed in mice in the presence of the therapeutic compound valproate, given in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 185548 BP; 58272 A; 40343 C; 37771 G; 49162 T; 0 U; 0 Other;
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US-10-664-025-3903_COPY_1_17 (1-17) x ADV34986 (1-185548) Length: Matches: Conservative: Mismatches: Indels: 1.71e+04 52.00 92.9% 64.3% 64.2% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB: ò

RESULT 15

from base 600001 (Human SLIT-3 genomic sequence.) LOCUS ADO34435 Accession Ado34435 34886 8 6 0 0 length: Matches: Conservative: Mismatches: Indels: 110000 210000 310000 410000 510000 634886 ADO34435 fr fragments Begin 7.52e+03 49.00 82.4% 47.1% 60.5% 100001 200001 300001 400001 500001 600001 AD034435_6/c
Continuation (7 of 7) of AD
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WP AD034435_1 1
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6 Alignment Scores:

US-10-664-025-3903_COPY_1_17 (1-17) x ADO34435_6 (1-34886)

Percent Similarity: Best Local Similarity: Query Match:

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Search completed: May 9, 2006, 13:30:11 Job time: 92.4 secs

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6972, Ap
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16307, Ap
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US-09-252-991A-3983

US-09-252-991A-3924

US-09-252-991A-3924

US-09-252-991A-3924

US-09-949-016-4565

US-09-949-016-16307

US-09-949-016-16307

US-09-949-016-16307

US-09-949-016-16307

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US-09-184-418C-104

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US-09-184-418C-105

US-09-184-000C-1205

US-09-184-000C-1205

US-09-184-18C-105

US-09-489-039A-6672

US-09-489-039A-6847

US-09-489-039A-6847

US-09-489-039A-6847

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US-09-489-039A-6847

US-09-485-0105-016-5492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Duran Milne Edwards, J.B.
APPLICANT: Duran Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET, 054 PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 1363
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Conservative:
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LOCATION: 137..154
NAME/KEY: sig_peptide
LOCATION: 137..187.
LOCATION: 137..187.
COTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 10.699998092651
OTHER INFORMATION: seq VLMLLAVLWTGA/EN
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US-09-621-976-1163
Sequence 1363, Application US/09621976
Pacent No. 6639063
GENERAL INFORMATION:
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                          TYPE: DNA
ORGANISM: Homo sapiens
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-LCOPEXT=0 - UNITS-Eits - START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi
-LIST=45 - DOCALIGN=200 - THR SCORE=pct - THR MAX=100 - THR MIN=0 - ALIGN=15
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-NCPU=6 - ICPU=3 - NO MMAP - NEG SCORES=0 - WAIT - DSPBLOCK=100 - LONGLOG
-DEV_TIMEOUT=120 - WARN_TIMEOUT=30 - THREADS=1 - XGAPOP=10 - XGAPEXT=0.5 - FGAPOP=6
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Sequence 2587, Appl
Sequence 2587, Ap
Sequence 1704, Ap
Sequence 15700, A
Sequence 25675, A
Sequence 2675, A
Sequence 10302, A
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                                                                                    9, 2006, 13:33:17 ; Search time 22.3 Seconds
             GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
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US-09-621-976-2887
US-09-621-976-1362
US-10-104-047-1704
US-09-621-976-15700
US-09-270-767-2675
US-09-270-767-10302
US-09-252-991R-4051
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Maximum Match 100%
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Maximum DB seq length: 200000000
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58.0
58.0
55.6
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81 81 81 81 81 47 47 47

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Result No.

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137 Argecerradaagrerreargerecrescrererraarregaecegreer 187
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                                                   US-10-664-025-3903_COPY_1_17 (1-17) x US-09-621-976-1363 (1-469)
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Fatent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dobart, S.
APPLICANT: Glordano, J.Y.
TILLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2587
LENGTH: 560
TYPE: DNA
ONGANISM: Homo sapiens
                                                                                                                                                                                                                                                            APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent, pm
SEQ ID NO 43
LENGTH: 512
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17
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Matches:
Conservative:
Mismatches:
Indels:
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 Indels:
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LOCATION: 53..511
NAME/KEY: sig_peptide
LOCATION: 53..103
COTHER INFORMATION: Von Heijne matrix
O'THER INFORMATION: score 10.699999092651
COTHER INFORMATION: seq VIMLLAVLIWTGA/EN
US-09-621-976-43
                    Gaps:
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81.00
100.0%
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100.0%
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Best Local Similarity:
Query Match:
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; LOCATION: 372..539
US-09-621-976-2587
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US-09-621-976-2587
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Pred. No.:
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 Query Match:
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53 AIGGCGITAGAAGICTIGAIGCTCCTCGCTGICTIGATTIGGACCGGGGCT 103
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                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
TITLE REFERENCE: GENSET. 054PR2
TITLE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
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Sequence 1704, Application US/10104047

Patent No. 6943241

GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE

TITLE OF INVENTION: No. 6943241e1 full length cDNA
FILE REFERENCE: H1-A0105

CURRENT APPLICATION NUMBER:

CURRENT FILING DATE: 2002-03-25

PRIOR FILING DATE:

NUMBER:

NUMBER:

NUMBER:

SOFTWARE: PATENTING NOS: 4096

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1704

LENGTH: 1492
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Matches:
Conservative:
Mismatches:
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Mismatches:
Indels:
              Length:
Matches:
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NAME/KEY: CDS
LOCATION: 53.-526
NAME/KEY: sig_peptide
LOCATION: 53..103
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 10.69999809251
OTHER INFORMATION: seq VLMLLAVLIWTGA/EN
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; Patent No. 6639063
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ORGANISM: Homo sapiens
                                           Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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Alignment Scores:
Pred. No.:
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APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic 37326-094
CURRENT APPLICATION NUBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62217
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25675
LENGTH: 564
                                                                                                                                                                                                                                                    1 MetAlaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAla 17
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                                                                                                                                                                                                                                                                                                                    Sequence 1500, Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:

APPLICANT: Dunas Milne Edwards, J.B.

APPLICANT: Glordano, J.Y.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.

FILE REFERENCE: GENEET. 054PR2.

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

LENGTH: 372
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Matches:
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Matches:
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Sequence 25675, Application US/09270767
Patent No. 6703491
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CRGANISM: Drosophila melanogaster
US-09-270-767-25675
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94.1$
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1704
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LOCATION: 351
                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Query Match:
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RESULT 9
US-09-252-991A-4051/C
US-09-252-991A-4051/C
Sequence 4051, Application US/09252991A
TITLE OF INVENTION: ARUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR SEQ ID NOS: 33142
SEQ ID NO 4051
                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10302
LENGTH: 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. MetAlaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAla 17
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               Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                        US-09-270-767-10302/c
; Sequence 10302, Application US/09270767
; Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Drosophila melanogaster
                    27.4
47.00
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52.9$
58.0$
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47.00
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Best Local Similarity:
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Alignment Scores:
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Pred. No.:
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                                                                                                         Query Match:
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DB:
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ORGANISM: Aspergillus oryzae
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
DB:
                ÚS-09-949-016-163017
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                        US-09-533-559-6972
                                                         Alignment Scores:
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US-09-949-016-163017/c

i Sequence 163017, Application US/09949016

i Patent No. 681239

j GENERAL INFORMATION:

i APPLICANT: VENTER, J. Craig et al.

i TITLE OF INVENITION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

i TITLE OF INVENITION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

i TITLE OF INVENITION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

i FILE REFERENCE: CLOO1307

i CURRENT APPLICATION NUMBER: US/09/949,016

i CURRENT PILING DATE: 2000-04-14

i PRIOR FILING DATE: 2000-10-20

i PRIOR PLICATION NUMBER: 60/237,768

i PRIOR PLICATION NUMBER: 60/231,498

i PRIOR PLING DATE: 2000-10-03

i PRIOR PLING DATE: 2000-09-08

i NUMBER OF SEQ ID NOS: 207012

i SOUTHARE: PEBLISCE for Windows Version 4.0

i LENGTH: 601
                                                                                                                                                                                                                                                 WENCH TO 100-949-016-163016/C

Sequence 163016, Application US/09949016

Patent No. 6812339

Patent No. 6812339

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 06/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR PELICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FESTER SESER FOR WINDOWS VERSION 4.0

SEQ ID NO 163016
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                  Conservative:
Mismatches:
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; ORGANISM: Human
US-09-949-016-163016
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Best Local Similarity:
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                                                                                                                                                                                                                                           LENGTH: 1977
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Job time
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AREGUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AREGUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
SEQ ID NOS: 33142
SEQ ID NOS: 33142
SEQ ID NO 3896
                                                                                                                                                                      NAME/KEX: unsure; NAME/KEX: unsure; LOCATION: (504), (604), (604), (753); OTHER INFORMATION: Identity of nucleotide at the above locations are unknown. US-09-252-991A-3983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: unsure; LOCATION: (12), (50), (150); COTHER INFORMATION: Identity of nucleotide at the above locations are unknown. US-09-252-991A-3896
                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-664-025-3903_COPY_1_17 (1-17) x US-09-252-991A-3983 (1-1077)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AlaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGly 16
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Mismatches:
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Matches:
Conservative:
Mismatches:
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3924, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
                                                                                                                          ORGANISM: Pseudomonas aeruginosa FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                               45.00
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US-09-252-991A-3924
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                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
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score:

Title: Perfect

Sequence:

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Scoring table:

Searched:

Sequence 1704, Apple Sequence 27, Appl Sequence 27, Appl Sequence 175, Appl Sequence 175, Appl Sequence 62, Appl Sequence 62, Appl Sequence 63920, A Sequence 13037, A Sequence 13037, A Sequence 24373, A Sequence 6527, Ap Sequence 6528, Ap Sequence 6528, Ap Sequence 121354, Sequence 121354, Sequence 121354, Sequence 121354, Sequence 121354, Sequence 23666, A Sequence 121354

Sequence 23665, A Sequence 28396, A Sequence 1, Appli Sequence 1, Appli

Sequence 133, App Sequence 137049, Sequence 137050, Sequence 137050, Sequence 137050, Sequence 137050,

ALIGNMENTS

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Sequence 24, Application US/09731872

Sequence 24, Application US/09731872

Batent No. US20020102604A1

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Jobert, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78 US3.RSC
CURRENT FILING DATE: 2000-12-07

PRIOR PRILING DATE: 1999-12-08

PRIOR FILING DATE: 1999-12-08

PRIOR FILING DATE: 2000-03-06

MUMBER OF SEQ ID NOS: 482

SEQ ID NO 24

FULL SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: CDE
LOCATION: 137..454
NAME/KEX: 8ig_peptide
LOCATION: 137..187
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 10.7019149919754
COTHER INFORMATION: seq VLMLLAVLIWTGA/EN
US-09-731-872-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
RESULT 1
US-09-731-872-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 470
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Length DB

Query

Score

Result 2

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Published Applications NA Main:*

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6: /cgn2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*

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9: /cgn2_6/ptodata/1/pubpna/USIOF_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USIOF_PUBCOMB.seq:*

-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Sequence 24, Appl Sequence 24, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 2, Appli

US-09-731-872-24 US-09-876-997-24 US-10-643-836-24 US-09-876-997-19 US-09-876-997-19 US-10-643-836-19 US-10-467-046-2

470 470 691 691 691

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Sequence 24, Description

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Sequence 19, Application US/09731872
; Sequence 19, Application US/09731872
; Sequence 19, Application US/09731872
; Batent No. US20020102604A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Dupost, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78.032 REG
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MetAlaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAla 17
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NAME/KEY: CDS
LOCATION: 42..515
LOCATION: 42..92
COTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 10.7019149919754
COTHER INFORMATION: seq VLMLLAVLIWITGA/EN
US-09-731-872-19
CURRENT APPLICATION NUMBER: US/10/643,836
CURRENT FILING DATE: 2003-08-19
PRIOR PILLING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR FILING DATE: 1999-12-08
PRIOR FILING DATE: 1999-12-08
PRIOR FILING DATE: 1999-12-08
PRIOR FILING DATE: 2000-03-06
NUMBER OF SEQ ID NOS: 482
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: sig_peptide
LOCATION: 137.187
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 10.7019149919754
OTHER INFORMATION: seq_VLMLLAVLIWTGA/EN
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ORGANISM: Homo sapiens
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NAME/KEY: CDS
LOCATION: 137..454
FEATURE:
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Query Match:
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Pred. No.:
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                                                                                                                                                                                                         SEQ ID NO 24
LENGTH: 470
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                                                                                                                                                                                                                                                                                                    RESULT 2
US-09-876-997-24
IS-09-876-997-24
Sequence 24, Application US/09876997
Shublication No. US20030152921A1
GENERAL INFORMATION:
APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
APPLICANT: Jober, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78.US4.CIP
CURRENT APPLICATION NUMBER: US/09/876,997
CURRENT FILING DATE: 2000-12-07
PRIOR PAPLICATION NUMBER: US 60/187,470
PRIOR PLING DATE: 2000-03-06
PRIOR PLING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 482
SEQ ID NO 24
LENGTH: 470

LENGTH: 470

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Publication No. US20050096458A1
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78.US3.REG
                                                                                                                                                                                                                                                                      137 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT 187
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Mismatches:
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LOCATION: 137..454
NAME/KEY: 81g_peptide
LOCATION: 137..187
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: 8core 10.7019149919754
OTHER INFORMATION: 8cq VLMLLAVLWTGA/EN
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ORGANISM: Homo sapiens
                                                                           Percent Similarity:
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US-10-643-836-24
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No.:
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APPLICANT: Salter-Cid, Luisa
APPLICANT: Ebbets-Reed, Dana
APPLICANT: Chicca, Barbara A.
APPLICANT: Chicca, John
APPLICANT: Chicca, John
APPLICANT: Ven-Potin, Frances
APPLICANT: Yen-Potin, Bernard
APPLICANT: Bihain, Bernard
APPLICANT: Bihain, Bernard
APPLICANT: Bihain, Bernard
APPLICANT: Word Sepsion of Seps
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: sig_peptide
LOCATION: 42..92
COTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 10.7019149919754
OTHER INFORMATION: seq VLMLLAVLWTGA/EN
US-10-643-836-19
   PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR FILING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR FILING DATE: 2000-03-06
NUMBER OF SEQ ID NOS: 482
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10467046; Publication No. US20040235709A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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LOCATION: (104)..(526)
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LOCATION: (53)..(103)
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Best Local Similarity:
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Best Local Similarity:
Query Match:
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LOCATION: 42..515
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Pred. No.:
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Pred. No.:
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APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Bougueleret, Lydie
APPLICANT: Jobert, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78, US3.REG
CURRENT APPLICATION NUMBER: US/10/643,836
CURRENT FILING DATE: 2003-08-19
PRIOR APPLICATION NUMBER: US/09/731,872
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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LOCATION: 42..515

NAME/KEY: sig_peptide

LOCATION: 42..92

CTHER INFORMATION: Von Heijne matrix

OTHER INFORMATION: score 10.7019149919754

US-09-876-997-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.00017
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ORGANISM: Homo sapiens
               Percent Similarity:
Best Local Similarity:
Query Match:
D8:
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Best Local Similarity:
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Matches:
Conservative:
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Matches:
Conservative:
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TITLE OF INVENTION: 62 Human Secreted Proteins
FILE REPERENCE: PS039P1
FULRENT APPLICATION NUMBER: US/10/050,704
CURRENT FILING DATE: 2002-01-18
FRIOR APPLICATION NUMBER: 09/684,524
PRIOR PILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: PCT/US00/08979
PRIOR FILING DATE: 2000-04-06
PRIOR PILING DATE: 1999-04-06
PRIOR PILING DATE: 1999-04-09
PRIOR PILING DATE: 1999-04-06
NUMBER OF SEQ. ID NOS: 344
SOFTWARE: PALENTIN VET: 2.0
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LOCATION: (1428)
OTHER INFORMATION: n equals a,t,g, or c
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ORGANISM: Homo sapiens
FEATURE:
NAME/FEX: SITE
LOCATION: (1398)
OTHER INFORMATION: n equals a,t,g, or
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; PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1704
LENGTH: 1492
                                                                                                                              TYPE: DNA
CORGANISM: Homo sapiens
US-10-104-047-1704
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Best Local Similarity:
Query Match:
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US-10-798-512-27
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                                                                                                                                                                                                                                            Sequence 16, Application US/10467335
Publication No. US20040146970A1
GENERAL INFORMATION:
APPLICANT: VUE, Henry: YAO, Monique G.
APPLICANT: APPLICANT: ANGREW, Bridget A.; ELLIOTT, Vicki S.
APPLICANT: APPLICANT: ANGREW, Bridget A.; ELLIOTT, Vicki S.
APPLICANT: ANGRAW, Mariah R.; DING, Li
APPLICANT: TANG, Tom Y.; Lal, Preed G.
APPLICANT: TANG, Tom Y.; KHARE, Reen A.
APPLICANT: TANG, Tom Y.; KHARE, Reen A.; RICHARDSON, Thomas W.
APPLICANT: TAN, Uyen K.; KHARE, Reen A.; RICHARDSON, Thomas W.
APPLICANT: CHAWLA, Narinder K.
APPLICANT: CHAWLA, Narinder K.
APPLICANT: CHAWLA, Narinder K.
APPLICANT: CHAWLA, TOWERN: US/01/467,535
CURRENT FILING DATE: 2003-08-02
PRIOR APPLICATION NUMBER: US 60/271,175
PRIOR APPLICATION NUMBER: US 60/271,175
PRIOR PLING DATE: 2001-03-08
PRIOR PLING DATE: 2001-03-09
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                                                   US-10-664-025-3903_COPY_1_17 (1-17) x US-10-467-046-2 (1-1337)
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TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
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Mismatches:
Indels:
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OTHER INFORMATION: Incyte ID No: 5284076CB1
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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US-10-104-047-1704
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; LOCATION: (1428)..(1428)
; OTHER INFORMATION: n equals a,t,g, or US-10-472-533-175
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DB:
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Matches:
Conservative:
Mismatches:
Indels:
GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: 62 Human Secreted Proteins
FILE REFERENCE: P2039P1
CURRENT APPLICATION NUMBER: US/10/798,512
CURRENT FILING DATE: 2004-03-12
PRIOR APPLICATION NUMBER: US/09/684,524
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 1090-04-06
PRIOR FILING DATE: 1090-04-06
PRIOR PAPLICATION NUMBER: 60/128,693
PRIOR PLING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-06
SOFTWARE: PACHIN VINBER: 60/130,991
PRIOR PILING DATE: 1999-04-26
SOFTWARE: PACHIN VET: 2.0
SEQ ID NO 27
LENGTH: 1898
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FUDLICARION NO. US20050197285A1
GENERAL INFORMATION:
APPLICANT: HUMAN GENOME Sciences, Inc.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS906PCT
CURRENT FILING DATE: 2003-09-20
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/331,287
PRIOR APPLICATION NUMBER: US 60/306,171
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/306,171
PRIOR PILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc_feature
LOCATION: (1398)..(1398)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAMES/KEY: SITE
LOCATION: (1398)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.000561
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100.0%
100.0%
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 175
LENGTH: 1898
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: SITE
LOCATION: (1428)
OTHER INFORMATION: n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-472-533-175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score:
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US-140-140-140-1

Sequence 1, 90-14

Dublication No. US20040235709A1

GENERAL INFORMATION:

APPLICANT: Salter-Cid, Luisa

APPLICANT: Chicca, Barbara A.

APPLICANT: Chicca, John

APPLICANT: Chicca, John

APPLICANT: Prances

APPLICANT: Brinain, Bernard

TITLE OF INVENTION: GSSP3 Polynucleotides and Polypeptides and Uses Thereof

FILE REFERENCE: 2003-08-01

FURRENT APPLICATION NUMBER: US/10/467,046

CURRENT FILING DATE: 2003-08-01

PRIOR PELICATION NUMBER: US 60/266,156

NUMBER OF SEQ ID NOS: 3

SEGURATION PRICE NOS: 3

SEGURATION NOSE: PRICE NOS: 3
                                                                                                                                                                                             1 MetAlaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAla 17
                                                                                                                                                                                                                      15 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT 65
                                                                                                                                                       US-10-664-025-3903_COPY_1_17 (1-17) x US-10-472-533-175 (1-1898)
    Length:
Matches:
Conservative:
Mismatches:
                                                                                        Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (4107)..(4109)
OTHER INFORMATION: n is a, c, g, or
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LOCATION: (2986)..(2986)
OTHER INFORMATION: n is a,
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LOCATION: (3879)..(3879)
OTHER INFORMATION: n is a,
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LOCATION: (3847)..(3848)
OTHER INFORMATION: n is a,
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LOCATION: (4105)..(4105)
OTHER INFORMATION: n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: exon
LOCATION: 5443...5646
FEATURE:
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LOCATION: 6649...6747
FEATURE:
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LOCATION: 2387...2501
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LOCATION: 8907...9774
FEATURE:
                                          Percent Similarity:
Best Local Similarity:
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Length: Matches:

Conservative: Mismatches: Indels:

Gaps:

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US-10-664-025-3903_COPY_1_17 (1-17) x US-10-175-523-62 (1-185548)
                                                                                  1.72e+04
52.00
92.9%
64.3%
; ORGANISM: Mus musculus
US-10-175-523-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: MUS musculus
                                                                                                                Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
Query Match:
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                                                                    Alignment Scores:
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Pred. No.:
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                                                                                         Pred. No.:
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US-10-175-521-62/C

US-10-175-521-62/C

US-10-175-521-62/C

Sequence 6.2, Application US/1015523

Publication No. US200300962641

GENERAL INPORMATION:

APPLICANT: Brockman, Jeffrey

APPLICANT: Brockman, Jeffrey

APPLICANT: Laeng, Pascal

APPLICANT: Laeng, Pascal

APPLICANT: Rajan, Prithi

APPLICANT: 2001-06-18

PRIOR PILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: US 60/333,047

PRIOR APPLICATION NUMBER: US 60/333,047

PRIOR APPLICATION NUMBER: US 60/333,047

PRIOR APPLICANTION NUMBER: US 60/333,047

PRIOR PRILING DATE: 2002-01-18

PRIOR PRILING DATE: 2002-01-18

PRIOR PRILING DATE: 2002-01-18

PRIOR PRILING DATE: 2002-01-18

PRIOR PRILING DATE: 2002-03-04

NUMBER OF SEQ ID NOS: 197

SEQTUMAR: PARCHIN VERSION 3.1

SEQTUMAR: BASABB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetAlaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAla 17
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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! LOCATION: (9942)..(9942)

! OTHER INFORMATION: n is a, c, g, or t

US-10-467-046-1
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LOCATION: (8342)..(8349)
OTHER INFORMATION: n is a, c, g,
                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
LOCATION: (8334)..(8336)
OTHER INFORMATION: n is a, c, g,
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                  NAME/KEY: misc feature
LOCATION: (7347)..(7348)
OTHER INFORMATION: n is a, c,
                                                                                    FEATURE:
NAME/KEY: misc_feature
LOCATION: (8197)..(8197)
OTHER INFORMATION: n is a, c,
                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (8293)..(8293)
OTHER INFORMATION: n is a, c,
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81.00
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                              FEATURE
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RESULT 15
US-11-099-266-62/c
Sequence 62, Application US/11099266
Sequence 15, Application US/11099266
GENERAL INFORMATION:
APPLICANT: Brockman, Jeffrey
APPLICANT: Hook, Derek
APPLICANT: Klimczak, Leszek
APPLICANT: Laeng, Pascal
APPLICANT: Laeng, Michael
APPLICANT: Rajan, Michael
APPLICANT: Rajan, Michael
APPLICANT: Rajan, Prithi
TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
FILE REPRENCE: 03255/1004755-US4
FILE REPRENCE: 03255/1004755-US4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-664-025-3903_COPY_1_17 (1-17) x US-11-099-266-62 (1-185548)
178598 CAAGTACTTTTTCTAATATCTGTTGTTATATGGACTGGGGCT 178557
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Matches:
Conservative:
Mismatches:
Indels:
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CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: US 10/17,5.23
PRIOR FILING DATE: 2005-06-18
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2002-01-18
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Job time : 126.5 secs
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52.00
92.9%
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Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Sequence 564, Description

Sequence 178689, Sequence 792096, Sequence 792097,

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Sequence 564, Application US/10475075
Publication No. US20060053498A1
GENERAL INFORMATION:
APPLICANT: Bejanin, Stephane
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Glordano, Jean-Yves
TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins
FILE REFERENCE: G-081US03PCT
CURRENT APPLICATION NUMBER: US/10/475,075
CURRENT FILING DATE: 2003-10-17
FRIOR APPLICATION NUMBER: PCT/IB01/00914
FRIOR FILING DATE: 2001-04-18
NUMBER OF FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 918
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Sequence 194738,
Sequence 1108146,
Sequence 111111112,
Sequence 11111112,
Sequence 845855,
Sequence 848855,
                                                                          Sequence 563, App
Sequence 1704, Ap
Sequence 77448, A
Sequence 77449, A
Sequence 77450, A
Sequence 17868,
                                                                                                                                                                                                                                                                                                                           Sequence 16510,
Sequence 16510,
Sequence 16510,
Sequence 12283,
Sequence 122834,
Sequence 87557,
Sequence 87557,
Sequence 87655,
Sequence 87447,
Sequence 834245,
Sequence 834245,
Sequence 834245,
Sequence 432235,
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US-09-925-065A-77448
US-09-925-065A-77449
US-09-925-065A-77449
US-09-925-065A-77450

11 US-10-301-480-178689
12 US-10-301-480-178689
12 US-10-301-480-792096
12 US-10-301-480-792096
13 US-10-301-480-792096
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17 US-10-99-182A-166510
17 US-10-99-182A-166510
17 US-09-925-065A-857547
18 US-10-301-480-220836
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17 US-09-925-065A-848053
17 US-09-925-065A-848053
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US-10-301-480-285525
US-10-301-480-898331
US-10-301-480-898331
US-10-301-480-898332
US-10-301-480-898332
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ORGANISM: Homo sapiens
                                                                                                                            Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-475-075-564
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-DB=Published_Applications_NA_New -QFWT=fastap -SUFFIX=pan.mpbn -MINMATCH=0.1
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-WALERS-2000000000 -HOST=abss08
-USER-US10664025_acGN_1 1_981_arunat_08052006_173656_29587 -NCPU=6 -ICPU=3
-NO WMAP -NEG_SCORES=0 -WAIT -DSPBLCCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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1370.049 Million cell updates/sec
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1: /SIDS5/ptodata/1/pubpna/USO8_NEW_PUB.seq1:*

2: /SIDS5/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

3: /SIDS5/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

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6: /SIDS5/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

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10: /SIDS5/ptodata/1/pubpna/USIO_NEW_PUB.seq:*

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18: /SIDS5/ptodata/1/pubpna/USII_NEW_PUB.seq:*

19: /SIDS5/ptodata/1/pubpna/USII_NEW_PUB.seq:*

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                       GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                         - nucleic search, using frame plus p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9306428 seqs, 2036268586 residues
                                                                                                                                                                                                                                                                US-10-664-025-3903_COPY_1_17
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1 MALEVIAMILAVLIWTGA 17
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Maximum Match 100%
Listing first 45 summaries
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, Ygapext
, Fgapext
, Delext
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Maximum DB seq length: 2000000000
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Xgapop 10.0 ,
Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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Database :

Result

Sequence 168824, Sequence 782233, Sequence 285522, Sequence 285523 Sequence 285525

Sequence Sequence

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72 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT 122
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Mucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR PALING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MetAlaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAla 17
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Conservative:
Mismatches:
                                                                                                                                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHIN, YUNA
APPLICANT: ISONO, YUNKO
APPLICANT: ISONO, YUNKO
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMEGHIKA, ICHIRO
APPLICANT: TAMEGHIKA, ICHIRO
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: NOGHIKAWA, TSUTOWU
APPLICANT: NOGHIKAWA, TSUTOMU
APPLICANT
APPLICANT: NOGHIKAWA, TSUTOMU
APPLICANT
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                                                                                                                        ; Sequence 1704, Application US/11072512; Publication No. US20060029945A1; GENERAL INFORMATION:
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Best Local Similarity:
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                                                                                                    US-11-072-512-1704
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Mismatches:
Indels:
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Mismatches:
Indels:
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Matches:
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                                                                                            NAME/KEY: sig_peptide
10CATION: 52..102
7 OTHER INFORMATION: 8core 10.699998092651
7 OTHER INFORMATION: 8core 10.699998092651
US-10-475-075-564
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LOCATION: 72..122
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 10.6999998092651
OTHER INFORMATION: seq VLMLLAVLIWTGA/EN
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; OTHER INFORMATION: n = a, g, c or
US-10-475-075-563
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Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
Query Match:
                           NAME/KEY: CDS
LOCATION: 52..495
FEATURE:
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LOCATION: 72..500
FEATURE:
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Pred. No.:
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Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
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DB:
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GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REPERENCE: 10897.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT PILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-05-09

PRIOR FILING DATE: 2001-05-09

NUMBER FOR SEQ ID NOS: 957086

SOPTWARE: FREESEQ for Windows Version 4.0

SEQ ID NO 77449

LENGTH: 1642
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SEQ ID NO 77448
LENGTH: 1642
TYPE: DNA
TYPE: DNA
CSGANISM: Home sapiens
US-09-925-065A-77448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-09-925-065A-77449/C
Sequence 77449, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
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US-09-925-065A-77450/c
; Sequence 77450, Application US/09925065A
; Publication No. US20040181048A1
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64.3$
56.8$
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US-09-925-065A-77449
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Best Local Similarity:
Query Match:
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Query Match:
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APPLICANT: Wang, David G.

TITLE OF INVENTION: In the Human Genome
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR PILING DATE: 2002-08-09
PRIOR PILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR SEQ ID NOS: 1226818
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 178687
JOURNEAL INFOGULATION:

JAPLICANT: WAIG, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR PELING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PELING DATE: 2001-01-16
PRIOR PELING DATE: 2001-01-16
PRIOR PELING DATE: 2001-01-16
PRIOR PELING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957066
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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85.7<del>$</del>
64.3<del>$</del>
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85.7%
64.3%
56.8%
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; ORGANISM: Homo sapiens
US-09-925-065A-77450
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US-10-301-480-178687
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US-10-301-480-792096/c

is Sequence 732096, Application US/10301480

is Sequence 732096, Application US/20060057564A1

is GENERAL INPORMATION:

if APPLICANT: Wang, David G.

if TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms

if TITLE OF INVENTION: in the Human Genome

if TITLE OF INVENTION: in t
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                                                        1160 AAAGTTCTCCTGTTGTTGTTGTTGCTCCCTGGACTGGGGCC 1119
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Conservative:
Mismatches:
Indels:
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US-10-301-480-792096
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Best Local Similarity:
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ORGANISM: HOMO
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LENGTH: 1642
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Pred. No.:
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                                                                                                                 US-10-301-480-178688/C

US-10-301-480-178688/C

Sequence 178688, Application US/10301480

Sequence 178688, Application US/10301480

Sequence 178688, Application No. US20060057564Al

GENERAL INFORMATION:

TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms

TITLE OF INVENTION: identifiction and Mapping of Single Nucleotide Polymorphisms

TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms

TITLE OF INVENTION: identifiction and Mapping of Single Nucleotide Polymorphisms

TITLE OF INVENTION: identifiction and Mapping of Single Nucleotide Polymorphisms

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TITLE OF INVENTION: identification and Mapping of Single Nucleotide Polymorphisms

TITLE OF INVENTION: identification and Mapping of Single Nucleotide Polymorphisms

TITLE OF INVENTION: i
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| Publication No. US20060057564A1
| Publication No. US20060057564A1
| GENERAL INFORMATION:
| APPLICANT: Wang, David G. |
| TITLE OF INVENTION: In the Human Genome |
| TITLE OF INVENTION: In the Human Genome |
| TITLE OF INVENTION: In the Human Genome |
| TITLE OF INVENTION: In the Human Genome |
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| TITLE OF INVENTION: In the Human Genome |
| TITLE OF INVENTION: In the Human Genome |
| TITLE OF INVENTION: In the Human Genome |
| FORMENT FILING DATE: 2002-01-02 |
| PRIOR FILING DATE: 2001-08-10 |
| PRIOR PRILING DATE: 2001-08-10 |
| NUMBER OF SEQ ID NOS: 1226818 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 178689 |
| LENGTH: 1642
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1160 AAAGTTCTCCTGTTGTTGTTGTTGCTCCCTGGACTGGGGCC 1119
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Matches:
Conservative:
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Matches:
Conservative:
Mismatches:
Indels:
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56.8%
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; CRGANISM: Homo sapien
US-10-301-480-178688
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Best Local Similarity:
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US-10-301-480-178689
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ORGANISM: HOMO
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DB:
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Sequence 792097, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION
FURNALING David
APPLICANT WANG, David G.
TITLE OF INVENTION: In the Human Genome
TITLE OF INVENTION: In the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT PILING DATE: 2002-11-21
FRIOR APPLICATION NUMBER: US 10/215,598
FRIOR FILING DATE: 2001-08-10
REIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                      1160 AAAGTICTCCTGTTGTTGTCTGTTGCTCCCTGGACTGGGGCC 1119
4 GluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAla 17
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CURRENT FILE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
FILE REFERENCE: 09531-128001
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: US/11/099,686
PRIOR PLILNG DATE: 2005-10-01
PRIOR PLILNG DATE: 2003-10-01
PRIOR PLILNG DATE: 2003-10-04
NUMBER OF SEQ ID NOS: 11433
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9464
LENGTH: 492
                                                                                                                                                                                APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAO, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: FUJIMURA, TOMHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REPREBNCE: 030685-043
CURRENT APPLICATION NUMBER: US/10/932,182A
CURRENT FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 1970-23
SOFTWARE: PATENTIN VERSION 3.3
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      2 AlaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAla 17
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Matches:
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Gaps:
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                                                                                                                         ; Sequence 166510, Application US/10932182A; Publication No. US20060046253A1; GENERAL INFORMATION:
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Publication No. US20060024696A1
GENERAL INFORMATION:
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US-11-098-686-9464
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Best Local Similarity:
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Best Local Similarity:
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LENGTH: 294
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US-11-098-686-9464
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                                                                                                               Sequence 792098, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: In the Human Genome
TITLE OF INVENTION: In the Human Genome
TITLE APPLICATION NUMBER: US/10/301,480
CURRENT APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FactSEQ for Windows Version 4.0
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APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOWKO
APPLICANT: FUJIMURA, TOWKO
APPLICANT: RAHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: 030688-048
CURRENT APPLICATION NUMBER: US/10/932,182A
CURRENT FILING DATE: 2004-09-02
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                       1160 AAAGTTCTCCTGTTGTTGTTGTTGCTCCCTGGACTGGGGCC 1119
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 166510
LENGTH: 294
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ORGANISM: Homo sapien
                                                                                              -10-301-480-792098/c
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Best Local Similarity:
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Best Local Similarity:
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LENGTH: 1642
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Pred. No.:
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Search completed: May 9, 2006, 22:09:30 Job time: 76.8 secs

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CA28912 SCBFRT309

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AW011198 ST17H06 P

DR154376 49153495

DR139602 49190150

DR154420 4913973

CE551157 tigr-988-

AL141132 Anopheles

BF57187 602076741

AZ624138 1M0462M06

CG350468 OGSAN06TC

CG715063 CGADW37TF

CG221053 OGSANO6TC

CG221053 OGSANO6TC

CG221053 OGSANO6TC

CG212053 OGSANO6TC

CG212053 OGSANO6TC

CG212053 OGSANO6TC
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qd99c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1737606
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information can be
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AV422253
IP1 36 B1
RHIZ2 23
LjNEST96a
SCEZLR100
LjNEST677
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P11 32 C0
ETH1 11 B
AJ414707
AG-ND-102
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SCRLFL300
SCUTSD102
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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I (bases 1 to 331)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M. Fatima
                                                                                                                                                                                                                                                                                                       AW428893 AW4228893 BY02253 AW42253 AW42253 AW729005 BG102437 FCA121482 AW719616 BW324073 BW324073 BW5594345 GA208211 SW5594345 BW3414707 BW314707 BW314707 BW314707 BW32706 AW414707 BW32706 AW41
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CA226596 S
CA290401 S
AW720591 I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M.
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: washington University Genome Sequ
Clone distribution: NCI-CGAP Clone distribution info
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 395 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                           CF715063
CG212053
AZ558974
                                          BX118111
CA289989
CA278912
BG741530
AW011198
DR139602
DR154420
CE251157
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AW422893
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BIO99005
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BEJ02437
CBG22960
CA121482
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CA22440
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AI138881
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AI138881/c
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DEFINITION
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TITLE
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-MODEL=frame+_p2n.model -DEV=x1h
-0=/abss/AbsSWEB spool/US10664025/runat 08052006 173646 29404/app query.fasta_1
-0=/abss/AbsSWEB spool/US10664025/runat 08052006 173646 29404/app query.fasta_1
-0=/abss/AbsSWEB spool/US10664025.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-DN=EST -QFWT=fastap -SUPFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=12 -ALIGN=12 -OUTFWT=pto -NORM=EXT -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abss07
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-NO WMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEY TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPPEXT=7
-YGAPFOP=10 -YGAPEXT=7
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BE972717 d61652136
B1433012 603204535
BUS61151 AGENCOURT
BG772527 602720619
B1459538 603200545
B1520154 603071295
                                                                                                                 (without alignments)
1996.103 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                 9, 2006, 13:30:21 ; Search time 597.7 Seconds
            GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                       using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                   41078325 segs, 23393541228 residues
                                                                                                                                                                                                                                                                                                                                             Fotal number of hits satisfying chosen parameters:
                                                                                                                                                            US-10-664-025-3903_COPY_1_17
81
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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9b_est2::*
9b_est4::*
9b_est5::*
9b_est6::*
9b_gss6::*
9b_gss7::*
                                                                       nucleic search,
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/organism="Homo sapiens"
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                                                                                                                                                                                          0.000728
81.00
100.0%
100.0%
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                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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JOURNAL
COMMENT
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AUTHORS
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KEYWORDS
SOURCE
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BI463012
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                                                                                          /lab_host="DH10B"
/clone_lib="Soares testis_NHT"
/clone_lib="Soares testis_NHT"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_l: Not 1; Site_2: Eco RI; lst strand cDNA
was prepared from mRNA obtained_from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                Double-stranded CDNA was ligated to ECC RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I and ECC RI sites of the modified pyT73 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:3935288"
/lab_host="DH10B (T1 phage-resistant)"
/clone lib="NIH MGC 82"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1: Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc); S' and 3' adaptors were used in cloning as follows: 5' adaptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE972717 516 bp mRNA linear EST 04-OCT-2000 601652136F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935288 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Context: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Place: LLCM777 row: h column: 09
High quality sequence stop: 505.
Location/Qualifiers
rce
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                 Hominidae, Homo.
1 (bases 1 to 516)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (WGC)
Unpublished (1999)
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Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
              mol_type="mRNA"

db_xref="taxon:9606"

clone="IMAGE:1737606"
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Homo sapiens
                                                                            'sex="male"
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BE972717
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Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11682 row: e column: 09
High quality sequence stop: 624.
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCGGGCGGCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pBluescript Ks+); Site 1: BamHI; Site 2: Sal1-XhoI (gtcgag); Oligo-dT primed using primer average insert size 2:2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMMI/NHGRI, wational Institutes of Health). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 21-AUG-2001
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603204535F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5270384 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5270384"
/lab host=="BH10B"
/clone_lib="NIH MGC_97"
/note="Organ: testis; Vector: pBluescriptR (modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             516
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Mismatches:
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Matches:
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Pred. No.:

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/lab host="Dulibs"
/(Jab host="Dulibs")
/(Jone lib="NHH MGC 97"
/(Jone lib="NHH MGC 97"
/(Jone lib="Organ: restis; Vector: pBluescriptR (modified pBluescript KS+); Site_l: BamH1; Site_2: Sall-XhoI (gtcgag); Oligo-dT primed using primer
5-TTTTTTTTTTTTTTTTTTYN 3. size-selected for average insert size_2.2 kb and normalized to ROT5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NFM/MRRI, National Institutes of Health). Note: this is a NH_MGC Library."
                                                                                                                             BG772527 776 bp mRNA linear EST 15-MAY-2001
602720619F1 NIH_MGC_97 Homo sapiens CDNA clone IMAGE:4837612 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BI459538 778 bp mRNA linear EST 21-AUG-2001
603200545F1 NIH_MGC_97 Homo sapiens CDNA clone IMAGE:5266642 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: Cgapbs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10770 row: e column: 05
                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 776)

11 (bases 1 to 776)

Nath-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
           316 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT 266
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Matches:
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:4837612"
                                                                                                                                                                                                                                           BG772527.1 GI:14083180
                                                                                                                                                                                                                                                                                              Homo sapiens (human)
Homo sapiens
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TITLE
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                                                                 RESULT 5
BG772527
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BI459538
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/wol type="mRNA"
/db_xref="taxon:9606"
/clone="INMES:6592356"
/lab host="INMES:6592356"
/lab host="DH108 (T1 phage-resistant)"
/clone=lib="NIH MGC_82"
/clone=lib="NIH MGC_82"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (9gccgctcggcc); Site_2: Sfil (9gccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATANTGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGACATGATGGT (30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.35 kb (range 0.9-4.0 kb): 14/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homindae; Homo.

1 (Dases 1 to 753)

1 (Dases 1 to 753)

2 NIH-MGC http://mgc.nci.nih.gov/.

3 NIH-MGC http://mgc.nci.nih.gov/.

4 National Institutes of Health, Mammalian Gene Collection (MGC)

5 Notional Institutes of Health, Mammalian Gene Collection (MGC)

6 Ontact: Robert Strausberg, Ph.D.

7 Email: cgapbs-remail.nih.gov

7 Tissue Procurement: CLONTECH Laboratories, Inc.

7 CDNA Library Preparation: CLONTECH Laboratories, Inc.

8 CDNA Library Preparation: CLONTECH Laboratories CONTECH Lab
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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

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RESULT 4

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BI459538 BI459538.1 GI:15250194

ACCESSION VERSION KEYWORDS

MetAlaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAla 17

Query Match: DB:

Pred. No.:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_tref="taxon:9606"
/db.tref="taxon:9606"
/clone="IMAGE:526642"
/lab_host="DH10B"
/clone=lib="WHH MGC 97"
/clone=lib="WHH MGC 97"
/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHf; Site_2: Sal1-XhoI (Grogan: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHf; Site_2: Sal1-XhoI (Grogan: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHf; Site_2: Sal1-XhoI (Grogan: testis; Vector: dull-length constructed and normalized to ROT 5: This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (WIMH/NHGRI, National Institutes of Health). Note: this is
                                                                                                              E 1 (bases 1 to 778)

S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

L Contact: Robert Strausberg, Ph.D.
Email: cgapbe-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL at:
http://image.llnl.gov
Plate: LLAMIG72 row: i column: 11
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 878)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Location/Qualifiers
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1 (bases 1 to 778)
                        Homo sapiens
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H3059H12-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
H3059H12 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgeun.grc.nia.nih.gvc.nia.nih.g
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1 (Bases 1 to 598)
Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X., Grahovac,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,H., Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
m column: 24
High quality sequence stop: 851.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
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Matches:
Conservative:
Mismatches:
Indels:
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this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligo (d7) -Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse development placenta and embryo using a 15,000 mouse development conNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse develolpment, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear EST 17-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="MINA Mouse 15K CDNA Clone Set"
/clone lib="With Mouse 15K CDNA Clone Set"
/note="Vector: pSPORT1; Site_1: Sal1; Site_2: NotI; This
clone is among a rearrayed set of 15,247 clones from 11
embryo. cDNA libraries (including preimplantation stage
embryos from unfertilized egg to blastocyst, embryonic
part of E7.5 embryos, extraembryonic part of E7.5
embryos, and E12.5 female mesonephros/gonad) and one
newborn ovary CDNA library. Average insert size 1.5 kb.
All source libraries are cloned unidirectionally with
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus
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Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
Hume,D.A., Quackenbuhy,T., Schriml,L.M., Kanapin,A., Matsuda,H.,
Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.
                                                                                                                                                                                                                                                                                                                                                /sex="Clones arrayed from a variety of cDNA libraries"
|dev_stage="Clones arrayed from a variety of cDNA
visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details.
Plater. H3059 row: H column: 12
Seg primer: -21M13 Reverse
High quality sequence stop: 598
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                             /db_xref="niaEST:H3059H12-5"
/db_xref="taxon:10090"
/clone="H3059H12"
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                                                                                                                                                                                  /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                              lab_host="DH10B"
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BY731676
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KEYWORDS
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                                                                                                                                FEATURES
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Fletcher, C. Constitution, Constitution, Caralago, Placther, C. Constitution, Castler, C. Godzik, A., Gough, J., Gardendar, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Garibondi, S., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Garibondi, S., Gustincch, S., Hirokawa, N., Jackensi, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Mari, M., Maglott, D.R., Numata, K., Okido, T., Pavan, M.J., Pertea, G., Pesole, G., Percosky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Raig, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Varado, R., Wagner, L., Wahlestedt, C., Wang, Y., Wacanabe, Y., Wells, C., Willming, L.G., Wynshaw, Boris, A., Yanagasawa, K., Kang, I., Yang, I., Yang, L., Yuan, Z., Zavodan, M., Zhu, Y., Zimmer, A., Carninci, P., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawa, J.J., Azawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Indhi, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shirakya, A., Yasunishi, A., Yoshino, W., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y. Analysis of the mouse transcriptome based on functional annotation of 60,700 cull.—Inangh hospita
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Normalization and subtraction of cap-trapper selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence full-length cDNA encyclopedia: real-time sequenced in Mouse Genome Computers was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Science Laboratory in Riken Genomic Science Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
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Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Rukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishli,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
Zano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Direct Submission
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Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Site 1: Sail; Site 2: BamHI; cDNA library war
prepared and sequenced in Mouse Genome Encyclopedia
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/db_xref="taxon:10090"
/clone="E330031A07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="female"
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/ organism="Mus musculus"
/mol type="mRNA"
/db Xref="taxon:10090"
/clone="IMAGE:30931566"
/lab host="DH10B TonA"
/clone="lab"organ: oocyte; Vector: pExpress-1; Site 1: EcoRV;
Site 2: Not1; cDNA was primed using oligo-dT primer:
5'-pGACTACATCTCAGATCGGAGCGCCC(T(1)25-3' and cloned into
the EcoRV/Not1 sites of pExpress-1. Size-selection >0.5 kb
resulted in an average insert size of 1.0kb. This is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COB10251

AGENCOURT 30258260 NIH MGC 257 Mus musculus cDNA clone
IMAGES30931566 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-WGC http://wgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
Office of Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethead, MD 20892
Email: Gapbs-r@mail.nih.gov
Tissue Procurement: Dr. Kathleen Horner, Stanford University
CDNA Library Preparation: Express Genomics
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
http://inage.llnl.gov
Plate: NDAMI179 row: h column: 07
High quality sequence stop: 654.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetalaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAla 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 ATGGCTTTAGAGGTCCTGGTTTATCTTGCTGTCTTGGTTTTGGACTTGTGCT 96
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EST.
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76.5%
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Best Local Similarity:
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VERSION
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/clone libe Soares testis NHT"
/note="Vector: pT7I3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
normalized library (primary library is NIH MGC 256) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MGC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 07-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                       BX118111 Soares testis NHT Homo sapiens CDNA clone IMAGp998D122574 INAGE:1030619, mRNA Fequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seg primer: M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hominidae; Homo.

1 (bases 1 to 577)

Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
Radelof,U., Schneider,D. and Korn,B.
Human UnigeneSet - RZPD3
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Ina Rolfs
RAPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
IR Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZDD; INAGp998D122574.
RZDDLB; I.M.A.G.B. CDNA Clone Collection;
Human UnigeneSet - RZDD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/Cgi-
bin/ShowLib.pl.cgi/response7libNo-972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Fel: +49 30 32639 101
Fax: +49 30 32639 111
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                                                                                                                                                                                                                                                                                                            1 MetAlaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAla
                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
| Mol Lype="mRNA"
| Ab xref="texon:9606"
| Clone="IMAGD998D122574 ; IMAGE:1030619"
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Mismatches:
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Matches:
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BX118111.1 GI:27881212
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76.5
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                                                                                                                                                                                       Best Local Similarity:
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                                                                                                                                                                Percent Similarity:
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DB:
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AUTHORS
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SCBFRT3091G01.g RT3 Saccharum officinarum cDNA clone SCBFRT3091G01
5', mRNA sequence.
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/note="Gram: Root apex from adult plants; Vector:
pSportl; Site_l: Sall; Site_2: NotI; An unidirectional
pSportl; Site_l: Sall; Site_2: NotI; An unidirectional
cDNA library generated from [Root apex from adult
plants]. cDNA was prepared from polyA+ mRNA using
SuperScript Plasmid System Kit (Invitrogen). The
Guble-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucest.lad.ic.unicamp.br/public"
                                                                                                                                                                                                                                                                                                        Saccharum officinarum
Saccharum officinarum
Eukaryoty, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 091 row: G column: 01
Seq primer: T7 Promoter Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                           (Dasses 1 to 1009)
Vetrore, A.L., da Silva, F.R., Kemper, B.L. and Arruda, P. The libraries that made SUCEST
Contact: Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Universidade Estadual de Campinas
Caixa Poetal 610, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
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                                           2 AlaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThr 15
                                                                    18 GCGATGGAGCTCCTGATGTTACTGGCCTTCATGATATGGACG 59
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/organism="Saccharum officinarum"
/mol type="mRNA"
/db Xref="taxon:4547"
/clone="SCBFRI3091G01"
/lab_host="DH10B"
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US-10-664-025-3903_COPY_1_17 (1-17) x CA289989 (1-589)
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TITLE
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/clone lib="FLB"
/clone lib="FLB"
/clone lib="FLB"
/clone lib="FLB"
/note="Organ: Developing inflorescence and rachis
/note="Organ: Developing inflorescence and rachis (10cm-long); Vector: pSport1; Site_1: Sal1; Site_2: NotI;
An unidirectional cDNA library generated from [Developing inflorescence and rachis (10cm-long)]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharum officinarum
Saccharum officinarum
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
                                                                                                                                                                                                                                                                                                                                                        EST 26-SEP-2003
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SCAGFL8011C05.g FL8 Saccharum officinarum cDNA clone SCAGFL8011C05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 011 row: C column: 05
Seq primer: T7 Promoter Primer.
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I (bases 1 to 589)
Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P. Vettore, A.L., and Silva, F.R., Kemper, E.L. and Arruda, P. The libraries that made SUCEST Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda Molecular e Engenharia Genetica Universidade Estadual de Campinas Genetica Caixa Postal 6010, 13083-970, Campinas SP, Brazil Tel: 55 19 3788 1137
Fax: 55 19 3788 11089
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Mismatches:
Indels:
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                                                                                                                                                                                                                 LeuMetLeuLeualavalLeuIleTrpThrGlyala 17
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Conservative:
Mismatches:
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/db_xref="taxon:4547"
/clone="SCAGFL8011C05"
                                                                                                                                                                                                                                                                                                                                                                                                                                             CA289989.1 GI:36043353
                  6.16
59.00
100.0%
100.0%
72.8%
                                                                                                                                                                                                                                                                                                                                                                                                  5', mRNA sequence.
CA289989
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AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                      RESULT 12
CA289989
                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
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Search completed: May 9, 2006, 15:10:12
Job time : 600.7 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ST17H06 Pine TriplEx shoot tip library Pinus taeda cDNA clone ST17H06, mRNA sequence.
AW011198.1 GI:5859976
AST.
                 BG741530 863 bp mRNA linear EST 15-MAY-2001
602635139F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4780232 5',
                                                                                                                                                                                                                  Hominidae, Homo.

In (bases I to 863)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Londact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.

CDNA Library Parayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov
Plate: LiAM10638 row: n column: 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/mol_type="mRNA"
/mol_xref="taxon:9606"
/clone="ImAGES:4780232"
/lab_host="DH10B (T1 phage-resistant)"
/clone="lorgan: sKin, Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: sKin, Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall, Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. I (bases I to 59%)
Whetten, R. W., Kinlaw, C.S., Retzel, E. and Sederoff, R.R.
The Pine Gene Discovery Project
Thupblished (1999)
Contact: Ross Whetten
Forest Biotechnology Group
                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MetAlaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAla 17
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Matches:
Conservative:
Mismatches:
Indels:
              mRNA
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Location/Qualifiers
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BG741530.1 GI:14052183
                                                                                                                                          Homo sapiens (human)
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Best Local Similarity:
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AW011198
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/wol type="mrwa" cacua"
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/db xref="warna" 352"
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/clone lib="pine TriplEx shoot tips sand TriplEx; Site_1:
/clone lib="pine TriplEx shoot tips sand TriplEx; Site_1:
/clone lib="pine during the spring, frozen and used for mRNA isolation. The SMART-PCR method (Clontech) was used to prepare a library from 1 ug total RNA, using the Lambda TriplEx vector. Plasmid subclones in pTriplEx were recovered by cre-lox excision in E. coli strain BM25.8 and sequenced from the 5' end."
North Carolina State University
Dept. of Forestry, NC State University, 6113 Jordan Hall,
Raleigh,NC, 2769-8008
Tel: 919-515-7800
Fax: 919-515-7800
Email: rosswhet@unity.ncsu.edu
Seq primer: 5' lambda TriplEx2 Sequencing Primer.
Location/Qualifiers
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Conservative:
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                                                                                                                                                                                                          organism="Pinus taeda"
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May 9, 2006, 10:10:22 ; Search time 11.7 Seconds (without alignments) 638.414 Million cell updates/sec
GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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81
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Maximum Match 100%
Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: geneseqp1980s:*
2: geneseqp2000s:*
4: geneseqp2001s:*
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aaq89145 Human sec	Human	Human	Aag89140 Human sec	Abg97353 Human CGD	Abg31324 Human GSS	Abr47931 Human sec		Adb91675 Human sec	Adb65520 Human pro		Aab38337 Human sec	Adx40751 HIV Vpu p	8 HIV		Abb94049 Human sec	Abb94025 Human sec	Abg65110 Human alb	Abg65111 Human alb	Adl78378 Albumin f	Adl78377 Albumin f	Aau20830 Human nov	Aag72080 Human olf	Adq03086 P. aerugi
SUMMARIES	ID	AAG89145	ABP76237	ABP76238	AAG89140	ABG97353	ABG31324	ABR47931	ABR00175	ADB91675	ADB65520	ADC74338	AAB38337	ADX40751	ADX40648	ADX40735	ABB94049	ABB94025	ABG65110	ABG65111	ADL78378	ADL78377	AAU20830	AAG72080	ADQ03086
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Abo71749 Pseudomon Abu33173 Protein e Aeb41559 L. pneumo Aeb69261 HTV-1 non Aab69261 HTV-1 non Ad288786 Breast sp Ad23456 Acinetoba Abr58443 Human NOV Abr58445 Human NOV Abr58445 Human NOV Adj57406 Secretory Abm80171 Tumour-as Aab71408 Human pro Abr58444 Human NOV Adj57405 Secretory Abm80170 Tumour-as	NTS				vaccine; treatment; diagnosis;						Jobert S;		is encoding potentially secreted vaccination against a variety of diseases.		The invention relates to full length GENSET human nucleic acids encoding potentially secreted proteins. The nucleic acids and the polypeptides they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GENSET gene expression. For example, they be used to treat disorders associated with decreased GENSET gene expression by rectifying mutations or deletions in a patient's genome that affect the activity of GENSET or by supplementing the patients own production of GENSET polypeptides. Conversely, antisense nucleic acid molecules may be administered to down regulate GENSET expression by binding with the cells' own genes and preventing their
ABO71749 ABU33173 AEB41559 AEB18276 AAB69261 AAB69344 AAB69344 AAB8442 ABR58442 ABR58442 ABR58445 ABR58445 ABR58445 ABR58445 ABR58445 ABR60171 AAB60171 AAB011408 AAB11408	ALIGNMENTS	106 AA.		ID NO: 265.	ene therapy;				· ·		Bougueleret L,		nucleic acids therapy and va sis of those di	English.	is. The nucles of the prevention of the prevention of disconding mutations ity of GENSET polyke administent of the cells' of the
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U U U U U α α α α α α α α α α α α α α α		1 45 AG89145	AAG89145; 11-SEP-2001	Human secret	Human; secreted GENSET.	Homo sapiens	0200142451	4-JUN-2001 7-DEC-2000	8-DEC-1999 6-MAR-2000	(GEST) GENSI	Dumas Milne	WPI; 2001-36' N-PSDB; AAH6	Full length proteins, us diseases, an	Claim 21; Pa	he inventic otentially hey encode iseases as xample, the ene express enome that atients own ucleic acid
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	+.:	389 389	•					- 0	X K K S						

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expression. The sense and antisense nucleic acids may also be used as DNA
                probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence to determine which spatients may be in need of restorative therapy. The GENSET polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of GENSET polypeptide expression and activity. The present sequence is a GENSET polypeptide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New GENSET polynuclectides and polypeptides, useful for treating heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, CNS, cardiovascular or gastrointestinal effects of the
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                                                                                                                                                                                             Score 81; DB 4; Length 106;
Pred. No. 6.2e-05;
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Matches 17; Conserv
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The present invention relates to novel GENSET polynucleotides (ABZ36404-ABZ36911) encoding polypeptides (ABP75953-ABP76368). The polynucleotides and polypeptides are useful in screening and diagnostic assays for abnormal GENSET expression and/or biological activity. They are also useful for screening of compounds for treating or preventing GENSET-teated disorders, such as heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, central nervous system (CNS), cardiovascular or gastrointestinal effects of the toxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New GENSET polymucleotides and polypeptides, useful for treating heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, CNS, cardiovascular or gastrointestinal effects of the
                                                                                                                                                                                                              Cytostatic; antiinflammatory; nootropic; neuroprotective; cardiant; gastrointestinal; gene therapy; GRNSET; heavy metal toxicity; cancer; inflammatory disease; immune disorder; neuromuscular; toxicity; central nervous system; cardiovascular; gastrointestinal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Giordano J;
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100.0%; Pred. No. 8.8e-05;
ive 0; Mismatches 0;
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                                                                                        ABP76238 standard; protein; 148 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bejanin S,
                                                                                                                       ABP76238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           toxicity.
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Gaps

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Indels

100.0%; Score 81; DB 6; Le 100.0%; Pred. No. 8.5e-05; ive 0; Mismatches 0;

Local Similarity 100. 108 17; Conservative

Query Match Best Local S: Matches 17,

Length 143;

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1 MALEVLMLLAVLIWTGA 17
                                                                                          Homo sapiens
                                                                                                                                         19-SEP-2002
                                                                                                                                                                                                                                                                                             Ding L,
Lu DAM,
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                                                                                                                                                                                                                                                                                                                                                     potentially secreted proteins. The incleic acids and the polypeptides they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GENSET gene expression. For example, they be used to treat disorders associated with decreased GENSET gene expression by rectifying mutations or deletions in a patient's genome that affect the activity of GENSET or by supplementing the patients own production of GENSET polypeptides. Conversely, antisense nucleic acid molecules may be administered to down regulate GENSET expression by binding with the cells' own genes and preventing their expression. The sense and antisense nucleic acids may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence to determine which probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence to determine which parobes be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of GENSET polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                            invention relates to full length GENSET human nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cell growth, differentiation; death; CGDD; cancer; cell proliferative disorder; arteriosclerosis; atherosclerosis; cirrbosis; hepatitis; paroxysmal nocturnal haemoglobinuria; psoriasis; polycythaemia vera; primary thromobocytopaenia; developmental disorder; renal tubular acidosis, anaemia; mental retardation; epilepsy; AIDS; neurological disorder; Alzheimer disease; Parkinson's disease; asthma;
Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;
                                                                                                                                                                                                                                                               Full length GENSET human nucleic acids encoding potentially secreted proteins, useful in gene therapy and vaccination against a variety of diseases, and for diagnosis of those diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 81; DB 4; Length 15:
100.0%; Pred. No. 9.5e-05;
                                                                                                                                                                                                     Jobert S;
                                                                                                                                                                                                     Bougueleret L,
                                                                                                                                                                                                                                                                                                                   Claim 21; Page 804; 921pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG97353 standard; protein; 158 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human CGDD4, INCYTE 5284076CD1.
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                                                                                                            07-DEC-2000; 2000WO-IB001938
                                                                                                                                    08-DEC-1999; 99US-0169629P.
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                                                                                                                                                                                                 Dumas Milne Edwards J,
                                                                                                                                                                                                                           WPI; 2001-367870/38.
                                                                                                                                                                                                                                        N-PSDB; AAH64743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 158 AA;
                                                            WO200142451-A2.
                                                                                                                                                                        (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention
                                     Homo sapiens
                                                                                      14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG97353;
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             GENSET.
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The invention relates to an isolated polypeptide comprising CGDD1-12 (cell growth, differentiation and death), a naturally occurring amino acid sequence at least 90% identical to CGDD, a biologically active acid sequence at least 90% identical to CGDD, a biologically active fragment or an immunogenic fragment. Also included are the polymucleotides encoding CGDD1-12, a recombinant polymucleotide or comprising a promoter sequence operably! Inked to the CGDD polymucleotides, a cell transformed with the recombinant polymucleotide, a transgenic organism comprising the recombinant polymucleotide, an anti-cCGD polymucleotides a cell transformed with the recombinant polymucleotide and active cCGDD antibody, screening for compounds which bind to/modulate or are anti-dagonists of CGDD or alter the expression of CGDD polymucleotide microarray. The polypeptides, polymucleotide and active cCGDD polymucleotide microarray. The polypeptides, polymucleotide and active cCGD antibodists are useful for diagnosing, treating or cCGDD polymucleotide microarray. The polypeptides, polymucleotides associated with aberrant expression of CGDD, particularly cell proliferative (e.g. arteriosclerosis, atherosclerosis, apericals, particularly cell proliferative (e.g. arteriosclerosis, atherosclerosis, cirrhossis, polymorial pacroysmal nocturnal haemoglobinuria, polycythaemia correction for a disorders (e.g. renal tubular acidosis, anaemia or mental retardation), neurological disorders (e.g. Alzheimer disease, parkma, autoimmune correction in the menstrual cycle), or autoimmune/inflammatory disorders (e.g. Alzheimer disease, disbetes mellitus, cortact dermatitis, crom's disease, disbetes mellitus, cortact dermatitis, crom's disease, disbetes mellitus, cortact dermatitis, crom's disease, disbetes mellitus, cortact dermatitis, fungal, parasitic, processis, proteins associated with cGDD. The present sequence cortact cortact dermatitis, fungal, parasitic, processis or helminate associated with cGDD. The present sequence cortact cortact dermatities
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reproductive disorder, infertility; autoimmune disorder; gout; allergy; inflammatory disorder; acquired immunodeficiency syndrome; uveitis; autoimmune thyroiditis; contact dermatitis; Crohn's disease; infection; diabetes mellitus; glomerulonephritis; irritable bowel syndrome; multiple sclerosis; osteoarthritis; osteoporosis; pancreatitis; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baughn MR;
Burford N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . Lu Y, Warren BA, Elliott VS,
ζJ, Tang TY, Lal PG, Duggan BM,
Tran UK, Khare R, Walia NK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 158;
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100.0%; Pred. No. 9.5e-05;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-FEB-2001; 2001US-0268111F.
23-FEB-2001; 2001US-0271F5P.
08-MAR-2001; 2001US-0274403P.
09-MAR-2001; 2001US-0274552P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atherosclerosis or hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-FEB-2002; 2002WO-US003715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yao MG, Ison CH, I.
Xu Y, Gietzen KJ,
Richardson TW, Tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             represents a CGDD protein
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Best Local Similarity 100.
Matches 17; Conservative
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Sequence 158 AA;

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polypeptide, and polymucleotide sequences that encode it. The GSSP3
polypeptide, and polymucleotide sequences that encode it. The GSSP3
polypeptide reduces circulating blood glucose levels, increases insulin
sensitivity, and/or reduces body mass. The GSSP3 polypeptide and
conjunctedide sequences are useful in serum glucose regulation, fatty
acid metabolism, body weight loss, and prevention of body weight gain.
Compositions comprising GSSP3 polypeptides are useful for controlling
blood glucose levels, for treating metabolic-related diseases or
clasorders (e.g. obssity, impaired glucose tolerance, insulin resistance,
hyperlipidaemlas, attherosclerosis, heart disease, hypertension, stroke,
cyndrome C, type I or II diabetes, diabetes related complications,
microangiopathy, retinopathy, neuropathy, nephropathy, polycystic ovarian
syndrome, ocular lesions, microangiopathic lesions, or syndromes such as
canthosis nigricans, leprechaunism and lipoatrophy). The polypeptides
are also useful to improve physical performance during work or exercise,
and to treat dyslexial, attention-deficit disorders such as
cdeficit/hyperactivity disorder, and psychiatric disorders such as
controphrenia. The present sequence represents human GSSP3 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      body mass; serum glucose regulation; body weight loss; obesity; metabolic-related disorder; impaired glucose tolerance; stroke; insulin resistance; hyperlipidaemia; atheocalerosis; heart disease; hypertension; syndrome C; type I diabetes; type II diabetes; microangiopathy; retinopathy; neuropathy; nephropathy; ocular lesion; polycygtic ovarian syndrome; acanthosis nigiran; leptechaunism; lipoatrophy; physical performance; exercise; dyslexia; schizophrenia; attention-deficit disorder; hyperactivity disorder; psychiatric disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; GSSP3; circulating blood glucose level; insulin sensitivity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chicca J, Yen-Potin F;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18. .158
/label= Mature_GSSP3_polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .17
/label= Signal_peptide
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                                                                                                                                                                                                                                                 ABG31324 standard; protein; 158 AA
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01-FEB-2002; 2002WO-IB001333.
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                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human GSSP3 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002-608487/65.
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                                                                                                                                                                                                                  ABG31324
                                                                                                                                                                       RESULT
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ABR48145) and their coding sequences (ACC50856). The proteins and their coding sequences (ACC50856). The proteins and their coding sequences (ACC50856). The proteins corp pharmaceutical composition for diagnosing or treating a cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary areriosclerosis and myocardial ischaemia), neural disorders, immune system disorders, muscular disorders, reproductive disorders, immune gastrointestinal disorders, pulmonary disorders, renal disorders, pulmonary disorders, renal disorders, for proliferative disorders and/or cancerous diseases and conditions, for infection, for treating thrombosis and arteriosclerosis, for treating or preventing neural damage which occurs in neuronal disorders or neurodegenerative conditions such as Alzheimer's disease and Parkinson's disease, to enhance bone and periodontal regeneration and aid in tissue transplants or bone grafte, to prevent skin aging or hair loss, to stimulate growth and differentiation of heamstopoietic cells and bone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention relates to novel human secreted proteins (ABR47633-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human secreted proteins, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating cardiovascular disorders such as arrhythmia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 marrow cells when used in combination with other cytokines, to maintain organs before transplantation or for supporting cell culture of primary tissues, to increase or decrease differentiation or proliferation of embryonic stem cells, or to modulate mammalian characteristics or metabolism. Note: The sequence data for this patent was published in electronic format and is available from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                        Cardiant, antiarrhythmic, antiarteriosclerotic, vasotropic, cytostatic,
                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                               vulnerary; antiinflammatory; nootropic; neuroprotective;
antiparkinsonian; gene therapy; human; cardiovascular disorder.
    Score 81; DB 5; Length 158;
Pred. No. 9.5e-05;
                                           Indels
                                              Mismatches
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                                                                                                                                                                                                                             ABR47931 standard; protein; 158 AA.
                                                                                                                                                                                                                                                                                                                                                  Human secreted protein, SEQ ID 822.
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                                                                                                                   1 MALEVLMLLAVLIWTGA 17
      100.08;
                                                                                   1 MALEVLMLLAVLIWTGA 17
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
                       100.08;
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                                                                                                                                                                                                                                                                                                             (first entry)
Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen CA, Ruben SM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                     ABR47931;
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Sequence 158 AA;
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                                                                                                                                                                            RESULT 9
                                                                                                                                                                                          ADB91675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABZ71190-ABZ71478 represent CDNAs corresponding to 178 human secreted

Drotein genes, and ABP00011-ABP00299 represent the proteins they encode.

ABZ71479-ABZ714540 represent human secreted protein genomic fragments. The
invention also encompasses antibodies specific for the secreted proteins,

the use of the secreted proteins in drug screening, and recombinant

certains and host cells comprising a nucleic acid of the invention. The
secreted proteins, nucleic acids encoding them, antibodies or antibody

fragments specific for the secreted proteins, and modulators of protein

certivity are useful for diagnosing, treating, ameliorating or preventing
digestive disorders. Such conditions include disorders of protein

cesophagus, stomach, small intestine, large intestine, liver, biliary

tract and pancreas, and include cancers of these organs and tissues. The
secreted proteins and their nucleic acids may also be used in the

treatment of immune disorders, inflammation, infection,

hyperproliferative disorders, and to promote wound healing. Nucleic acids

of the invention may be used for chromosome identification, chromosome

mapping, in gene therapy, for identifying individuals from minute

biological samples, as hybridisation probes, and as molecular weight

anxiers.
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                                                                                                                                                                                                                                                                                                 Human; secreted protein; digestive disorder; gastrointestinal disorder; mouth; oesophagus; stomach; small intestine; large intestine; liver; billary tract; pancreas; cancer; tumour; hyperproliferative disorder; immune disorder; inflammation; infection; wound healing; drug screening; chromosome identification; chromosome mapping; cytostatic; antiinflammatory; immunosuppressive; vulnerary; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human secreted proteins and nucleic acids, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating e.g. gastrointestinal diseases and disorders, or cancers.
                                                            Gaps
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                                                                                                                                                                                                                                                                        Human gene 165 encoded secreted protein HTELS08, SEQ ID NO:464.
                            100.0%; Score 81; DB 6; Length 158; 100.0%; Pred. No. 9.5e-05; .ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; Page 1048; 1216pp; English.
                                                                                                                                                                                  ABR00175 standard; protein; 158 AA
                                                                                    1 MALEVLMLLAVLIWTGA 17
                                                                                                       1 MALEVLMLLAVLIWTGA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAR-2002; 2002WO-US008276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                            (first entry)
                                         Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-029900/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ABZ71354.
Sequence 158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                               WO200276488-A1.
                                                                                                                                                                                                                                                                                                                                                                                                    Ното варіеля
                                                                                                                                                                                                                                          03-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-OCT-2002
                                                                                                                                                                                                              ABR00175;
                             Query Match
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                                            Best Loc
Matches
                                                                                                                                                        RESULT 8
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The invention relates to isolated nucleic acid molecules ADB91065-
ADB91448 and ADB91815-ADB91911 encoding human secreted proteins ADB91449-
ADB91448 and ADB91815-ADB91911 encoding human secreted proteins ADB91449-
CADB91834. Also disclosed is a recombinant vector comprising a
polymucleotide of the invention, and a recombinant host cell comprising
the recombinant vector. The polypeptide of the invention is useful in
the recombinant vector. The polypeptide of the invention is useful in
the recombinant vector. The polypeptide of the invention is useful in
decreases activity of the polypeptide. The bolypeptide, polymucleotide,
antibody or its fragment, agonist or antagonist are useful for preparing
a pharmaceutical composition for diagnosing or treating diabetes or
conditions related to diabetes. The present sequence is that of the human
immunoglobulin Fc portion used to generate fusion proteins, increasing
the stability of the fused protein as compared to the secreted protein
conly. Note: The sequence data for this patent did not form part of the
printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pot_sequences.
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                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Secreted protein; gene therapy; antidiabetic; diabetes; human.
         Length 158;
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                                                                    Indels
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100.0%; Score 81; DB 6; L. 100.0%; Pred. No. 9.5e-05; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein #SEQ ID 621.
                                                                                                                                                                                                                                                                                                                                                 ADB91675 standard; protein; 158 AA.
                                                                                                                                                                1 MALEVIMILAVLIWIGA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                 17; Conservative
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Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruben SM;
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Query Match
Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-DEC-2003
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Gaps

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Mismatches

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17; Conservative

Matches

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The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel polypeptides. Also claimed its a polypeptide encoded by the polynucleotide, an antibody binding to the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide with the antibody of the encoded proctein, and observing the binding between the two, a transformant carrying the polypeptide or peptide with the antibody of the encoded proctein, and observing the binding between the two, a transformant carrying the polynucleotide in an expressible manner and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesising the polynucleotide, or as a probe for detecting the polynucleotides and encoded proteins are useful as pharmaceutical agents and many diseaser-related proteins are useful as paramaceutical agents and many diseaser-related proteins for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell regeneration. Membrane proteins, disease-related proteins and genes encoding them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours. The colly, and genes are concern, tumours. The colly, and second is the activity or expression of the encoded protein to treat diseases. The account of the activity or expression of the invention. Note: Some of the concern of the activity or expression of the invention. Our brained for the activity or expression of the invention. Our brained for the activity or expression of the invention. Our brained for the activity or expression of the invention. Our brained brained for the activity or expression of the invention. Our brained for the activity or expression of the invention. Our brained for the activity or expression of the invention of t
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Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                          Human, pharmaceutical, diagnostic, gene therapy, tissue regeneration,
cell regeneration, membrane protein, signal transduction-related protein,
transcription-related protein, osteoporosis, neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 81; DB 7; Length 158; 100.0%; Pred. No. 9.5e-05;
                                                                                                                                                                                                                                                                                                                           Human protein encoded by clone TESTI20282420.
ADB65520 standard; protein; 158 AA.
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-MAR-2002; 2002EP-00007401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-NOV-2001; 2001JP-00379298.
25-JAN-2002; 2002US-00350978.
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                                                                                                                                                                                                                (first entry)
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Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP1308459-A2.
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                                                                                                                                                                                                                04-DEC-2003
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                                                                                                          ADB65520;
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Best Local Similarity

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The invention relates to a novel human secreted polypeptide comprising a defined sequence given in the specification. The polypeptide, nucleic acid molecule, antibody, agonist or anisagonist of the invention may be useful for preparing a composition for diagnosing or treating a hemopoietic or haematologic disorder such as anaemia, autoimmune disorders such as rheumatold arthitis; inflammation, Grave's disease, diabetes, systemic lupus erythematosus or gloomerulonephritis, eurodegenerative disorders including Parkinson's disease and Alzheimer's atherosclerosis or cancer, as well as bacterial, viral, fungal or parasitic infections. The polypeptide may also be used during gene the polypeptide with a binding partner and determining whether the binding partner increases or decreases the activity of the polypeptide. The current sequence is that of the human secreted protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human secreted polypeptide for diagnosing, preventing or treating hematopoietic or hematologic disorders (e.g. anemia), autoimmune disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or atherosclerosis).
                                                                                                                                                                                                                                                                                  antianaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;
                                                                                                                                                                                                                                                                                                 antidiabetic, immunosuppressive, dermatological; nephrotropic; antidabetic, immunosuppressive, dermatologic, antibacterial; virucide, fungicide; antiparasitic; antiarteriosclerotic; vulnerary; cytostatic; haemopoietic; haematologic, anaemia, autoimmune disorder; rheumatoid arthritis; inflammation; Grave's disease; diabetes; systemic lupus erythematosus; glomerulonephritis; neurodegenerative; Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis; cancer; bacterial; viral; fungal; parasitic infection; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 16; SEQ ID NO 971; 2272pp; English.
                                                                                                                                                                                                                                              Human secreted protein - SEQ ID 971.
                                                                                                                                  ADC74338 standard; protein; 158 AA.
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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                   1 MALEVIMILIAVLIWIGA
MALEVIMILIAVLIWTGA
                                                                                                                                                                                                             01-JAN-2004 (first entry)
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N-PSDB; ADC73723.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                     ADC74338;
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                                                                                              RESULT 11
                                                                                                                ADC74338
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ADX40751 standard; protein; 80 AA.

(first entry)

21-APR-2005

ADX40751;

Human immunodeficiency virus.

WO2005012502-A2

10-FEB-2005.

Immune stimulation; Vpu.

HIV Vpu protein #160.

29-MAR-2004; 2004WO-US009510.

28-MAR-2003; 2003US-0458026P.

(EPIM-) EPIMMUNE INC

1 MALEVLMLLAVLIWTGA 17

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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequences ABB38121-B38396 represent the amino acid sequences of 62 human secreted proteins encoded by the genes AAC69512-C69587. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the ucidanosis, treatment and prevention of: (a) autoimmune disease e.g. rheumatoid arthritis; (b) hyperproliferative disorders e.g. cardiac arrest; (c) cardiovascular disorders e.g. cardiac arrest; (d) crebrovascular disorders e.g. cardiac arrest; (f) nervous system disorders e.g. cerbral inschemia; (e) andiogenesis; (f) nervous system disorders e.g. Allaheimer's disease; (g) infections caused by bacteria, viruses and fungi; and (h) ocular disorders e.g. cardiac arresting call cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid molecules encoding 62 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
                                                                                                                                                                                                                                                                               Immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytoëtatic; cardiant; vasotropic; cerebroprotective; neuroprotective; nootropic; antibacterial; virucide; fungicide; opthalmalogical; human; vulnerary; gene therapy; infection; secreted protein.
                                 Gaps
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Birse CE;
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Query Match 100.0%; Score 81; DB 7; Length 158; Best Local Similarity 100.0%; Pred. No. 9.5e-05; Matches 17; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Score 81; DB 3; Length 159;
Best Local Similarity 100.0%; Pred. No. 9.5e-05;
Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen CA, Soppet DR,
Florence KA, Moore PA,
                                                                                                                                                                                                                                                     Human secreted protein encoded by gene 17 clone HTELS08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 608-609; 716pp; English.
                                                                                                                                                            AAB38337 standard; protein; 159 AA.
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Olsen HS, Ebner R,
                                                          1 MALEVLMLLAVLIWTGA 17
                                                                                    1 MALEVLMLLAVLIWTCA 17
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99US-0130991P.
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                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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26-APR-1999;
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Lafleur DW,
                                                                                                                                                                                                                                                                                                                                                                                                                    19-0CT-2000
                                                                                                                                                                                         AAB38337;
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Newman MJ

Sette A,

Chesnut RW,

Livingston BD,

Baker DM,

WPI; 2005-132661/14.

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                                                                                                                                              The invention relates to a method of identifying a candidate peptide epitope which induces an HLA class I CTL response against variants of the peptide epitope. comprising identifying, from a particular antispen of an infectious agent, variants of a peptide epitope comprising primary anchor residues of the same HLA class I binding motif. The method is useful for identifying a candidate peptide epitope, which induces an HLA class I CTL response against variants of the peptide epitope. This sequence represents an HIV Vpu protein used in the scope of the invention.
Identifying a candidate peptide epitope, which induces a HLA class I CTL response comprises identifying variants of a peptide epitope 8-11 amino acids in length comprising primary anchor residues of the same HLA class I binding motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                          Score 46; DB 9; Length 80;
Pred. No. 14;
6; Mismatches 2; Indels
                                                                                                             Disclosure; Page 364-369; 458pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADX40648 standard; protein; 80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                    , 9
                                                                                                                                                                                                                                                                                                                                                                                      56.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MALEVLMLLAVLIWT 15
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                                                                                                                                                                                                                                                                                                                                                                      9 VALVVALILAIIVWT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIV Vpu protein #57.
                                                                                                                                                                                                                                                                                                                                                  Sequence 80 AA;
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Gaps

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Query Match
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                                                                                                                                                                                                                                                                          The invention relates to a method of identifying a candidate peptide epitope which induces an HLA class I CTL response against variants of the peptide epitope, comprising identifying, from a particular antigen of an infectious agent, variants of a peptide epitope comprising primary anchor residues of the same HLA class I binding motif. The method is useful for Identifying a candidate peptide epitope, which induces an HLA class I CTL response against variants of the peptide epitope. This sequence represents an HLV Vpu protein used in the scope of the invention.
                                                                                                                                                                                               response comprises identifying variants of a peptide epitope 8-11 amino acids in length comprising primary anchor residues of the same HLA class I binding motif.
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                                                                                                                                                                                    Identifying a candidate peptide epitope, which induces a HLA class I CTL
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                                                                                                                                 Newman MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                            55.6%; Score 45; DB 9; Length 80; 40.0%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                 Sette A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Mismatches
                                                                                                                                                                                                                                                     Disclosure; Page 362-368; 458pp; English.
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                                                                                                                                Chesnut RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADX40735 standard; protein; 81 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAR-2004; 2004WO-US009510.
                                                    29-MAR-2004; 2004WO-US009510
                                                                           28-MAR-2003; 2003US-0458026P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | | | | : : : | | | 10 VALVVVLIIAIVVWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immune stimulation; Vpu.
                                                                                                                                Livingston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIV Vpu protein #144.
                                                                                                       (EPIM-) EPIMMUNE INC.
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                                                                                                                                                         WPI; 2005-132661/14.
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Best Local Similarity
WO2005012502-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2005012502-A2
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 80 AA;
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                                                                                                                                 Baker DM,
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PS Disclosure; Page 364-369; 458pp; English.

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CC The invention relates to a method of identifying a candidate peptide comprising identifying, from a particular antigen of an CC infectious agent, variants of a peptide epitope comprising primary anchor cc residues of the same HLA class I Dinding motif. The method is useful for identifying a candidate peptide epitope, which induces an HLA class I CTL CC response against variants of the peptide epitope. This sequence CC response against variants of the peptide epitope. This sequence CC represents an HLV Vpu protein used in the scope of the invention.

XX
SQ Sequence 81 AA;

Query Match

Best Local Similarity 46.7%; Pred. No. 20;

Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MALEVLMILAVLWT 24

Db 10 VALVVALILAIVWT 24

Search completed: May 9, 2006, 10:15:16

Job time: 12.7 secs
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36424, A 51641, A 12693, A 8218, Ap 23230, A 17311, A 2300, Ap

92, Appl 90, Appl

9667, FP 10023, A 2, Appli 9813, Ap 59, App 158, App 159, App 18, App

Sequence:

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Sequence Seq
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US-09-621-976-3903

Sequence 3903, Application US/09621976

Patent No. 6629063

GENERAL INFORMATION:

APPLICANT: Dunas Milne Edwards, J.B.

APPLICANT: Glordano, J.Y.

TITLE REPERENCE: GENSET.054PR2

CURRENT APPLICATION: BSTS and Encoded Human Proteins.

TILE REFERENCE: GENSET.054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 3903
US-09-270-76-51641

US-09-489-039A-12693

US-09-489-039A-12693

US-09-252-991A-23230

US-09-252-991A-23230

US-10-104-047-2300

US-09-602-777A-92

US-09-602-777A-92

US-09-489-039A-10023

US-09-489-039A-10023

US-09-489-039A-10023

US-09-489-039A-10023

US-09-489-039A-10023

US-09-489-039A-10023

US-09-489-039A-10023

US-09-489-039A-188

US-10-290-579A-158

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US-10-290-579A-159
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APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 5223, Application US/09621976; Patent No. 6639063; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
      US-09-621-976-5223
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LENGTH: 106
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                               GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-09-621-976-5222

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US-10-290-579A-248

US-09-328-352-5855

US-09-004-502-1

US-10-290-579A-166

US-10-290-579A-166

US-10-290-579A-166

US-10-290-579A-171

US-10-290-579A-171

US-10-290-579A-14283

US-10-290-579A-14283

US-10-290-579A-157

US-10-290-579A-169

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Maximum Match 100%
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                                                                           100.0%; Score 81; DB 2; Length 153; 100.0%; Pred. No. 9.4e-06; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR.
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5222
LENGTH: 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3674, Application US/10104047
; Sequence 3674, Application US/10104047
; Patent No. 69432416;
; TITER PERENCE: HISTION: No. 694324161 full length cDNA;
; TITER PERENCE: HISTON: NO. 694324161 full length cDNA;
; TITER PERENCE: HISTON: NO. 694324161 full length cDNA;
; CURRENT FILING DATE: 2002-03-25
; CURRENT FILING DATE: 2002-03-25
; RIGHT APPLICATION NUMBER: ; PRIOR RELIGHED DOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 81; DB 2; Le Best Local Similarity 100.0%; Pred. No. 9.7e-06; Matches 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 81, DB 2, I
Best Local Similarity 100.0%; Pred. No. 9.7e-06;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                  Sequence 5222, Application US/09621976 Patent No. 6539063 Patent No. 6539063 Patent APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MALEVIMILAVLIWTGA 17
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                                                                     Query Match
Best Local Similarity 100.0
Matches 17; Conservative
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; ORGANISM: Homo sapiens
US-10-104-047-3674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
; NAME/KEY: SIGNAL
; LOCATION: -17..-1
US-09-621-976-3903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , LOCATION: -17..-1
US-09-621-976-5222
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                                                                                                                                                                                                                                                                                    US-09-621-976-5222
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Sequence 20455, Application US/0925291A

Sequence 20455, Application US/0925291A

Patent No. 655175

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

RIOR APPLICATION NUMBER: US 60/094,190

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 20495

FENTILIAND CASE OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (15),(28),(61); CTHER INFORMATION: Identity of amino acid at the above locations are unknown. US-09-252-991A-20495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
US-10-290-579A-165
US-10-290-579A-165
Sequence 165, Application US/10290579A
Patent No. 6897301
GENERAL INFORMATION:
APPLICANT: Hahn, Beatrice
APPLICANT: Gao, Fenge
APPLICANT: Shaw, George
TITLE OF INVENTION: CLONES AND SEQUENCES FOR NON-SUBTYPE B ISOLATES OF HUMAN
TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS TYPE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: isolate=94IN476.104; gene=vpu
US-10-290-579A-165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44; DB 2;
Pred. No. 1.8;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.6%; Score 45; DB 2; 66.7%; Pred. No. 30; iive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/290,579A CURRENT FILING DATE: 2002-11-08 PRIOR APPLICATION NUMBER: US 09/184,418 PRIOR FILING DATE: 1999-11-02 NUMBER OF SEQ ID NOS: 270 SEQ ID NO 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
US-10-290-579A-248
; Sequence 248, Application US/10290579A
                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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149 ALLALVLLAVLAWLG 163
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ORGANISM: artificial sequence
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16 ALIVALILAIIVWT 29
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Best Local Similarity 50.0
Matches 7; Conservative
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Best Local Similarity
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22;
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GENERAL INCORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Caley, Nevi
APPLICANT: Corley, Nevi
TITLE OF INVENTION: HUMAN MEMBRANE RECYCLING
TITLE OF INVENTION: HUMAN MEMBRANE RECYCLING
TITLE OF INVENTION: HUMAN MEMBRANE RECYCLING
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                               COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,502
FILING DATE: Filed Herewith
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 36,749
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEROMMUNICATION INFORMATION:
TELERAM: 650-845-655
TELERAM: 247 amino acids
LUNFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/360,125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
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Pred. No. 2
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/004,502
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ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 347 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 60...
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LIBRARY: TONGTUT01
; CLONE: 980615
US-09-004-502-1
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COUNTRY:
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US-09-360-125-1
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Patent No. 656295
Batent No. 656295
GENERAL INFORMATION:
FAPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GT-99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5855
LENGTH: 180
         GENERAL INFORMATION:
APPLICANT: Hahn, Beatrice
APPLICANT: Gao, Fenda, Beatrice
APPLICANT: Shaw, George
TITLE OF INVENTION: CLONES AND SEQUENCES FOR NON-SUBTYPE B ISOLATES OF HUMAN
TITLE OF INVENTION: IMMUNODERICIENCY VIRUS TYPE 1
FILE REFERENCE: D6287D
CURRENT FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: US 99/184,418
PRIOR FILING DATE: 1999-11-02
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Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 54.3%; Score 44; DB 2; Length 86; Best Local Similarity 50.0%; Pred. No. 4.9; Matches 7; Conservative 5; Mismatches 2; Indels
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APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN MEMBRANE RECYCLING
TITLE OF REQUENCES: 5
CORRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: isolate=94IN476.104; gene=vpu
US-10-290-579A-248
                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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Patent No. 5962263
GENERAL INFORMATION:

    TYPE: PRT
    ORGANISM: Acinetobacter baumannii
US-09-328-352-5855

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Best Local Similarity 53.8%;
Matches 7; Conservative
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16 ALIVALILAIIVWT 29
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140 KVLILISLLIWSG 152
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                                                                                                                                                                                                                                                                          SEQ ID NO 248
LENGTH: 86
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Query Match
Best Local Similarity
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                                                                                                           FEATURE:
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; Sequence 166. Application US/10290579A
; Patent No. 6897301
; GENERAL INFORMATION:
; APPLICANT: Hahn, Beatrice
; APPLICANT: Shaw, George
; APPLICANT: Gao, Feng
; TITLE OF INVENTION: CLONES AND SEQUENCES FOR NON-SUBTYPE B ISOLATES OF HUMAN
; TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS TYPE 1
; FILE REFERENCE: D62870
; CURRENT APPLICATION NUMBER: US/10/290,579A
; CURRENT APPLICATION NUMBER: US 09/184,418
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 270
; SEQ ID NO 166
; LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hahn, Beatrice
APPLICANT: Gao, Feng
APPLICANT: Gao, Feng
APPLICANT: Shaw, George
TITLE OF INVENTION: CLONES AND SEQUENCES FOR NON-SUBTYPE B ISOLATES OF HUMAN
TITLE OF INVENTION: LIMMUNODEFICIENCY VIRUS TYPE 1
FILE REFERENCE: D6287D
CURRENT APPLICATION NUMBER: US/10/290,579A
CURRENT FILING DATE: 2002-11-08
PRIOR FILING DATE: 1999-11-02
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US-10-290-579A-166
                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
REGISTRATION NUMBER: 36,749
REFERENCE JOCKET NUMBER: PF-0456 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: 650-845-0555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TONOTUT01
CLONE: 980615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 245, Application US/10290579A Patent No. 6897301 GENERAL INFORMATION:
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50.0%;
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274 AVSVLMLLVALLFTG 288
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16 ALIVALLIAIVUWT 29
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Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 60.0
Matches 9; Conservative
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

APPLICANT: Gary Breton et. al

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US 60/117,747

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR PILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 13843

LENGTH: 547
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US-10-290-579A-171

Sequence 171, Application US/10290579A

Patent No. 6897301

GENERAL INFORMATION:

APPLICANT: Hahn, Beatrice

APPLICANT: Gao, Feng

TITLE OF INVENTION: CLOUBERCIENCY VIRUS TYPE 1

FILE REFRENCE: D62870

TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS TYPE 1

FURRENT FILING DATE: 2002-11-08

PRIOR PILICATION NUMBER: US 09/184,418

PRIOR FILING DATE: 1999-11-02

NUMBER OF SEQ ID NOS: 270

SEQ ID NO 171

LENGTH: 27

TYPE: PRI

SEQ ID NO 171

TYPE: REF
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Pred. No. 52;
6; Mismatches 3; Indels
                                                                                                                                                                                      Length 86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Consenus sequence of deduced Vpu gene US-10-290-579A-171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.9%; Score 42; DB 2; 50.0%; Pred. No. 3;
                                                                                                                                                                                        Score 43; DB 2;
Pred. No. 7.1;
                                                                                                                           ; OTHER INFORMATION: isolate=96ZM651.8; gene=vpu
US-10-290-579A-245
                                                                 TYPE: PRT ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13843, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Klebsiella pneumoniae US-09-489-039A-13843
                                                                                                                                                                                        53.1%;
50.0%;
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371 ALAALLVIVLMLWTG 385
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16 ALIVALLIAIVVWT 29
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Best Local Similarity 40.0.
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NUMBER OF SEQ ID NOS: 270
SEQ ID NO 245
LENGTH: 86
                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 7; Conserv
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RESULT 15
US-10-290-579A-168
i Sequence 168, Application US/10290579A
i Sequence 168, Application US/10290579A
i Patent No. 6897301
i GENERAL INFORMATION:
i APPLICANT: Hahn, Bearrice
i APPLICANT: Shaw, George
i TITLE OF INVENTION: CLONES AND SEQUENCES FOR NON-SUBTYPE B ISOLATES OF HUMAN
i TITLE OF INVENTION: LONES AND SEQUENCES FOR NON-SUBTYPE B ISOLATES OF HUMAN
i TITLE OF INVENTION: LONES AND SEQUENCES FOR NON-SUBTYPE B
i FILE REPERENCE: D62870
i CURRENT FILING DATE: 2022-11-08
i PRIOR APPLICATION NUMBER: US 09/184,418
i PRIOR PILING DATE: 1999-11-02
i NUMBER OF SEQ ID NOS: 270
i LENGTH: 28
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51.9%; Score 42; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 3.1;
Matches 6; Conservative 6; Mismatches 2; Indels
    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: artificial sequence
| FEATURE:
| NAME/KEX: Xaa=unknown | LOCATION: 5 | OTHER INFORMATION: Consenus sequence of deduced Vpu gene US-10-290-579A-168
  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: May 9, 2006, 10:17:43 Job time : 5.5 secs
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10 ALVVTFIIAVIWT 23
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11 ALVVALIIAIVVWT 24
7; Conservative
Matches
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TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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; LOCATION: -17...-1
US-09-731-872-265
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Sequence 4, Appli
Sequence 113, App
Sequence 3, Appli
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1860, Ap
974, App
34, Appl
61097, A
165, App
248, App
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464, App
251583,
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                                                                                                May 9, 2006, 10:15:27 ; Search time 7.4 Seconds (without alignments) 959.878 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 260, 7
Sequence 260, 7
Sequence 113, 7
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(cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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(cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
           GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-643-818-265
US-09-876-997-260
US-10-10-050-704-113
US-10-104-047-3674
US-10-104-047-3674
US-10-798-512-113
US-10-643-818-26
US-10-472-513-464
US-10-472-513-464
US-10-125-715-81583
US-10-125-761-11775
US-09-813-245-1860
US-10-115-57-14
US-10-115-1258
US-10-115-1175
US-10-118-97-34
US-11-118-597-16
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US-10-262-839-162
US-10-262-839-166
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US-09-790-852-5
US-10-262-839-164
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1 MALEVIAMILAVINTGA 17
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Maximum Match 100%
Listing first 45 summaries
                                                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Perfect score:
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No.
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Sequence 265 Application US/09731872

Patent No. US20020102604A1

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Bougneleret, Lydie

APPLICANT: Bougneleret, Lydie

APPLICANT: Bougneleret, Lydie

APPLICANT: Bougneleret, Severin

TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS

FILE REFERENCE: 78-US/09/731,872

CURRENT APPLICATION NUMBER: US/09/731,872

CURRENT FILING DATE: 1999-12-08

PRIOR APPLICATION NUMBER: US 60/169,629

PRIOR APPLICATION NUMBER: US 60/187,470

PRIOR APPLICATION NUMBER: US 60/187,470

PRIOR PELING DATE: 1999-12-08

SOFTWARE: Patent.pm

SEQ ID NO 265

LENGTHARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78.US4.CIP
CURRENT APPLICATION NUMBER: US/09/876,997
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/731,872
PRIOR FILING DATE: 2000-12-07
  Sequence 1745, Ap
Sequence 166, App
Sequence 314, App1
Sequence 11, App1
Sequence 29, App1
Sequence 29, App1
Sequence 35, App1
Sequence 46, App1
Sequence 78, App1
Sequence 78, App1
Sequence 78, App1
Sequence 1632, App1
Sequence 1632, App1
Sequence 8077, App1
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14947,
12205,
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Pred. No. 0.00011;
Mismatches 0; Indels
US-10-732-923-1745
US-11-135-597-166
US-10-945-115-344527
US-10-190-435-306
US-10-135-597-245
US-09-912-976-46
US-09-912-976-46
US-09-912-976-46
US-09-912-976-46
US-09-912-976-46
US-09-912-976-49
US-10-369-493-14391
US-10-369-493-14788
US-10-369-493-11685
US-10-369-493-11685
US-10-369-493-11685
US-10-369-493-11685
US-10-369-493-112205
                       -11-135-597-166
-10-425-115-344527
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Publication No. US20030152921A1
GENERAL INFORMATION:
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100.0%; Pre
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VS-09-08-76-997-260

Sequence 260, Application US/09876997

Publication No. US2030152921A1

Publication No. US2030152921A1

Publication No. US2030152921A1

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Bougueleret, Lydie

APPLICANT: Jobert, Severin

TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS

FILE REFERENCE: 78.045-CIP

CURRENT APPLICATION NUMBER: US/09/876,997

CURRENT FILING DATE: 2000-10-6-08

PRIOR FILING DATE: 2000-12-06

PRIOR FILING DATE: 2000-12-06

PRIOR FILING DATE: 1999-12-08

NUMBER OF SEQ ID NOS: 482

SOFTWARE: Patent.pm

SEQ ID NO 260

LENGTH: 158
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TITLE OF INVENTION: 62 Human Secreted Proteins
FILE REFERENCE: PZ039P1
CURRENT APPLICATION NUMBER: US/10/050,704
CURRENT FILING DATE: 2002-01-18
                        PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR FILING DATE: 1999-12-08
PRIOR PELICATION NUMBER: US 60/187,470
PRIOR PILING DATE: 2000-03-06
NUMBER OF SEQ ID NOS: 482
SOFTWARE: Patent.pm
SSOFTWARE: Patent.pm
LENGTH: 158
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         2000-12-07
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Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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         CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                     ; NAME/KEY: SIGNAL
; LOCATION: -17...1
US-09-731-872-260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: -17..-1
US-09-876-997-260
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US-10-050-704-113
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; Sequence 255, Application US/10643836
; Publication No. US20050096458A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bougueleret, US-10/643,836
; CURRENT APPLICATION NUMBER: US/10/643,836
; CURRENT PTLING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR PILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 265
; LENGTH: 106
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Patent No. US20020102604A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Bougueleret, Lydie
APPLICANT: Jobert, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78.US3.REG
CURRENT APPLICATION NUMBER: US/09/731,872
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PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR PILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 482
SOCTHARE: Patent.pm
SSOTHARE: Patent.pm
LENGTH: 106
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Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                          ; NAME/KEY: SIGNAL
; LOCATION: -17..-1
US-09-876-997-265
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; LOCATION: -17...1
US-10-643-836-265
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US-09-731-872-260
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Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 17; Conservative 0; Mismatches 0; Indels
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Publication No. US20040152164A1

GENERAL INPORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: 62 Human Secreted Proteins

FILE REPRENCE: PZ039P1

CURRENT APPLICATION NUMBER: US/10/798,512

CURRENT FILING DATE: 2004-03-12.

PRIOR APPLICATION NUMBER: US/09/684,524

PRIOR FILING DATE: 2000-04-06

PRIOR APPLICATION NUMBER: 60/128,693

PRIOR APPLICATION NUMBER: 60/128,693

PRIOR APPLICATION NUMBER: 60/128,693

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

NUMBER OF PRIOR FILING DATE: 1999-04-09

NUMBER OF PRIOR PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 5284076CD1
US-10-467-535-4
          PRIOR APPLICATION NUMBER: PCT/USO2/03715
PRIOR FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/268,111
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-23
PRIOR FILING DATE: 2001-02-3
PRIOR PILING DATE: 2001-03-08
PRIOR PILING DATE: 2001-03-08
PRIOR PILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PERL PROGram
SEQ ID NO 4
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Publication No. US20040235709A1
GENERAL INFORMATION:
APPLICANT: Salter-Cid, Luisa
APPLICANT: Ebbers-Reed, Dana
APPLICANT: Chicca, Barbara A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MALEVLMLLAVLIWTGA 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 158
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-467-046-3
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APPLICANT: SON, Craig H.; Lu, Yan
APPLICANT: BAUGHN, Mariah R.; ElloTT, Vicki S.
APPLICANT: BAUGHN, Mariah R.; ElloTT, Vicki S.
APPLICANT: TANG, Tom Y.; LAL, Preetl G.
APPLICANT: TANG, Tom Y.; LAL, Preetl G.
APPLICANT: TANG, Tom M.; BURRORD, Neil
APPLICANT: TANG, Tom M.; RICHARDSON, Thomas W.
APPLICANT: LU, Dyung Aina M.; RICHARDSON, Thomas W.
APPLICANT: TRAN, Uyen K.; KHARE, Reena
APPLICANT: CHAWIA, Narinder K.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
FILE REFERENCE: PPOGOJ USN
CURRENT APPLICATION NUMBER: US/10/467,535
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Publication No. US20030236392A1

GENERAL INFORMATION:

TITLE OF INVENTION: No. US20030236392Ae1

TITLE OF INVENTION: No. US20030236392Ae1

TITLE OF INVENTION: No. US20030236392Ae1

CURRENT APPLICATION NUMBER: US/10/104,047

CURRENT APPLICATION NUMBER:

NUMBER OF SEQ ID NOS: 4096

SOFTWARE PATENTIN VET. 2.1

SOFTWARE PATENTIN VET. 2.1

LENGTH: 158
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Pred. No. 0.00017;
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PRIOR APPLICATION NUMBER: 09/684,524
PRIOR FILING DATE: 2000-10-10
PRIOR PELLING DATE: 2000-04-06
PRIOR PILING DATE: 2000-04-06
PRIOR PELLING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-05
PRIOR PILING DATE: 1999-04-05
SEQ ID NOS: 344
SOFTWARE: PALENTIN VET. 2.0
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; Sequence 4, Application US/10467535
; Publication No. US20040146970A1
; GENERAL INFORMATION:
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Best Local Similarity 100.0%; Po
Matches 17; Conservative 0;
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Best Local Similarity 100.0
Matches 17; Conservative
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US-10-050-704-113
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US-10-104-047-3674
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US-10-472-533-464
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ORGANISM: Zea mays
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; Sequence 260, Application US/10643836
; Publication No. US20050096458A1
; GENERAL INFORMATION:
; APPLICANT: Dunas Milne Edwards, Jean Baptiste
; APPLICANT: Dunas Milne Edwards, Jean Baptiste
; APPLICANT: Jobert, Lydie
; APPLICANT: Jobert, Severin
; TILE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
; TILE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
; CURRENT APPLICATION NUMBER: US/10/643,836
; CURRENT FILING DATE: 2000-12-07
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 482
; SEQ ID NO 260
; LENGTH 1: 158
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APPLICANT: Chicca, John
APPLICANT: Yen-Potin, Frances
APPLICANT: Yen-Potin, Frances
APPLICANT: Bihain, Bernard
TITLE OF INVENTION: GSSP3 Polymucleotides and Polypeptides and Uses Thereof
FILE REFERENCE: G-102US03REG
CURRENT APPLICATION NUMBER: US/10/467,046
CURRENT APPLICATION NUMBER: US 60/266,156
PRIOR APPLICATION NUMBER: US 60/266,156
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
LENGTH: 158
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100.0%; Score 81; DB 5; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 17; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0
Matches 17; Conservative
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; LOCATION: (1)..(17)
US-10-467-046-3
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APPLICANT: In COURTY La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Applicant and Younghair and Younghair and Younghair and Younghair and Younghair Cao, Yongwai TITLE OF INVENTION: Plants
FITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 251583
LENGTH: 75
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Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 17; Conservative 0; Mismatches 0;
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TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS906CT
CURRENT APPLICATION NUMBER: US/10/472,533
CURRENT FILING DATE: 2003-09-20
PRIOR APPLICATION NUMBER: US 60/331,287
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 650
SOFTWARE: Patentin Ver. 2.0
LENGTH: 158
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKKHI, YOSHIYUKI
APPLICANT: BAKKHI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
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; Publication No. US20030119018A1
; GENERAL INFORMATION:
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Publication No. US20040010134A1
GENERAL INPORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REPERENCE: PF546FOT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PALOR OF SEQ ID NOS: 2267
SEQ ID NO 1859
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR PLING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 11775
LENGTH: 694
                                                                                                                                                                                                      TYPE: PRT ; ORGANISM: Streptomyces avermitilis US-10-156-761-11775
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; ORGANISM: Homo sapiens
US-09-833-245-1859
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Sequence 14, Appl Sequence 460, Appl Sequence 16, Appl Sequence 12650, A Sequence 12650, A

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1 US-11-087-719-73

1 US-11-087-719-75

1 US-11-087-719-71

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US-11-096-568A-12649
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100.0%; Pred. No. 1.2e-05;
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APPLICANT: Tanaka, Hiroaki
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
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Best Local Similarity 100.
Matches 17; Conservative
    TYPE: PRT
ORGANISM: Homo sapiens
    NAME/KEY: SIGNAL
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Perfect score:
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Result No.

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; Publication No. US20060084794A1
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: Albumin Fusion Proteins
; TITLE OF INVENTION: Albumin Fusion Proteins
; TITLE OF INVENTION: Albumin Fusion Proteins
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR PILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
; PRIOR FILING DATE: 2000-04-12
; PRIOR FILING DATE: 2000-04-21
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PALENTIN WENTER: 60/199, 384
; SOFTWARE: PALENTIN WENTER: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
                                                                                                                                                                                                                                                              5; Mismatches
                                                                                                                                                                        1 MALEVLMLLAVLIWTGA 17
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13 LAFFSLVLISVLLWTG 28
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13 LAFFSLVLISVLLWTG 28
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 50.0°
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Conservative
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US-11-264-096-1859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-11-264-096-1860
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Best Local Similarity
Matches 8; Conserv
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US-11-264-096-1860
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us-10-664-025-39

LOBERT: Jobert, Severin

APPLICANT: Glordano, Jean-Yves

TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins

FILE REFERENCE: G-081US03PCT

CURRENT APPLICATION NUMBER: US/10/475,075

CURRENT APPLICATION NUMBER: PCT/1801/00914

PRIOR PILING DATE: 2003-04-18

NUMBER OF SEQ ID NOS: 918

SEQ ID NO 788

LENGTH: 148

LENGTH: 148
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Pred. No. 1.3e-05;
Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SEKI, NACHIKO
APPLICANT: SEKI, NACHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: MAGNIKA, MOTOVUKI
APPLICANT: MAGNIKA, KENJI
APPLICANT: MAGNICA, KENJI
APPLICANT: MAGNICA, KENJI
APPLICANT: MAGNICA, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REPERENCE: 084335-0191
CURRENT PEPLICATION NUMBER: US 60/350,978
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR PILING DATE: 2001-11-05
NUMBER OF SEQ 1D NOS: 4096
SOFTWARE: PATCHIN VET. 2.1
SEQ 1D NO 3674
LENGTH: 158
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100.0%; Score 81; DB
Best Local Similarity 100.0%; Pred. No. 1.3
Matches 17; Conservative 0; Mismatches
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Publication No. US20060029945A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISONO, YUUKO
APPLICANT: ISONO, YUUKO
APPLICANT: HOO, YUKO
APPLICANT: HOO, YUKO
APPLICANT: HOO, YUKO
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NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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; LOCATION: -17..-1
US-10-475-075-788
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RESULT 6
US-11-098-686-10809
i Sequence 10809, Application US/11098686
j Publication No. US20060024696A1
i GENERAL INFORMATION:
APPLICANT: Kapur, Vivek and Gebhart, Connie J.
TITLE OF INVENTION: RROM LAWSONIA INTRACELLULARIS SEQUENCES
TITLE OF INVENTION: RROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
FILE REFERENCE: 09531-128001
CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR FILING DATE: 2003-10-01
PRIOR FILING DATE: 2003-10-04
NUMBER OF SEQ ID NOS: 11433
SOFTWARE: FESTESQ for Windows Version 4.0
SEQ ID NO 10809
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APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
ITILE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT PILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR PILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 1379
LENGTH: 247
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Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STARHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45; DB : Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Mismatches
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Publication No. US20050255114A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10809
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Best Local Similarity 60.07
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US-10-821-234-1379
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Best Local Similarity
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US-11-079-463-9820
Sequence 9820, Application US/11079463
Sequence 9820, Application US/11079463
Sequence 9820, US-120060073161A1
Sequence 9820, US-120060073161A1
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FR.
TITLE OF INVENTION: VOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: US/120
CURRENT APPLICATION NUMBER: US/11/079,463
CURRENT APPLICATION NUMBER: US/11/079,463
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2000-04-04
PRIOR FILING DATE: 2000-04-04
NUMBER: OF SEQ ID NOS: 10444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 467;
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Publication No. US20060075522A1

GENERAL INFORMATION:

APPLICANT: Abad, Mark S. et al.

TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT

FILE REFRENCE: 38-21(5452)B

CURRENT APPLICATION NUMBER: US/11/188,298

CURRENT APPLICATION NUMBER: 05/592,978

PRIOR RILING DATE: 2004-07-31

PRIOR FILING DATE: 2004-07-31

NUMBER OF SEQ ID NOS: 22569
                                                                                                                                                                                                                                                                                                                      Score 41; DB 9; Length 329;
Pred. No. 38;
4; Mismatches 0; Indels
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Pred. No. 54;
4; Mismatches 0;
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CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION WUMBER: 60/164,258
PRIOR FILING DATE: 1990-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 1942
LENGTH: 329
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                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 60.0
Matches 6; Conservative
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253 LLIMAILIWT 262
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Best Local Similarity
Matches 6; Conserv
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US-11-188-298-3902
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LENGTH: 547
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AFPLICANI: Gashad, Ference

TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REFERENCE: 21402-251

CURRENT APPLICATION NUMBER: 00/262,892

PRIOR APPLICATION NUMBER: 00/262,892

PRIOR PILING DATE: 2001-01-9

PRIOR FILING DATE: 2001-01-9

PRIOR PILING DATE: 2001-01-24

PRIOR PILING DATE: 2001-01-24

PRIOR APPLICATION NUMBER: 60/264,117

PRIOR APPLICATION NUMBER: 60/264,117

PRIOR PILING DATE: 2001-01-24

PRIOR PILING DATE: 2001-01-24

PRIOR PILING DATE: 2001-01-25

PRIOR PILING DATE: 2001-01-26

PRIOR PILING DATE: 2001-01-14

PRIOR PILING DATE: 2001-01-14
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NUMBER OF SEQ ID NOS: 512
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Pred. No. 86;
2; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53452)B
CURRENT APPLICATION NUMBER: US/11/188,298
CURRENT FILING DATE: 2005-07-22
PRIOR PELLING DATE: 2004-07-31
NUMBER OF SEQ ID NOS: 22569
SEQ ID NO 15594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-11-188-298-15594
; Sequence 15594, Application US/11188298
; Publication No. US2060075522A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MALEVLMLLAVLIWT 15
                     Shenoy, Suresh
Li, Li
Casman, Stacie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 52.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
, ORGANISM: Vibrio cholerae
US-11-188-298-15594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Mus musculus
US-10-055-877-234
       Pena, Carol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                JULIOLANT: Hybrigenics
TITLE OF INVENTION: Protein-protein interactions in Human Immunodeficiency Virus
FILE REFERENCE: B555AA
CURRENT APPLICATION NUMBER: US/10/853,807A
CURRENT FILING DATE: 2004-05-26
PRIOR APPLICATION NUMBER: US 60/333,346
PRIOR APPLICATION NUMBER: US 60/333,346
PRIOR APPLICATION NUMBER: US 60/335,132
PRIOR PILING DATE: 2002-11-26
PRIOR PILING DATE: 2002-05-31
PRIOR PILING DATE: 2002-05-31
PRIOR PILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 132
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 81
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                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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Query Match 50.6%; Score 41; DB 11; Length 547; Best Local Similarity 37.5%; Pred. No. 63; Matches 6; Conservative 6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 49.4%; Score 40; DB 9; Length 81; Best Local Similarity 40.0%; Pred. No. 14; Matches 6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Translation of SEQ ID No7
                                                                                                                                                                                                                               US-10-853-807A-14
, Sequence 14, Application US/10853807A
; Publication No. US20060034860A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 234, Application US/10055877
Publication No. US20050288241A1
GENERAL INFORMATION:
APPLICANT: DeCristofaro, Marc
APPLICANT: Padigaru, Muralidhara
APPLICANT: Miller, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shimkets, Richard
Gusev, Vladimir
Vernet, Corine
Taupier Jr., Raymond
                                                                                                                         463 LSIQTIMLYIVLMWIG 478
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Zhong, Mei
Anderson, David
Ballinger, Robert
Gerlach, Valerie
Spytek, Kimberly
Ratelli, Luca
Kekuda, Ramesh
Guo, Xiaojia
Zerhusen, Bryan
Andrew, David
                                                                                          1 MALEVLMILAVLIWTG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patturajan, Meera
Burgess, Cahterine
Eisen, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baumgartner, Jason
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MALEVLMLLAVLIWT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
US-10-055-877-234
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PRIOR APPLICATION NUMBER: DE 19932127.2
PRIOR PELICATION NUMBER: DE 19932127.2
PRIOR PELICATION NUMBER: DE 19932128.0
PRIOR PELICATION NUMBER: DE 19932129.9
PRIOR FILING DATE: 1999-07-19
PRIOR FILING DATE: 1999-07-19
PRIOR PILING DATE: 1999-07-19
PRIOR PILING DATE: 1999-07-19
PRIOR PLING DATE: 1999-07-14
PRIOR PILING DATE: 1999-07-14
PRIOR FILING DATE: 1999-07-14
PRIOR PLING DATE: 1999-07-14
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Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-454-437-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: May 9, 2006, 10:17:28 Job time : 2.2 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: OTGURA, KAORU
APPLICANT: NAGAI, KEJICHI
APPLICANT: NAGAI, KEJICHI
APPLICANT: TAMECHIKA, TCHIRO
APPLICANT: TAMECHIKA, TCHIRO
APPLICANT: SEKI, NAOHIKO
APPLICANT: SCHIKAMA, TSUTOMU
APPLICANT: OTGURA, MOTOVUKI
APPLICANT: OTGURA, MOTOVUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGHARI, KENJI
APPLICANT: NAGHARI, KENJI
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2005-03-07
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOCTWARE: PALENTIN VET. 2.1
SOCTWARE: PALENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                            Sequence 2300, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
                                                                                                                                                                                   APPLICANT: 1SOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | || | || |:|
95 MRLEALSLLHTLVW 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -10-454-437-92
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Sequence 92, Aprication US/10454437

Publication No. US20050277115A1

GENERAL INFORMATION:

APPLICANT: Pompejus, Markus

APPLICANT: Schroder, Hartwig

APPLICANT: Schroder, Hartwig

APPLICANT: APPLICANT: Calder, Oskar

APPLICANT: APPLICANT: Alberhauer, Gregor

ITITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS

ITITLE OF INVENTION: LANGOLUED IN HOMEOSTASIS AND ADAPTATION

FILE REFERENCE: BGI-128CPCN

CURRENT APPLICATION NUMBER: US/10/454,437

CURRENT APPLICATION NUMBER: US 60,141031

PRIOR PLING DATE: 1999-07-08

PRIOR FILING DATE: 1999-07-08

PRIOR PLING DATE: 1999-07-09

PRIOR FILING DATE: 1999-07-09

PRIOR PLING DATE: 1999-07-09

PRIOR FILING DATE: 1999-07-09

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9, 2006, 10:13:22; Search time 1.9 Seconds (without alignments) 860.887 Million cell updates/sec
GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                             OM protein - protein search, using sw model
                                                                                                                                                                      Run on:
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US-10-664-025-3903_COPY_1_17 81 1 MALEVLMLLAVLIWTGA 17 BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Scoring table: Sequence:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100% 1: pirl: * 2: pir2: * 3: pir3: * 4: pir4: * PIR_80:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

conserved hypothet	sensor histidine k	cytochrome-c oxida	FixI2 E1-E2 type c	vpu protein - huma	hypothetical prote	hypothetical prote	hypothetical prote	stage V sporulatio	conserved hypothet	hypothetical prote	probable glutathio	glutathione-regula	ATP-binding protei	proline dehydrogen	hypothetical prote
AE3201	E82176	E69609	E95302	G44001	F83105	C83632	H71568	SZBSE	C81722	H83104	A82256	JC5652	AG2455	T28435	T20664
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303	462	622	755	81	245	264	363	366	367	487	528	528	615	1127	294
9.05	50.6	50.6	50.6	49.4	49.4	49.4	49.4	49.4	49.4	49.4	49.4	49.4	49.4	49.4	48.8
41	41	41	41	40	40	40	40	40	40	40	40	40	40	40	39.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	· E HIVE	•	
	LTOSHY	Т.	
	H69148		
	hypothet	hypothetical protein MTH378 - Methanobacterium thermoautotrophicum (strain Delta H)	noautotrophicum (strain Delta H)
	C;Specie	C; Species: Methanobacterium thermoautotrophicum	•
	C, Date:	C;Date: 05-Dec-1997 #sequence revision 05-Dec-1997 #text change 09-Jul-2004	text change 09-Jul-2004
	C, Accese	C;Accession: H69148	
	R;Smith,	R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;	; Lee, H.; Dubois, J.; Aldredge, T.;
	, Qiu, I	D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wi	erzbowski, J.; Gibson, R.; Jiwani, N
	ki, S.;	Church, G.M.; Daniels, C.J.; Mao, J.; Rice,	P.; Noelling, J.; Reeve, J.N.
	J. Bacte	eriol. 179, 7135-7155, 1997	
	A;Title:	A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func	um thermoautotrophicum Delta H: func
	A;Refere	A; Reference number: A69000; MUID: 98037514; PMID: 9371463	1463
	A; Access	A,Accession: H69148	
	A;Status	A; Status: preliminary; nucleic acid sequence not shown; translation not shown	own; translation not shown
	A; Molecu	A; Molecule type: DNA	•
	A;Residu	A;Residues: 1-334 <mth></mth>	
	A;Cross-	A; Cross-references: UNIPROT: 026478; UNIPARC: UP100001396F5; GB: AE000823; GB: AE000666; NI	1396F5; GB:AE000823; GB:AE000666; NI
	A, Experi	A;Experimental source: strain Delta H	
	C;Genetics:	ics:	
	A;Gene: MTH378	MTH378	
	C;Superf	C, Superfamily: conserved hypothetical protein MTH887	
	Ouery	Match 61.7%; Score 50; DB 2;	Length 334;
	Best I	Best Local Similarity 53.3%; Pred. No. 3.5;	
	Matches	8; Conservative 5; Mismatches	2; Indels 0; Gaps 0;
	ò	2 ALEVIMILAVIIWTG 16	
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11 ALSILLILALIWMG 25 g

hypothetical protein 274 - Rhodobacter capsulatus
L;Species Rhodobacter capsulatus
C;Species Rhodobacter capsulatus
C;Species Rhodobacter capsulatus
C;Accession: S17804
C;Accession: S17804
S;Burke, D.H.; Alberti, M.; Armstrong, G.A.; Hearst, J.E.
submitted to the EMBL Data Library, November 1991
A;Pescription: The complete nucleotide sequence of the 46 kb photosynthesis gene cluste
A;Reference number: S17803
A;Reference number: L274 ckmb>
A;Residues: 1-274 ckmb>
A;Residues: 1-274 ckmb>
A;Cosssion: S17804
A;Cossion: S17804
A;Cosssion: S17804
A;Cosssion: S17804
A;Cosssion: S17804
A;Cosssion: S17804
A;Cosssion: S17804
A;Cossion: S17804
A;Cossi 58.0%; Score 47; DB 2; 57.1%; Pred. No. 8.3; iive 3; Mismatches Query Match
Best Local Similarity 57.1
Matches 8; Conservative nitrogen fixation nitrogen fixation conserved hypothet multidrug-efflux t threonine-serine p threonine-serine p threonine-serine p iron (II) transpor vpu protein - huma
hypothetical prote probable receptor-

3 LEVLMLLAVLIWTG 16

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hypothetical

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Gaps

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Length 274; 3; Indels

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DB 2;
30;
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Pred. No. 28;
                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: yfnI
C;Superfamily: membrane sulfatase, HI1246 type
                                           Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: translated from GB/EMBL/DDBJ
                                           55.6%;
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52 ALLALVLLAVLAWLG 66
                                                                                                                                                                                                            2 ALEVIMILAVLIWIG 16
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LDIIILIAVLIW 152
                                                                                                                              10; Conservative
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                                       Query Match
Best Local Similarity
Matches 10; Conserv
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NiAtternate names: hypothetical protein G1895
Cispeciae: Saccharomyces crevisiae
Cispeciae: Saccharomyces crevisiae
Cispeciae: Saccharomyces crevision 19-Apr-1996 #text_change 09-Jul-2004
Cispeciae: Saccharomyces crevision 19-Apr-1996 #text_change 09-Jul-2004
Cispeciae: Sachai; S64163; S64165
Rijames, C.M.; Indge, K.J.; Oliver, S.G.
Yeast 11, 1413-1419, 1995
A;Fille: DNA sequence nallysis of a 35 kb segment from Saccharomyces crevisiae chromosc
A;Reference number: S60417; MUD:96158061; PMID:855324
A;Reference number: S60418
A;Reference number: S60419
A;Reference number: S60418
A;Reference number: S64183
A;Reference number: S64185
A;Reference numbe
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ALLYVLSLALLIWTGS 20
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Conserved hypothetical protein yfnI - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Decorporation os-Dec-1997 #text_change O5-Oct-2004
C;Accession: D69815
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Broni, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch.
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler,
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Levine, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Scanlon,
A;Authors: Schlaich, S.; Sumatein, E.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Tamaka, T.; Terpstra, P.; Tosato, V.; Uchiyama,
A;Authors: Yoshikawa, H.F.; Zumatein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: Acosso; Muld. Anders. Acosso; Muld. Anders. Acosso; M.; Aller, M.; A
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A;Residues: 1-347 <WIN>
A;Cross-references: UNIPROT: 014828; UNIPARC: UPI00001696B1; EMBL: AF023268; NID: 92564910;
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A;Introns: 22/3; 48/3; 89/3; 130/1; 173/1; 226/2; 260/2; 299/3
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Pred. No. 34;
5; Mismatches
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A;Cross-references: UNIPROT:O44587; UNIPARC:UP10000079AF2; EMBL:AF039044; PIDN:AAC47948 B;Rxporimental source: strain Bristol N2; clone F48G7 C;Genetics: A;Gene: CESP:F48G7.8 A;Gene: CESP:F48G7.8 A;Map postition: 5 A;Map postition: 5 A;Introns: 55/1 C;Superfamily: Caenorhabditis elegans hypothetical protein F48G7.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Bscherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: G85850
R;Perna, M.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe'
iller, L.; Grobeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca
Nature 409, 529-533, 2001
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R;Blattner, F.R; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C. Science 277, 1455-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Title: The Complete genome sequence of Escherichia coli K-12.

A;Title: The F64981

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Reference number: A85480; MUD:21074935; PMID:11206551
A;Accession: G85850
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-203 <STO>
A;Esexidues: 1-203 <STO>
A;Cross-references: UNIPROT:QBXEC7; UNIPARC:UPIO000165866; GB:AE005174; NID:g12516443;
A;Experimental source: strain O157:H7, substrain EDL933
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Pred. No. 25;
4; Mismatches
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A;Cross-references: UNIPROT:Q8XEC7;
A;Experimental source: strain K-12,
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1 MLLRVVFLTFVILWAGA 17
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183 LVLEVLLALTVILW 196
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                                                                                                                                                                                                                                                                                       C. Accession: T01671
R.Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.
Cell 46, 63-74, 1986
A.Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isol A.Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isol A.Reference number: Z14389; MUID:86245056; PMID:2424612
A.Accession: T01671
A.Accession: T01671
A.Accession: T01671
A.Residue: preliminary; translated from GB/EMBL/DDBJ
A.Residues: 1-81 cALI>
A.Residues: 1-81 cALI>
A.Cross-references: UNIPARC:UPI000017865F; EMBL:K03456; NID:g328018
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                                                                                                                                                                                                                        vpu protein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vpu protein - human immunodeficiency virus type 1
C.Species: human immunodeficiency virus type 1, HIV-1
C.bate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
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C;Date: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 09-Jul-2004
C;Accession: T28742
R;Clarke, K.; Wohldmann, P.; Harrison, M.
submitted to the BMBL Data Library, January 1998
A;Description: The sequence of C. elegans cosmid F48G7.
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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RyCohen, B.A.; Terwilliger, B.P.; Sodroski, J.G.; Haseltine, W.A.
Nature 334, 532-534, 1988
A;Title: Identification of a protein encoded by the vpu gene of HIV-1.
A;Reference number: S06409; MUID:88302445; PMID:3043230
A;Accession: S06409
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  Indels
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A,Residues: 1-81 <COH>
A;Cross-references: UNIPROT:P05925; UNIPARC:UPI0000138D35
C;Superfamily: HIV-1 vpu protein
  3;
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A;Molecule type: DNA
A;Residues: 1-165 <CLA>
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Pred. No. 12;
7; Mismatches
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Pred. No. 12;
5; Mismatches
Mismatches
3,
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Best Local Similarity 40.0%;
Matches 6; Conservative 7
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274 AVSVLMLLVALLFTG 288
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10 VALVVTLIIAIVVWT 24
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ALVVAIILAIVVWT 24
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Best Local Similarity 50.00
Best Local 7; Conservative
                                                 2 ALEVIALLAVLIWTG
Conservative
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6
Matches
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Wed May 10

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Gaps

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1; Indels

53.1%; Score 43; DB 2; 58.3%; Pred. No. 76; iive 4; Mismatches

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A,Molecule type: DNA,
Mesidues: 1-773 cKAH.
A,FResidues: 1-773 cKAH.
A,FCTOSB-references: UNIPROT:P18398; UNIPARC:UPI000012A7F3; EMBL;Z21854; NID:g49403; PIDN
C,Superfamily: Enterococcus copper-transporting ATPase copA, ATPase nucleotide-binding d
C,Steywords: phosphoproteain; transmembrane protein homology cATT>
F;162-495/Domain: ATPase transduction domain homology cATT>
F;557-699/Domain: ATPase nucleotide-binding domain homology
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137 IMLLSVSVWSGA 148
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Best Local Similarity 58.3
Matches 7; Conservative
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A;Status: preliminary
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                                                          P91006
hypothetical protein EC83022 [imported] - Escherichia coli (strain O157:H7, substrain RI C; Species: Escherichia coli #1. 
C; Date: 18-Jul-2004 #1. 
C; Accession: F91006
R; Hayashi, T; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. 
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Residues: 1-203 cHAX>
A; Residues: 1-204 cHAX>
A; Residues: 1-205 cHAX>
A; Residues: 1-205
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ACCESSION: 13.

ACCESSION: 13.

ACCESSION: ACCESSION: Control melitensis
C;Specias: Brucella melitensis
C;Specias: Grand Brocession: ACCESSION: Bequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: ACCESSION: C; Kapatral, V; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
S; Mazur, M.; Goltsman, E.; Selkov, E.; Blzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Reference number: AD3252; PMID:11756688
A;Rocession: ACCESSION: ACMRA
A;Residues: 1-752 acMRA
A;Residues: 1-752 acMRA
A;Residues: 1-752 acMRA
A;Residues: 1-752 acMRA
A;Gene: BWEI1569
A;Genetics:
A;Genetics:
A;Genetics:
C;Genetics:
C;Superfamily: Enterococcus copper-transporting ATPase copA; ATPase nucleotide-binding of C;Keywords: hydrolase
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C32052
Fix protein - Rhizobium meliloti
C;Species: Rhizobium meliloti
C;Species: Rhizobium meliloti
C;Species: Rhizobium meliloti
C;Date: 13-Jul-1989 #sequence revision 13-Jul-1989 #text_change 09-Jul-2004
C;Accession: C32052; S32847; S39994
R;Kahn, D:, David, M.; Domergue, O.; Daveran, M.L.; Ghai, J.; Hirsch, P.R.; Batut, J.
J. Bacteriol. 171, 929-939, 1989
A;Title: Rhizobium meliloti fixGHI sequence predicts involvement of a specific cation pu
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Pred. No. 25;
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Pred. No. 75;
4; Mismatches 1; Indels
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58.3%;
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183 LVLEVLLALTVILW 196
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128 VMLLSVAVWSGA 139
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Matches 7; Conservative
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C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: C95344
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A;Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: UNIPROT: P18398; UNIPARC: UP1000012A7F3; GB: AE006469; PIDN: AAK65317.1; A; Experimental source: strain 1021, megaplasmid pSymA significant source: strain 1021, megaplasmid pSymA significant. F:; Pinan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001
A; Athors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A; Rieference number: Assonable symbiont Sinorhizobium meliloti.
A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Genome: plasmid
C;Superfamily: Enterococcus copper-transporting ATPase copA; ATPase nucleotide-binding d
FixIl copper transport ATPase fixIl [imported] - Sinorhizobium meliloti (strain 1021) ma
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Pred. No. 76;
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4; Mismatches
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58.3%;
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137 IMLLSVSVWSGA 148
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A;Molecule type: DNA
A;Residues: 1-757 <KUR>
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RAY TISSUE-Testis

RAY OLE T., SULLE SEQUENCE.

RAY OLE T., SULLKI Y., NISHIKAWA T., OLGUKI T., SUGIYAMA T., ITIE R.,

RAY OLE T., SULLKI Y., NISHIKAWA T., OLGUKI T., SUGIYAMA T., ITIE R.,

RAY ARAMMETEU A., HAYASHI K., SALO H., NOGAIK, K., MAKITA H.,

RAY SKINE M., ODAYASHI M., NISHI T., Shibahara T., Tanaka T., Ishii S.,

RAY MAGAMATI K., MULZKAMI K., YSUAGI T., PULTUYA T., ISHII S.,

RAY SUGAWATA M., TAKAHASHI M., KARAGA T., PULTUYA T., KIKAWA E.,

RAY SUGAWATA M., TAKAHASHI T., KAKU Y., KOGAIRA H., KIKAWA E.,

RAY SUGAWATA M., NINOMIYA K., ISHIBASHI T., YSMASHITA H., MULZKAWA K.,

RAY SUGAWATA M., NINOMIYA K., ISHIBASHI T., YSMASHITA H., MULZKAWA K.,

RAY LAHIGAS S., ONO Y., TAKIGUCHI S., WALANADA S., YOSIGA M., HOLUTA T.,

RAY NOWLA Y., TOGIYAS S., KOMATI F., WALANADA S., YOSIGA M., HOLUTA T.,

RAY NOWLA Y., TOGIYAS S., KOMATI F., WALANADA S., YOSIGA M., HOLUTA T.,

RAY NOWLA Y., MASSHINO K., YUNKI H., OSHIMA A., SABAKI N., ACTSHIA M.,

RAY MOSSHINO K., YUNKI H., OSHIMA A., SABAKI N., ACTSHIA M., SALO S.,

RAY NOWLA Y., MATSOHOLH H., OSHIMA A., SABAKI N., SALUKI S.,

RAY MARAGAWA S., SENOH A., MIROGUCH H., GOLO Y., SHIMIZU S., FULLULUMI Y.,

RAY PUJIMOTI Y., KOMAYAMA H., TSHIMIS A., TZAKMI S., TEKNOLUMI Y.,

RAY PUJIMOTI Y., KOMAYAMA H., TSHIMIS A., TAKAMAKAMI Y.,

RAY RAMADATA A., HIKIJI T., KODATAK N., INGAKI K., PULINGAR Y., SANDAT T.,

RAY RAMADATA A., HIKIJI T., NOSDATK K., HIRO M., OHMOTI Y.,

RAY ALSHIMA Y., MALSHIMA Y., MIZOHOLI S., ILOH T., SHIGHE K., SCHAB T.,

MATSUMINA K., NAWAKAMI T., NOSLAK K., TAKAHAMA S., SASAKI M.,

RAY MATSUMINA S., SALOH T., SHIRAI Y., TAKAHAMA S., SASAKI M.,

RAY MATSUMINA S., NAGARULA Y., MATSUMA S., SAGAN S.,

RAY MATSUMINA S., NAWAKAMI Y., NOGHOLI S., ILOH T., SHIGHE K., SCHAB T.,

RAY MATSUMINA S., NAWAKAMI Y., NOGHOLI S., ILOH T., SHIGHE K., SCHAB T.,

RAY MATSUMINA S., NAWAKAMI Y., NOGHOLI S., ILOH T., SHIGHE K., YAGAT N., NAKAMINA S., NAWAKAMI K., WAGAT K., WAKAMINA S., NAWAKAMI K., WAGAT K., YAMASH K., YAGA T., NOGHOLI S., ILOH T., SHIGHE K., YAGA T., NOGHOLI S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                 QBadcB
QBadko
QBadko
QBadkB
QBadxB
QBae75
QBae75
QBumdS
QSGw3
QSGw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nat. Genet. 36:40-45(2004).
EMBL, AK033517; BAC04191.1; -; mRNA.
Ensembl; ENSG0000149507; Homo sapiens.
SEQUENCE 158 AA; 17942 MW; EEB43D70A8A391E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ36198.
Homo sapiens (Human).
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Pred. No. 0.00036;
                 08ADC8_9HIV1
08ADE4_9HIV1
08ADE6_9HIV1
08ADE6_9HIV1
08ADE8_9HIV1
08AE51_9HIV1
08AE51_9HIV1
08UMD5_9HIV1
050CW3_9HIV1
05ACW3_9HIV1
05ACW3_9HIV1
04OX90_9HIV1
06UEX9_9HIV1
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   000000000000000
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QBN9U6 HUMAN PRELIMINARY;
   NUCLEOTIDE SEQUENCE.
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Best Local Similarity
NCBI_TaxID=9606;
 Q8N9U6;
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               GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                     2166443 seqs, 705528306 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q86WS3_HUMAN
Q4FZG8_MOUSE
Q8T8D7_TAESA
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Q5UEH5_9HIV1
Q6UF05_9HIV1
Q6X6S8_9HIV1
Q70661_9HIV1
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BIFLO
STRAW
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26LSD9 PHOPR
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81
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Maximum Match 100%
Listing first 45 summaries
                                                                                          using sw model
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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Match Length
                                                                                        - protein search,
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TISSUE-OCCYCES,

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TALESCHIE 223825;

TALESCHIE 223825;

TALESCHIE 223825;

TALESCHIE 223825;

TALESCHIE 2. Teingold E.A., Grouse L.H., Derge J.G.,

Altschil S.F., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschil S.F., Collins F.S., Wagner L., Mang J., Haieh F.,

Altschil S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Altschil S.F., Jordan H., Moore T., Max S.I., Waln G.M., Hong L.,

An Didchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., Malek J.A., Gunaratne P.H.,

Rosak S.A., McEwan P.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A., Gibbs R.A.,

Villalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,

Nhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Minting M., Madan A., Young A.C., Schwutz J., Myers R.M.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield X.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield X.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield X.S.N., Krzywinski M.I., Marra M.A.,

"Medicon and initial analysis of more than 15,000 full-length human
                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.5%; Score 62; DB 2; Length 164; 76.5%; Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH WGC Project;
Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC099498; AAH99498.1; -; mRNA.
Hypothetical protein:
SEQUENCE 164 AA; 18849 WW; 49ADE19216BE8606 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Taenia saginata (Beef tapeworm).
Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
Cyclophyllidea; Taenidae; Taenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                 13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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INGEVPRO; IPR003961; FN III.
SMRAT; SM00060; FN3; 1.
PROSITE; PS50853; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MALEVLMLLAVLIWTGA 17
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08T8D7 TAESA PRELIMINARY;
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                                                                                                                                Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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Altschul S.F., Zeeberg B. B., Buetow K.H., Schaefer C.R., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A physins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A papleron M., Soarse M.B., Bonaldo M.F., Gasavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,
Brownstein M.J., Wokernan K.J., Mahek J.A., Gunstane P.H.,
Brownstein M.J., Wokernan K.J., Makek J.A., Gunstane P.H.,
A soak S.A., McKwan P.J., McKernan K.J., Makek J.A., Gunstane P.H.,
A willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A phylon B.K. Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.R., Touchman J.W., Green B.D., Dickson M.C.,
Butterfield Y.S. M., Krzywinski M.I., Skalska U., Smailus D.E.,
B. Cheneration and initial analysis of more than 15,000 full-length human
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Pred. No. 0.00036;
      Indels
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Director MGC Project;
Director MGC Project;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 158 AA; 17971 MW; EEB43D6FB8AB81FF CRC64;
                                                                                                                                                                                                                                                                                                                                                         01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein FLJ36198.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nd mouse cDNA sequences.";
roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                  158 AA.
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   Mismatches
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Ensembl; ENSG00000149507; Homo sapiens.
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EMBL; BC048121; AAH48121.1; -; mRNA.
FWRT; BC036256; AAH36256.1; -; mRNA.
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                                                                                                     1 MALEVIMILAVLIWIGA 17
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                                                                   1 MALEVLMLLAVLIWTGA
                                                                                                                                                                                                                                                                                        Q86WS3_HUMAN PRELIMINARY,
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Matches 17; Conservative
   17; Conservative
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Q4FZG8 MOUSE
ID Q4FZG8 MC
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O86WS3_HUMAN
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Q4WR18_ASPFU PRELIMINARY;
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A Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
A Addredge T., Bashizzadeh R., Blakely D., Cook R., Gilbert K.,
Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
"Complete genome sequence of Methanobacterium thermoautotrophicum
T dltdh: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155 (1997).
                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                       Methanobacterium thermoautotrophicum.
Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
                                                                     Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.7%; Score 50; DB 1; Length 334; 53.3%; Pred. No. 27;
                                                                                                        0; Indels
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Hypothetical protein.
NON TER 1 1 SEQUENCE 174 Aa; 18702 MW; 645D04766AC068AF CRC64;
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46D280EC683CB611 CRC64;
                                                                     65.4%; Score 53; DB 2; 75.0%; Pred. No. 5.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Hypothetical UPF0104 protein.
                                                                                                    Mismatches
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TIGRFAMB; TIGR00374; Cons hypoth374; 1.
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                                                                                                                                                                                                                                                                                                                                                           OrderedLocusNames=MTH378;
                                                                                                    Conservative
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4 LMLLAILLWTGS 15
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                                                                                                                                                                                                                                                      STANDARD;
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218
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334 AA;
                                                            Query Match
Best Local Similarity
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Best Local Similarity
Matches 8; Conserv
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RETAINS—ACES SEQUENCE.

RA ALTOSTILE SEQUENCE.

RA ALTOST J., Berriman M., Abbe K., Archer D.B., Bernelo C., Bennett J., Bernelo C., Bennett J., Bernelo C., Den D., Collins M., Couleen R., Davies R., Dyer P.S., Raman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R., Goddman G.H., Gomi K., Garcia M.J., Goble A., Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B., Koller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R., Haas B., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R., Mangai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C., Mollar B., Murphy D., O'Neil S., Paulsen I., Mollam M., Monod M., Majoros W.H., May G.S., Murphy L., O'Neil S., Paulsen I., Ablinga S., Murphy L., O'Neil S., Paulsen I., Rabbinowitsch B., Rawlins N., Rajandream M.-A., Reichard U., Rabbinowitsch B., Rawlins N., Rajandream M.-A., Reichard U., Rabbinowitsch B., Rawlins N., Rajandream M.-A., Reichard U., Racher-Ferrero J.C., Saunders D., Seeger K., Squares R., Sanchez Perrero J.C., Saunders D., Seeger K., Squares S., Machida M., Hall N., Barrell B., Denning D.W., Machida M., Hall N., Barrell B., Denning D.W., Machida M., Hall N., Barrell B., Denning D.W., Submitted (MAY-2005) to the EWBL/GenBank/DDBJ databases

C. I. CAUTION: The sequence shown here is derived from an EmBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                  Aspergillus funigatus Af293.
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
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1. SIMILARITY: Balongs to the cytochrome P450 family.

REMBL, AAHFO1000005 EAL69316.1; -; Genomic_DNA.

RINTERPRO; IPR00128; Cytochrome_P450.

RINTERPRO; IPR00128; Cytochrome_P450.

RINTERPRO; IPR001865; Ribosomal_S2.

R Pfam; PF00067; P450.

R PRINTS; PR00463; B450.

R PRINTS; PR00463; P450.

R PRINTS; PR00965; CYTOCHROME P450; UNKNOWN 1.

R PROSITE; PS00962; RIBOSOWAL_S2_1; UNKNOWN 1.

R PROSITE; PS00962; RIBOSOWAL_S2_1; UNKNOWN 1.

R Heme; Iron; Metal-binding; Monocoxygenaee; Oxidoreductage.

SEQUENCE 507 AA; 57910 MW; 16F1DE6E90612F32 CRC64;
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                                                                                                             Cytochrome P450 monooxygenase, putative
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08AE43;

01-MAR-2003 (TEMBLE1. 23, C

01-MAR-2003 (TEMBLE1. 23, L

01-OCT-2003 (TEMBLE1. 25, L

Vpu protein.
13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31,
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                                                                                                                                         ORFNames=Afu4g14790;
                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                            NCBI_TaxID=330879;
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MEDLINE=22375625; PubMed=12487816; DOI=10.1089/088922202320886325;
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Serwadda S., Sewankambo N., Wabwire F., Kigozi G., Kiwanuka N.;
Submitred (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF494481; ARA19479-1; -1, Genomic_DNA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0019076; P:viral release; IEA.
InterPro; IPR008187; Vpu.
InterPro; IPR009032; Vpu.cyt.
Ffam; PF00558; Vpu. 1.
SEQUENCE 81 AA; 9322 MW; 98B7887582935D15 CRC64;
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Kim B., Phillips J.B., Lane J.R., Merling R., McCutchan F.E.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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Harris M.E., Birx D.L., Robb M.L.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                          Viruses; Retroid viruses; Retroviridae; Lentivirus;
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Human immunodeficiency virus 1
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Q8AD88;
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                                                   Primate lentivirus group
NCBI_TaxID=11676;
                                                                                                                     NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
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Matches 8; Conserva
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NUCLEOTIDE SEQUENCE
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Platyrrhini, Cebidae, Cebinae, Cebus.
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"Loss of Olfactory Receptor Genes Coincides with the Acquisition of Full Trichromatic Vision in Primates.";
PLOS Biol. 2:0120-0125(2004).
-!- SUBCELLUIAR LOCATION: Integral membrane protein (By similarity).
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
EMBL, AV454839; AAR19450.1; -; Genomic DNA.
GO; GO:0016021; C:integral to membrane, IEA.
Harris M.E., Serwadda D., Sewankambo N., Kim B., Kigozi G., Kiwanuka N., Phillips J.B., Wabwire F., Meehen M., Lutalo T., Liane J.R., Merling R., Gray R., Wawer M., Birx D.L., Robb M.L., McOttchan F.E.;
"Among 46 near full length HIV type 1 genome sequences from Rakai District, Uganda, subtype D and AD recombinants predominate.";
AIDS Res. Hum. Retroviruses 18:1281-1290(2002).
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BMBL, AP484520. AAN73822.1; -; Genomic_DNA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0019076; P:viral release; IEA.
InterPro; IPR008187; Vpu.
InterPro; IPR009032; Vpu.
SEQUENCE 81 AA; 9317 MW; 430257630240FDEC CRC64;
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=99UCK38855;
Meehen M., Wawer M.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
01factory receptor (Fragment).
Cebus apella (Brown-capped capuchin).
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Q6SNL4;
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Matches 8; Conservative
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Submitted (FEB-2002)
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NUCLEOTIDE SEQUENCE [GENOMIC DNA].
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Q8AD96;
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Submitted (FEB-2002)
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STRAIN=99UGF03726;
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GO; GO:0004984; F:olfactory receptor activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0007165; P:sreceptor activity; IEA.

GO; GO:0007165; P:signal transduction; IEA.

R InterPro; IPR000276; GPCR Rhodpsn.

InterPro; IPR000275; Olfact receptor.

R InterPro; IPR000175; Olfact receptor.

R PANTHER, PTHR11398; Olfact receptor.

R PROSITE; PS00024; OLFACTORYR.

R PROSITE; PS00024; GPROTEIN_RECEP_F1_1; 1.

R PROSITE; PS00024; GPROTEIN_RECEP_F1_2; 1.

R PROSITE; PS00024; GPROTEIN_RECEP_F1_2; 1.

R G-protein coupled receptor; Receptor; Transmembrane.

T NON_TER 219

T NON_TER 219

SEQÜENCE 219 AA; 24476 MW; 9B73B54D0446A130 CRC64;
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01-MAY-1992 (Rel. 22, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Hypothetical 30.4 kDa protein in pubh 5'region (ORF274).
Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacteraceae; Rhodobacteria; Rhodobacteria; Inaxib=1061;
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QELSD9_PHOPR PRELIMINARY; PRT; 223 AA.

QELSD9;

QELSD9;

OS-JUL-2004 (TrEMBLrel. 27, Last sequence update)

OS-JUL-2004 (TrEMBLrel. 27, Last annotation update)

OS-JUL-2004 (TrEMBLrel. 27, Last annotation update)

Hypothetical protein uv2139.

Name=VV2139; OrderedLocusNames=PBPRA1376;

Photobacterium profitundum (Photobacterium sp. (strain SS9)).

Bacteria, Proteobacteria, Gammaproteobacteria; Vibrionales;

Vibrionaceae; Photobacterium.
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55;
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73 MNWKVCMMLAVALWTG 88
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nes 9; Conservative
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P26158;
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Q6LSD9_PHO
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22375625; PubMed=12487816; DOI=10.1089/088922202320886325; Harris M.E., Serwadda D., Sewankambo N., Kim B., Kigozi G., Kiwanuka N., Phillips J.B., Wabwire F., Meehen M., Lutalo T., Lane J.R., Merling R., Gray R., Wawer M., Birx D.L., Robb M.L., McCutchan F.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Among 46 near full length HIV type I genome sequences from Rakai District, Uganda, subtype D and AD recombinants predominate."; AIDS Res. Hum. Retroviruses 18:1281-1290(2002).
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Serwadda S., Sewankambo N., Wabwire F., Kigozi G., Kiwanuka N.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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Burke D.H., Alberti M., Armstrong G.A., Hearst J.E.;
Submitted (NOV-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=99UGF03726;
Kim B., Phillips J.B., Lane J.R., Merling R., McCutchan
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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Harris M.E., Birx D.L., Robb M.L.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                             EMBL; Z11165; CAA77516.1; -; Genomic_DNA.
PIR; S17804; S17804.
Hypothetical protein; Photosynthesis.
SEQUENCE 274 AA; 30352 MW; 98A650B44B27A01E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human îmmunodeficiency virus 1.
Viruses, Retroid viruses, Retroviridae, Lentivirus,
Primate lentivirus group.
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3; Mismatches
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nes 8; Conservative
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123 ISALILCAVLVWTG 136
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PRT;

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STRAIN-01YE386;
Saad M.D., Al-Jaufy A., Graham R.R., Nadai Y., Earhart K.C.,
Sanchez J.L., Carr J.K.;
"HIV from Burope, Africa and Asia Co-circulate in Yemen.";
Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AY795903; AAW5733.1; -; Genomic_DNA.
GO; GO:0019076; P:viral release; IEA.
InterPro; IPR001877; Vpu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00558; Vpu; 1.
SEQUENCE 81 AA; 9274 MW; 5CA394AE497C5EC2 CRC64;
                                                                                                                                                                                 10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Vpu protein.
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Viruses; Retroid viruses; Retroviridae; Lentivirus;
Primate lentivirus group.
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9 VALVVALILAIIVWT 23
                                                                                                                                              QSG7F2_9HIV1 PRELIMINARY;
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                               Name=vpu;
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Viruses, Retro-transcribing viruses, Retroviridae, Orthoretrovirinae,
Lentivirus, Primate lentivirus group.
NCBI_TaxID=11676,
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
NCBI_TaxID=11676;
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Pred. No. 36;
6; Mismatches 2; Indels
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                                                                                                                                                                                                Score 46; DB 2; Length 78;
Pred. No. 35;
                                                                                                                                                                                                                                               Indels
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Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; DQ054370; AAY78574.1; -; Genomic DNA.
SEQUENCE 80 AA; 9183 MW; 46FA15083CDED1E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cho Y.; Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases. Submitted (APR-2005) to the EMBL, DQ054368; AAY78564.1; -; Genomic DNA. SEQUENCE 80 AA; 9184 MW; C4FA15083GD0DF09 CRC64;
EMBL; AF484519; AAN73813.1; -; Genomic_DNA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0019076; P:viral release; IEA.
InterPro; IPR009137; Vpu.
InterPro; IPR009032; Vpu.cyt.
Pfam; PF00558; Vpu; 1.
SEQUENCE 78 AA; 8998 MW; 23FA19937BABE989 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Vpu protein.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Vpu protein.
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10 VALVVALILAIIVWT 24
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9 VALVVALILAIIVWT 23
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Q4PUS8 9HIV1 PRELIMINARY;
Q4PUS8;
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Best Local Similarity 46.77
Conservative
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Q4PU48;
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Matches 7; Conservative
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STRAIN=04KBH8-1813;
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NUCLEOTIDE SEQUENCE
STRAIN=02KBH8-1798;
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9HIV1
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05 PUSB 13 - SBD 13 - SBD 13 - SBD 13 - SBD 14
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 Length 81;
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56.8%; Score 46; DB 2; 46.7%; Pred. No. 36; tive 6; Mismatches
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10 VALVVALILAIIVWT 24
                               Conservative
            Local Similarity
nes 7; Conserv
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AX748179 Sequence
AK035517 Homo sapi
BC036251 Homo sapi
BC036255 Homo sapi
BC075948 62 Human
AX574404 Sequence
AX574404 Sequence
AX000622 Homo sapi
AP00013807 Homo sapi
AR012807 Homo sapi
BD119756 EST and e
AR44203 Sequence
AX94897 Sequence
BC099498 Mus muscu
AC1276036 Mus muscu
AC1276036 Mus muscu
AC1276036 Mus muscu
AC1278036 Mus muscu
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AC13728 Rattus no
AC143727 Pan trogl
AC143727 Pan trogl
AC138103 Rattus no
AC163727 Pan trogl
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1 (Dases 1 to 469)

Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.

Est and encoded human protein

Patent: JP 2002010789-A 1356 15-JAN-2002;
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12 2002010789-A/1356
13-JAN-20002
107-AUG-2000 DP 2000280989
105-AUG-1999 US 60/147499
105-AUG-1999 US 60/147499
105-AUG-1999 US AUG-1999 UG-1999 UG-
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                              BD275948
AX574404
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BD119756
AR42491
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score 10.699998092651
seq VLMLLAVLIWTGA/EN
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JP 2002010789-A/1356.
Homo sapiens (human)
Homo sapiens
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1000.0 1492
1000.0 1502
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1000.0 101031
1000.0 100317
1000.0 176944
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CX737256
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                GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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PAT 05-MAY-2005

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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                 137. .187
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VLMLLAVLIWTGA/EN"
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                                  Length 469;
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iive 0; Mismatches 0;
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Sequence 24 from Patent W02001042451.
CS072276.1 GI:63089511
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/note="Von Heijne matrix score 10.699998092651 seq
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Query Match 100.0%; Score 51; DB 6; Length 469; Best Local Similarity 100.0%; Pred. No. 2.8e-08; Matches 51; Conservative 0; Mismatches 0; Indels
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Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
EST's and encoded human proteins
Parent: US 6639063-A 1363 28-OCT-2003;
Genset S.A.;;
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100.0%; Score 51; DB 6; I
Best Local Similarity 100.0%; Pred. No. 2.8e-08;
Matches 51; Conservative 0; Mismatches 0;
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Sequence 1363 from Patent EP1104808.
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JP 2002010789-A/36
15-JAV-2002
07-AUG-2000 JP 2000280989
05-AUG-1999 US 60/147499
JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI
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Homo sapiens (human)
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PC CI2NS/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12NS/00, PC
                                                         Bejanin, S., Tanaka, H., Dumas Milne Edwards, J.B., Jobert, S. and Giordano, J.Y.
Giordano, J.Y.
Full-length human cdnas encoding potentially secreted proteins Patent: WO 02083898-A 563 24-OCT-2002;
GENSET (FR)
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Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.
EST and encoded human protein

GEACH: JP 2002010789-A 36 15-JAN-2002;

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score 10.6999998092651
seq VLMLLAVLIWTGA/EN
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XIFADELHLGMGCPANRIHTYVYEFIYLVRDCGIRTRVVSEETLLFQTELYFTPRNID
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Full-length human cdnas encoding potentially secreted proteins Patent: WO 02083898-A 564 24-OCT-2002;
                                                                                                                                                                                                                                                                                      Gaps
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Motte="Von Heijne matrix score 10.6999998092651 seq
VLALLAVIJATGA\EN"
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                                                                                                                                                                                                                            Length 477;
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Best Local Similarity 100.0%; Pred. No. 2.8e-08;
Matches 51; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                          ch 100.0%; Score 51; DB 6; Similarity 100.0%; Pred. No. 2.8e-08; 51; Conservative 0; Mismatches 0;
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/note="unnamed protein product"
/codon start=1
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AX588688
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                                                                                /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
1. .477
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Best Local Similarity
Matches 51; Conserv
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AX588688
                         FEATURES
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1 (bases 1 to 560)

Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.

Ear and encoded human protein

Patent: JP 2002010789-A 2580 15-JAN-2002;
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JP 2002010789-A/2580
15-JAN-2002
07-AUG-2000 JP 2000280989
05-AUG-1999 US 60/147499
JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE
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VIMILAVLIWTGA/EN"
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Unclassified.
1 (bases 1 to 560)
Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
EST's and encoded human proteins
                                                                     100.0%; Score 51; DB 6; 100.0%; Pred. No. 2.8e-08; ive 0; Mismatches 0;
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Key Location/Qualifiers
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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BD110503
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JP 2002010789-A/2580.
Homo sapiens (human)
Homo sapiens
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PC C12N5
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//pbotein_id="CAF14348.1"
/db.xref="G1:40975400"
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini;
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Patent: EP 1104808-A 43 06-JUN-2001;
                                       100.0%; Score 51; DB 6; Length 512; 100.0%; Pred. No. 2.8e-08; ive 0; Mismatches 0; Indels
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Edwards, J.-B.D.M., Jobert, S. and Giordano, J.-Y.
EST's and encoded human proteins
and encoded human proteins
Geneet S.A.;;
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Best Local Similarity 100.0%; Pred. No. 2.8e-08;
Matches 51; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                 Sequence 43 from patent US 6639063.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 43 from Patent EP1104808.
AX569240 GI:40975399
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Unclassified.
                                       Query Match
Best Local Similarity
Matches 51; Conserv
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AX969240
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AR412406
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ML Patent: JP 2002010789-A 1355 15-JAN-2002;

GENSET CORP
OS Homo sapiens (human)
PN JP 2002010789-A/1355
PD 15-JAN-2002
PP 07-AUG-2000 JP 2002280989
PR 05-AUG-1999 US 60/147499
PR C12NS/10,C12P21/09,C12P21/08,C12Q1/68,C12N1/19, PC C12NN1/21,
PC C12NS/10,C12P21/02,C12P21/08,C12Q1/68,C12N1/19, PC C12NN1/21,
PC C12NS/10,C12P21/02,C12P21/08,C12Q1/68,C12N1/19, PC C12NN1/21,
PC C2 VON Heijne matrix
CC score 10.699999092651
CC seq VLMLLAVLIMTGA/EN
FR KSY Location/Qualifiers
FT sig_peptide 53..103.
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Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
EST's and encoded human proteins
Patent: US 6639063-A 1362 28-OCT-2003;
WOX;
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Best Local Similarity 100.0%; Pred. No. 2.8e-08;
Matches 51; Conservative 0; Mismatches 0;
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Sequence 1362 from patent US 6639063.
AR413725.
AR413725.1 GI:40168835
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signature 53. .103.
Location/Qualifiers
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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ESTs and encoded human proteins
PER 1104808-A 2587 06-JUN-2001;
Geneet (FR)
                                                                                                                                                                          ch 100.0%; Score 51; DB 6; Length 560; 1. Similarity 100.0%; Pred. No. 2.8e-08; 51; Conservative 0; Mismatches 0; Indels
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1 (bases 1 to 642)

Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.

EST and encoded human protein
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Best Local Similarity 100.0%; Pred. No. 2.8e-08;
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AX971784
Patent: US 6639063-A 2587 28-OCT-2003;
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JP 2002010789-A/1355.
Homo Bapiens (human)
Homo Bapiens
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Adw24026 Bacillus
Acd05503 cDNA enco
Ade81204 Orf16 cod
Ade0741 Novel cod
Adg84623 Human tum
Acc5989 Human tum
Acc5989 Human cDN
Adp10444 Reference
Ade1173 ML-236B s
Abl56459 Nucleotid
Abl56463 ALphae lo
Add5776 Human lun
Ade88030 Aspergill
Adx34451 Plant ful
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Adx3451 Plant ful
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Adx3451 Plant ful
Adx3451 Rabidops
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Aac50472 Arabidops
Aac1633 Human odo
Adt14765 Plant cDN
Adx8081 Rabidops
Adx1455 Plant cDN
Adx80817 OAS1 gene
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                                                                            ACC59890
ADB62163
ADP10174
ADP1174
ADB156459
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ADD56776
ADD6776
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ADD68490
ADY58490
ADX34451
ADX34451
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ABN98358
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AAC33280
AAS11693
ADT14765
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ADQ84623
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 P-PSDB; AAG89145.
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Ab236690 Human GEN
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Ab890053 DNA encod
Ab878646 Human cDN
Ad63550 Human sec
Acc50642 Human sec
Acc50642 Human sec
Ab271354 Secreted
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Ab87052 Human sec
Ad691291 Human sec
Ad673723 Human sec
Ad73723 Human pro
Ad46955 Human GSS
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Ad290379 Fusarium
Aav69879 Bacillus
Aav59478 Bacillus
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5173.506 Million cell updates/sec
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Result ě Seguence 497 BP; 127 A; 99 C; 117 G; 154 T; 0 U; 0 Other;

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genome that affect the activity of GENSET or by supplementing the patients own production of GENSET polypeptides. Conversely, antisense nucleic acid molecules may be administered to down regulate GENSET expression by binding with the cells' own genes and preventing their expression. The sense and antisense nucleic acids may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence to determine which patients may be in need of restorative therapy. The GENSET polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of GENSET nucleic acid of expression and activity. The present sequence is a GENSET nucleic acid of
expression by rectifying mutations or deletions in a patient's
                                                                                                                                                                                                                                                                                                                                                                        the invention
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Sequence 470 BP; 137 A; 87 C; 107 G; 139 T; 0 U; 0 Other;

Gaps ö Length 470; Indels 100.0%; Score 51; DB 5; L. Llarity 100.0%; Pred. No. 4.8e-10; Conservative 0; Mismatches 0; Best Local Similarity Matches 51; Conserv Query Match

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51 1 ATGCCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT 셤

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ABZ36691 standard; cDNA; 497 BP ABZ36691; RESULT 2 ABZ36691

(first entry) 21-FEB-2003 Human GENSET coding sequence SEQ ID 564.

Cytostatic; antiinflammatory; nootropic; neuroprotective; cardiant; gastrointestinal; gene therapy; GENSET; heavy metal toxicity; cancer; inflammatory disease; immune disorder; neuromuscular; toxicity; central nervous system; cardiovascular; gastrointestinal; gene; ss.

Homo sapiens,

WO200283898-A1

24-OCT-2002

18-APR-2001; 2001WO-IB000914.

18-APR-2001; 2001WO-IB000914

(GEST) GENSET

Giordano J; Jobert S, Dumas Milne Edwards J, Tanaka H, Bejanin S,

WPI; 2003-075548/07.

New GENSET polynucleotides and polypeptides, useful for treating heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, CNS, cardiovascular or gastrointestinal effects of the toxicity

Claim 12; Page 579; 735pp; English.

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Gaps

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21

72 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT 122

AAH64743 standard; cDNA; 691

AAH64743 ID AAH6 RESULT 4

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1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT

51; Conservative

Similarity

Local Matches

Query Match

The present invention relates to novel GENSET polynucleotides (ABZ36404-ABZ36911) encoding polypeptides (ABP75963-ABP76368). The polynucleotides and polypeptides are useful in screening and diagnostic assays for abnormal GENSET expression and/or biological activity. They are also useful for screening of compounds for treating or preventing GENSET-related disorders, such as heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, central nervous system (CNS), cardiovascular or gastrointestinal effects of the toxicity. The polynucleotides are useful for constructing or expanding chromosome maps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to novel GENSET polynucleotides (ABZ36404-ABZ36311) encoding polypeptides (ABP75963-ABP76368). The polynucleotides and polypeptides are useful in screening and diagnostic assays for abnormal GENSET expression and/or biological activity. They are also useful for screening of compounds for treating or preventing GENSET-related disorders, such as heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, central nervous system (CNS), cardiovascular or gastrointestinal effects of the toxicity. The polynucleotides are useful for constructing or expanding chromosome maps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treating heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               metal toxicity, cancer, inflammatory diseases, immune disorders, and t
neuromuscular, CNS, cardiovascular or gastrointestinal effects of the
                                                                                                                                                                                                                                                                                                                                                gastrointestinal; gene therapy; GENSET; heavy metal toxicity; cancer; inflammatory disease; immune disorder; neuromuscular; toxicity;
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                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                 central nervous system; cardiovascular; gastrointestinal; gene; ss.
                                                                                                                                                                                                                                                                                                                                 Cytostatic; antiinflammatory; nootropic; neuroprotective; cardiant;
                                                                                              52 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTTTTTGGACCGGTGCT 102
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                                                                              1 ATGCCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT
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             Length 497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 500 BP; 129 A; 100 C; 113 G; 155 T; 0 U; 3 Other;
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jobert S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENSET polynucleotides and polypeptides, useful for
             Score 51; DB 8; I
Pred. No. 4.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dumas Milne Edwards J,
                                                Mismatches
                                                                                                                                                                                                                                                                                                  Human GENSET coding sequence SEQ ID 563.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Page 578; 735pp; English.
100.0%; Scc.
100.0%; Pre
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                                                                                                                                                                                                ABZ36690 standard; cDNA; 500
                                                                                                                                                                                                                                                                   (first entry)
                                                51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tanaka
                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bejanin S,
                                                                                                                                                                                                                                  ABZ36690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   toxicity.
               Query Match
                                                Matches
                                                                                                                                                                 RESULT 3
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SEQ ID NO: 19.

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Full length GENSET human nucleic acids encoding potentially secreted proteins, useful in gene therapy and vaccination against a variety of diseases, and for diagnosis of those diseases.
                                                    Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;
                                                                                                                                                                                                                                                Claim 7; Page 579; 921pp; English.
                                      Human secreted protein cDNA,
                                                                                                                        07-DEC-2000; 2000WO-IB001938.
                                                                                                                                     08-DEC-1999; 99US-0169629P, 06-MAR-2000; 2000US-0187470P.
                      (first entry)
                                                                                                                                                                             Dumas Milne Edwards J,
                                                                                                                                                                                            2001-367870/38.
                                                                                                                                                                                                    P-PSDB; AAG89140.
                                                                                         WO200142451-A2.
                                                                                                                                                             (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                 the invention
                                                                           Homo sapiens.
                      11-SEP-2001
                                                                                                        14-JUN-2001
                                                            GENSET; 88
        AAH64743;
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Jobert

Bougueleret L,

The invention relates to full length GENSET human nucleic acids encoding potentially secreted proteins. The nucleic acids and the polypeptides they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GENSET gene expression. For example, they be used to treat disorders associated with decreased GENSET gene expression by rectifying mutations or deletions in a patient's genome that affect the activity of GENSET or by supplementing the comment that affect the activity of GENSET polypeptides. Conversely, antisense nucleic acid molecules may be administered to down resplate GENSET expression by binding with the cells' own genes and preventing their expression. The sense and antisense nucleic acids may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence to determine which patients may be used as antigenes in the production of antibodies and in assays to identify modulators (agonists and antegonists) of GENSET polypeptides expression and activity. The present sequence is a GENSET nucleic acid of

Gaps ö Sequence 691 BP; 198 A; 126 C; 151 G; 216 T; 0 U; 0 Other; Indels 100.0%; Score 51; DB 5; I 100.0%; Pred. No. 5.3e-10; 0; Mismatches Conservative Query Match Best Local Similarity Marches 51; Conserv

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ABK90053 standard; DNA; 1337 05-NOV-2002 ABK90053; RESULT 5 ABK90053 8X4X6X8

ВЪ

DNA encoding human GSSP3 polypeptide. (first entry)

body mass; serum glucose regulation; body weight loss; obesity; metabolic-related disorder; impaired glucose tolerance; stroke; insulin resistance; hyperlipidemia; atherosclerosis; heart disease; hypertension; syndrome C; type I diabetes; type II diabetes; microangiopathy; retinopathy; neuropathy; nephropathy; ocular lesion; polycystic ovarian syndrome; acanthosis nigrican; leprechaunism; lipoatrophy; physical performance; exercise; dyslaxia; schizophrenia; attention-deficit disorder; hyperactivity disorder; psychiatric disorder; Reducing circulating glucose levels or increasing insulin sensitivity, useful for reducing body mass or preventing body weight gain, comprises administering composition comprising GSSP3 polypeptide. GSSP3; circulating blood glucose level; insulin sensitivity; Chicca J, Yen-Potin F; "GSSP3 polypeptide" Bour BA, Location/Qualifiers 53. .529 Salter-Cid L, Ebbets-Reed D, 01-FEB-2002; 2002WO-IB001333. 02-FEB-2001; 2001US-0266156P. /*tag= a /product= /*tag= b 104. .526 /*tag= c 53. .103 WPI; 2002-608487/65 P-PSDB; ABG31324. WO200260466-A2. (GEST) GENSET Homo sapiens. 08-AUG-2002. sig peptide mat peptide gene; da. Bihain B; Human;

Disclosure; Page 95-96; 97pp; English.

The present invention relates to the isolation of human GSSP3

CO plypeptide, and polymucleotide sequences that encode it. The GSSP3

polypeptide reduces circulating blood glucose levels, increases insulin

sensitivity, and/or reduces body mass. The GSSP3 polypeptide and

caid metabolism, body weight loss, and prevention of body weight gain.

COMPOSITION COMPAINED GSSP3 polypeptides are useful for controlling

COMPOSITIONS COMPAINED GSSP3 polypeptides are useful for controlling

blood glucose levels, for treating metabolic-related diseases or

COMPOSITION COMPAINED GSSP3 polypeptides are useful for controlling

blood glucose levels, for treating metabolic-related diseases or

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Sequence 1337 BP; 457 A; 214 C; 240 G; 426 T; 0 U; 0 Other;

1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT 51

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100.0%; Score 51; DB 6; Length 1337; 100.0%; Pred. No. 6.3e-10; 0; Indels 0; Mismatches Local Similarity 100.

Query Match

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(cell growth, differentiation and death), a naturally occurring amino acid sequence at least 90% identical to CCDD, a biologically active acid sequence at least 90% identical to CCDD, a biologically active compared to an immunogenic fragment. Also included are the polymucleotides encoding CCDD1-12, a recombinant polymucleotide comparison operably linked to the CCDD polymucleotides, a cell transformed with the recombinant polymucleotide, a transgenic organism comprising the recombinant polymucleotide, an anti-comparison of CCDD polymucleotide and a comparison of CCDD polymucleotide and a comparison of CCDD polymucleotide and a cCDD polymucleotide microarray. The polypeptides, polymucleotide and a cCDD polymucleotide microarray. The polypeptides, polymucleotide and accomparase associated with aberrant expression of CCDD, particularly cell proliferative (e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary thromobocytopaenia or cancer), developmental currhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary thromobocytopaenia or cancer), developmental currhosis, ansemia or mental retardation), neurological disorders (e.g. Alzahemer disease, Parkinson's disease or epilepsy), reproductive disorders (e.g. infertility or a disruption in
                                                                                                                                                                                                                                                                                                      cell proliferative disorder; arreriosclerosis; atherosclerosis; cirrhosis; hepatitis; paroxysmal nocturnal haemoglobinuria; psoriasis; polycythaemia vera; primary thromobocytopaenia; developmental disorder; renal tubular acidosis; amental retardation; epilepsy; AllDS; neurological disorder; Alzheimer disease; Parkinson's disease; asthma; reproductive disorder; infertility; autoimmune disorder; gout; allergy; inflammatory disorder; acquired immunodeficiency syndrome; uveitis; autoimmune thyroiditis; contact dermatitis; Crohn's disease; infection; diabetes mellitus; glomerulonephritis; irritable bowel syndrome; multiple sclerosis; osteoporosis; pancreatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baughn MR;
Burford N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human proteins associated with cell growth, differentiation and death, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), cancer, atheroscierosis or hepatitis.
                                                                                                                                                                                                                                                                                     Human; 88; gene; cell growth; differentiation; death; CGDD; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lu Y, Warren BA, Elliott VS,
I, Tang TY, Lal PG, Duggan BM,
ran UK, Khare R, Walia NK;
                                                                                                                                                                                                                                        Human cDNA encoding, CGDD4, INCYTE 5284076CB1.
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                                                                                              ABS78646 standard; cDNA; 1480 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-FEB-2001; 2001US-0271175P. 08-MAR-2001; 2001US-0274503P. 09-MAR-2001; 2001US-0274552P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-FEB-2001; 2001US-0268111P.
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Xu Y, Gietzen KJ,
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                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rheumatoid arthritis.
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P-PSDB; ABG97353.
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                                                                                                                                                                                         16-DEC-2002
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                                                                                                                                             ABS78646;
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Lu DAM,
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                                                 RESULT 6
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(acquired immunodeficiency syndrome) allergies, asthma, autoimmune thyroidities, contact dermatitis, Crohn's disease, diabetes mellitus, glomerulonephritis, gout, irritable bowel syndrome, multiple sclerosis, uveitis, osteoporosis, panoreatitis, rheumatoid arthritis, uveitis, or viral, bacterial, fungal, parasitic, protozoal or helminthic infections. They are also useful in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of proteins associated with CGDD. The present sequence encodes a CGDD protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sato H, Ishii S;
K, Irie R, Tamechika I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ss; gene; pharmaceutical; diagnostic; gene therapy; tissue regeneration; cell regeneration; membrane protein; signal transduction-related protein; transcription-related protein; osteoporosis; neurological disease; cancer; tumour.
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                                                                                                                                                                                                                                                                                                                                                                                                 Length 1480;
                                                                                                                                                                                                                                                                                                                                       Sequence 1480 BP; 463 A; 244 C; 265 G; 508 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "Clone TESTI20282420 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                         6.4e-10;
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9
                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 51; DB 100.0%; Pred. No. 6.4e
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cDNA encoding clone TESTI20282420.
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-NOV-2001; 2001JP-00379298.
25-JAN-2002; 2002US-00350978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-MAR-2002; 2002EP-00007401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similaricy
hes 51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
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Yoshikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-450961/43.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADB63550;
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seki N,
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of the polynucleotide, immunologically assaying the polypeptide or peptide of the polynucleotide by contacting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polynucleotide in an expressible manner and an antisense polynucleotide. The oligonucleotide or as a probe CC is useful as a primer for synthesising the polynucleotide, or as a probe CC for detecting the polynucleotide. The polynucleotide and encoded proteins are useful as pharmaceutical agents and many disease-related proteins may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of genes may be included in them, for developing a diagnostic marker or cof gene therapy. The genes are involved in tissus and/or cell cranscription-related proteins, signal transduction-related proteins, transcription-related proteins, disease-related proteins and corristion or trade proteins and season of the encoded protein and genes cancer, tumours. The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The catal for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office.
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Gaps ö 100.0%; Score 51; DB 10; Length 1492; 100.0%; Pred. No. 6.5e-10; Sequence 1492 BP; 452 A; 250 C; 272 G; 518 T; 0 U; 0 Other; Indels ö 0; Mismatches 51; Conservative Query Match Best Local Similarity Matches 51; Conserv

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21 1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT

8 셤 RESULT 8 AAC69528

AAC69528 standard; DNA; 1898 BP AAC69528;

Human secreted protein gene 17 clone HTELS08.

(first entry)

31-JAN-2001

Immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective; noorcopic; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; gene therapy; infection; human; secreted protein; ss.

Homo sapiens,

WO200061623-A1

19-OCT-2000

06-APR-2000; 2000WO-US008979.

99US-0128693P. 99US-0130991P. 09-APR-1999; 26-APR-1999;

(HUMA-) HUMAN GENOME SCI INC.

Shi Y; Birse CE; Soppet DR, , Moore PA, Rosen CA, S Florence KA, ж Д, Komatsoulis n HS, Ebner Olsen HS, Z Lafleur DW, Young PE; Ruben SM,

WPI; 2000-647418/62.

New nucleic acid molecules encoding 62 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.

Claim 1; Page 543-544; 716pp; English.

The invention relates to the isolation of genes (AAC69512-C69587) encoding 62 human secreted proteins (AAB38131-B38396). The genes can be

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used to generate fusion proteins by linking to the gene for the human immunoglobulin G Fo portion (AAC69503) for increasing the stability of the fusion protein as compared to the human protein only. The genes and proteins are useful for preventing, amelicating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and entragonists are useful in the teumont and prevention of: (a) autoimmune disease e.g. rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms of the breast or liver; (c) cardiovascular disorders e.g. neoplasms of the breast or liver; (c) cardiovascular disorders e.g. neoplasms of (f) nervous system disorders e.g. Alzheimer's disease; (g) infections caused by bacteria, viruses and fungi; and (h) ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis
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Best Local Similarity
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RESULT 9 ACC50642

ACC50642 standard; cDNA; 1898 BP

ACC50642;

(first entry) 12-JUN-2003

Human secreted protein coding sequence, SEQ ID 309.

Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic; vulnerary; antiinflammatory; nootropic; neuroprotective; antiparkinsonian; gene therapy; human; cardiovascular disorder; gene; ss.

Homo sapiens.

WO200295010-A2.

28-NOV-2002.

19-MAR-2002; 2002WO-US009785.

21-MAR-2001; 2001US-0277340P. 19-JUL-2001; 2001US-0306171P. 13-NOV-2001; 2001US-0331287P.

(HUMA-) HUMAN GENOME SCI INC

Ruben SM; Rosen CA,

WPI; 2003-129429/12.

proteins, useful for detecting, preventing, icating, treating and/or ameliorating cardiovascular diagnosing, prognosticating, disorders such as arrhythmia. Novel human secreted

Claim 21; SEQ ID NO 309; 1881pp; English.

The present invention relates to novel human secreted proteins (ABR49613-ABR49145) and their coding sequences (ACC50344-ACC50856). The proteins and their coding sequences are useful for the preparation of a diagnostic or pharmaceutical composition for diagnosing or treating a cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary arteriosclerosis and myocardial ischaemia), neural disorders, immune

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system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders pulmonary disorders, renal disorders, pulmonary disorders, renal disorders, pulmonary disorders, renal disorders, for proliferative disorders and/or cancerous diseases and conditions, for wound healing and epithelial cell proliferation, to treat inflammation or infection, for treating thrombosis and arteriosclerosis, for treating or preventing neural damage which occurs in neuronal disorders or neurodegenerative conditions such as Alzheimer's disease and Parkinson's disease, to enhance bone and periodonial regeneration and aid in tissue transplants or bone grafts, to prevent skin aging or hair loss, to stimulate growth and differentiation of haemactopoletic cells and bone marrow cells when used in combination with other cyclokines, to maintain organs before transplantation or for supporting cell culture of primary tissues, to increase or decrease differentiation or proliferation of embryonic stem cells, or to modulate mammalian characteristics or metabolism. Note: The sequence data for this patent was published in electronic format and is available from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted protein; digestive disorder; gastrointestinal disorder; mouth; oesophagus; stomach; small intestine; large intestine; liver; billiary tract; panoreas; cancer; tumour; hyperproliferative disorder; immune disorder; inflammation; infection; wound healing; drug screening; chromosome identification; chromosome mapping; cytostatic; antiinflammatory; immunosuppressive; vulnerary; gene therapy; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                         1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT 51
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Pred. No. 6.9e-10;
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13-NOV-2001; 2001US-0331287P.
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Best Local Similarity 100.0
Entropy 51, Conservative
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P-PSDB; ABR00175.
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ABZ71479-ABZ71540 represent human secreted protein genomic fragments. The invention also encompasses antibodies specific for the secreted proteins, the use of the secreted proteins in drug screening, and recombinant vectors and host cells comprising a nucleic acid of the invention. The secreted proteins, nucleic acids encoding them, antibodies or antibody fragments specific for the secreted proteins, and modulators of protein activity are useful for diagnosing, treating, ameliorating or preventing digestive disorders. Such conditions include disorders of the mouth, coseophagus, stromach, small intestine, large intestine, liver, biliary tract and pancreas, and include cancers of these organs and tissues. The secreted proteins and their nucleic acids may also be used in the companient of immune disorders, inflammation, infection, hyperproliferative disorders, and to promote wound healing. Nucleic acids of the invention may be used for chromosome identification, chromosome continuously, in gene therapy, for identifying individuals from minute biological samples, as hybridisation probes, and as molecular weight markers. The present sequence represents a human secreted protein.
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ADB91448 and ADB91835-ADB91911 encoding human secreted proteins ADB91449-
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100.0%; Pred. No. 6.9e-10;
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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Gaps

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antibody or its fragment, agonist or antagonist are useful for preparing a pharmaceutical composition for diagnosing or treating diabetes or conditions related to diabetes. The present sequence is that of the human immunoglobulin Pc portion used to generate fusion proteins, increasing the stability of the fused protein as compared to the secreted protein only. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antidiabetic; antirheumatic; antiarthritic; antiinflammatory; antithyroid; antidiabetic; immunosuppressive; dermatological; nephrotropic; antiparthisonian; neuroprotective, nootropic; antibacterial; virucide; fungicide; antiparastic; antiparastic; antiarteriosclerotic; vulnerary; cytostatic; haemopoietic; haematologic; anaemia; autoimmune disorder; haemopoietic; haematologic; anaemia; autoimmune disorder; haemotodid arthritis; inflammation; Grave's disease; diabetes; systemic lupus erythematosus; glomerulonephritis; neurodegenerative; Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis; cancer; hacterial; viral; fungal; parastitc infection; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human secreted polypeptide for diagnosing, preventing or treating thematopoletic or hematologic disorders (e.g. anemia), autoimmune disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or atherosclerosis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel human secreted polypeptide comprising defined sequence given in the specification. The polypeptide, nucleic acid molecule, antibody, agonist or antagonist of the invention may be useful for preparing a composition for diagnosing or treating a haemopoietic or haematologic disorder such as anaemia, autoimmune disorders such as rheumatoid arthritis, inflammation, Grave's disease,
                                                                                                                                                                                                                                                                                                                                             15 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT 65
                                                                                                                                                                                                                                                                                                                       1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT 51
                                                                                                                                                                                                                                        Length 1898;
                                                                                                                                                                                        Sequence 1898 BP; 595 A; 315 C; 332 G; 654 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                    100.0%; Score 51; DB 9; I 100.0%; Pred. No. 6.9e-10;
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                             51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-430516/40.
                                                                                                                                                                                                                                                       Local Similarity
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diabetes, systemic lupus erythematosus or glomerulonephritis, neurodegemerative disorders including Parkinson's disease and Alzheimer's disease, wounds and hyperproliferative disorders including atherosclerosis or cancer, as well as bacterial, viral, fungal or parasitic infections. The polypeptide may also be used during gene therapy procedures and for identifying a binding partner by contacting the polypeptide with a binding partner and determining whether the binding partner increases or decreases the activity of the polypeptide. The current sequence is that of the human secreted protein-related DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; GSSP3; circulating blood glucose level; insulin sensitivity; body mass; serum glucose regulation; body weight loss; obesity; metabolic-related disorder; impaired glucose tolerance; stroke; insulin resistance; hyperlipidemia; atheroselse; heart disease; hypertension; syndrome C; type I diabetes; type II diabetes; microangiopathy; retinopathy; neuropathy; nephropathy; ocular lesion; polycystic ovarian syndrome; acanthosis nigrican; leprechaunism; lipoatrophy; physical performance; exercise; dyslexia; schizophrenia; attention-deficit disorder; hyperactivity disorder; psychiatric disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reducing circulating glucose levels or increasing insulin sensitivity, useful for reducing body mass or preventing body weight gain, comprises administering composition comprising GSSP3 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide, and polynucleotide sequences that encode it. The GSSP3 polypeptide reduces circulating blood glucose levels, increases insulin sensitivity, and/or reduces body mass. The GSSP3 polypeptide and polynucleotide sequences are useful in serum glucose regulation, fatty acid metabolism, body weight loss, and prevention of body weight gain. Compositions comprising GSSP3 polypeptides are useful for controlling
                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                              TIGATITIGACCGGIGCT 51
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                                                                                                                                                                                                                     Sequence 1898 BP; 595 A; 315 C; 332 G; 654 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                             100.0%; Score 51; DB 10; 100.0%; Pred. No. 6.9e-10;
                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 90-95; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK90052 standard; DNA; 10115 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salter-Cid L, Ebbets-Reed D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human GSSP3 genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-2002; 2002WO-IB001333.
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                                                                                                                                                                                                                                                                                                  51; Conservative
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                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                  the invention.
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(HUMA-) HUMAN GENOME SCI INC.
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                   Shi Y,
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       disorders (e.g. obesity, impaired glucose tolerance, insulin resistance, hyperlipidaemias, atherosclerosis, heart disease, hypertension, stroke, syndrome C, type I or II diabetee, diabetees related complications, microangiopathy, retinopathy, neuropathy, nephropathy, polycystic ovarian syndrome, ocular lesions, microangiopathic lesions, or syndromes such as acanthosis nigricans, leprechaunism and lipoatrophy). The polypeptides are also useful to improve physical performance during work or exercise, and to treat dyslexia, attention-deficit disorder, attention-deficit/hyperactivity disorder, and psychiatric disorders such as schizophrenia. The present sequence encodes human GSSP3 polypeptide
                                                                                                                                                                                                                                                                                                                                                      human immunodeficiency virus; arthritis; hyperproliferative disease; acquired immune deficiency syndrome; inflammation; asthma; myopathy; allergy; cancer; cardiac oedema; duodenal ulcer; psoriaais; sepsis; neutromuscular system disorder; multiple myeloma; pulmonary disorder; cardiovascular disorder; rabdomyosarcoma; gastrointestinal disorder; multiple sclerosis; immune-mediated thrombocytopaenia; myocarditis; leiomyosarcoma; autoimmune disorder; Crohn's disease; gene therapy;
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                             Human; immune system disorder; HIV infection; myocardial infarction;
                                                                                                                                                                                                  2439 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT 2489
                                                                                                                         Sequence 10115 BP; 2860 A; 1941 C; 1815 G; 3475 T; 0 U; 24 Other;
glucose levels, for treating metabolic-related diseases or
                                                                                                                                                                                       1 ATGCCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT 51
                                                                                                                                                                  ;
0
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                                                                                                                                             100.0%; Score 51; DB 6;
100.0%; Pred. No. 1e-09;
iive 0; Mismatches 0;
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1. .527
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Matches 51; Conservative
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1777. :
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AAD46949-AAD46954 represent cDNAs corresponding to novel human protein
genes, and AAB29290-AAB29295 represent the proteins they encode. AAD46955
-AAD46963 represent novel human protein genes and AAB29296- AAB29297
crepresent novel human protein fragments. Sequences of the invention are
useful for preventing, treating or ameliorating medical conditions or
council healing. These conditions include diseases or disorders of the
immune system (e.g. HIV infection, autoimmune disorders, arthritis,
athma, AIDS, sepsis, psoriasis or inflammation) or neuromuscular system
(e.g. multiple sclerosis, myocarditis, or myopathies), disorders
cassociated with Fc receptor binding by antibody (e.g. immune-mediated
thrombocytopaenia, inflammatory responses or allergic responses),
hyperproliferative diseases (e.g. multiple myeloma, rhabdomyosarcoma,
lung cancer, brain cancer or leiomyosarcoma), gastrointestinal disorders
(e.g. Crohn's disease or duodenal ulcers), pulmonary disorders
infections or cardiovascular disorders (e.g. hyperaemia, myocardial
cinfaction or cardiac oedemal. The invention is useful in gene therapy.
The present sequence represents human protein gene of the invention
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                                                                                                                                            New proteins encoded by genes contained in cDNA clones (e.g. HAPQL38 or HHFOS77), useful for preventing, treating, ameliorating or diagnosing e.g. AIDS, sepsis, brain cancer, Crohn's disease or myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Pusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma resest; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.2%; Score 25.6; DB 6; Length 40 70.8%; Pred. No. 10; ive 0; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 422-423; 429pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF08335 standard; cDNA; 534
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SM;
                                                                        WPI; 2002-759842/82.
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WPI; 2000-594572/56.

Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags.

Claim 86; Page 711; 3161pp; English

The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (BST). The ESTS are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of genes con a first filamentous fungal cells. Monitoring the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, cost them incroorganisms to be improved. New genes may be discovered, cost gene copy number variation and stability can be monitored. The expression of gene copy number variation and stability can be monitored. The expression of gene copy number variation and stability can be monitored. The expression of gene copy number variation and stability can be monitored. The expression conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering. Using ESTS provides several davantages over genomic or random cDNA clones including elimination of credundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF11247 copresents ESTS from Aspergillus niger: AAF18537 represents ESTS from Aspergillus oryzae; and AAF14879 to AAF18537 represents ESTS from Aspergillus or each in the present control or each in the present control or each in the area in the present control or each in the present entered or each invention %XCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

Sequence 534 BP; 132 A; 148 C; 103 G; 130 T; 0 U; 21 Other;

0; Gaps Score 25; DB 3; Length 534; Pred. No. 10; 0; Mismatches 11; Indels Query Match
Best Local Similarity 73.8%;
Matches 31; Conservative (31; Conservative

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Search completed: May 9, 2006, 14:08:20 Job time : 68.7 secs

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Sequence 43, Appl
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Sequence 1362, Ap
Sequence 1704, Ap
Sequence 15700, A
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Sequence 317, App
Sequence 468, App
Sequence 6972, Ap
Sequence 17094, A
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Sequence 54, Appl
Sequence 56, Appl
Sequence 60, Appl
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Sequence 5, Appli
Sequence 16292, A
Sequence 14514, A
                                                                    May 9, 2006, 12:55:51 ; Search time 16.3 Seconds (without alignments) 5561.696 Million cell updates/sec
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Sequence 3, Appli
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-09-621-976-15700
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US-09-68-11
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US-09-85-1133-468
US-09-949-016-17094
US-09-533-559-6972
US-09-949-016-17094
US-09-444-840-1
US-09-444-840-62
US-09-444-840-62
US-09-444-840-62
US-09-444-840-63
US-09-444-840-60
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US-09-949-016-12765
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                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                         1303057 seqs, 888780828 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                            US-10-664-025-43_COPY_53_103
51
1 atggcgttagaagtcttgat.....
                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                 nucleic search, using sw model
                                                                                                                                                       IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                              Issued Patents NA:
                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1732
1732
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13023
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156894
                                                                                                               Title:
Perfect score:
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24.2
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                                                                     Run on:
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Sequence 12766, A
Sequence 16957, A
Sequence 16959, A
Sequence 16959, A
Sequence 1, Appli
Sequence 2813, Ap
                                                                                                                             Sequence 1, Appli
Sequence 10565, A
Sequence 1, Appli
Sequence 2, Appli
Sequence 1072, A
Sequence 16072, A
Sequence 17806, A
Sequence 1532, Ap
Sequence 21819, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1363, Application US/09621976

Patent No. 6639063

GENERAL INPORMATION:
APPLICANT: Unbear Nine Edwards, J.B.
APPLICANT: Jobert S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTE and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SEQ ID NO 1363
LENGTH: 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 73, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
3 US-09-949-016-12766

3 US-09-949-016-16959

3 US-09-949-016-16959

3 US-09-949-016-16959

3 US-09-103-840A-1

3 US-09-621-976-2813

3 US-09-61-976-2813

3 US-09-470-661A-1

3 US-09-470-661A-1

3 US-09-411-132A-1

3 US-09-949-016-18119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 137.187
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: 8core 10.699999802651
OTHER INFORMATION: 8eq VLMLLAVLIWTGA/EN
   156894
156895
156895
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4411529
4411529
17450
17450
811
811
811
1210
1310
2352
2352
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ORGANISM: Homo sapiens
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NAME/KEY: sig_peptide
LOCATION: 137..187
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Query Match
Best Local Similarity 100.0
Matches 51; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-09-621-976-15700
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US-10-104-047-1704
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  SEQ ID NO 1362
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                   LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                        Length 512;
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100.0%; Score 51; DB 3; Length 560;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
Matches 51; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
ITLE OF INVENTION:
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT APPLICATION NUMBER: US/09/621,976
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Johns Milne Edwards, J.B.
APPLICANT: Johns Milne Edwards, J.B.
APPLICANT: Johns Milne Edwards, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2;
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT APPLICATION NUMBER: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2587
LENGTH: 560
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 51; DB 3; L
Best Local Similarity 100.0%; Pred. No. 2.7e-10;
Matches 51; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                          LOCATION: 53.7103
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 10.69999999551
OTHER INFORMATION: seq VLMLLAVLIWIGA/EN
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: PATENT, pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2587, Application US/09621976
Patent No. 6639063
                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 53..511
NAME/KEY: 819_peptide
LOCATION: 53..103
                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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; LOCATION: 372..539
US-09-621-976-2587
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US-09-621-976-1362
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                                                                             SEQ ID NO 43
LENGTH: 512
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; Sequent No. 6629063
; GENERAL INFORMATION:
; APPLICANT: Johnas Milne Edwards, J.B.
; APPLICANT: Johnas Milne Edwards, J.B.
; APPLICANT: Johnas Milne Edwards, J.Y.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; FILE REPERENCE: GENER-1054PR2.
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT PILING DATE: 2000-07-21
; NUMBER: PATENTENTENT NOS: 19335
; SOFTWARE: PATENTENT
; SEQ ID NO 15700
; LENGTH: 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1704, Application US/10104047

Patent No. 6943241

GENERAL INFORMATION:
FIRE PEPLICANT: HELIX RESERCH INSTITUTE

TITLE OF INVENTION: No. 6942241e1 full length cDNA
FILE REFERENCE: H1-A0105

CURRENT PILIG DATE:
PRIOR APPLICATION NUMBER: US/10/104,047

CURRENT FILIG DATE:
PRIOR APPLICATION NUMBER:
NUMBER OF SEQ ID NOS: 4096

SOFTWARE: PATENTING DATE:

NUMBER OF SEQ ID NOS: 4096

SEQ ID NO 1704
                                                                                                                                                                                                                                                                               100.0%; Score 51; DB 3; I
100.0%; Pred. No. 2.9e-10;
tive 0; Mismatches 0;
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100.0%; Pred. No. 3.5e-10;
iive 0; Mismatches 0;
TYPE: DNA
ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: CDS
LOCATION: 53..526
NAME/KEY: sig_peptide
LOCATION: 53..103
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: seeq VLMLLAVLIWTGA/EN
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LOCATION: 351
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Gaps
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US-09-854-133-468

US-09-854-133-468

Sequence 468, Application US/09854133

Patent No. 6795508

GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CURRENT APPLICATION NUMBER: US/09/854,133

CURRENT FILING DATE: 2001-05-11

NUMBER OF SEQ ID NOS: 735

SOFTWARE: FASTSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                      12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 317, Application US/10104047

Patent No. 6943241

GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE

TITLE OF INVENTION: No. 6943241e1 full length cDNA

FILE REFERENCE: H1-A0105

CURRENT APPLICATION UNMBER: US/10/104,047

CURRENT APPLICATION NUMBER: US/20/104,047

PRIOR APPLICATION NUMBER:

PRIOR APPLICATION NUMBER:

PRIOR SEQ ID NOS: 4096

SOFTWARE: PATENTING DATE:

NUMBER OF SEQ ID NOS: 4096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 CTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT 51
                                                                                                                                                                                                                                                                                                                     Query Match

48.6%; Score 24.8; DB 3;
Best Local Similarity 72.7%; Pred. No. 4.5;
Matches 32; Conservative 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3;
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      PCT/US98/01613
                                                                                                                                                                                                        OTHER INFORMATION: Strain: KSM-P15; NAMB/KRX: CDS; NAMB/KRX: CDS; LOCATION: (1)..(591)
    PRIOR APPLICATION NUMBER: PCT/US;
PRIOR FILING DATE: 1998-04-09;
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 591
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il Similarity 78.4%;
29; Conservative
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; ORGANISM: Homo sapiens
US-10-104-047-317
                                                                                                                                           TYPE: DNA
ORGANISM: Bacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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LENGTH: 4156
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LENGTH: 573
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; Sequence 858, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
   APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFRERNES: 8849.200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; BARLIER PILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.0%; Score 25; DB 3; Length 534; 73.8%; Pred. No. 3.7; ative 0; Mismatches 11; Indels
                                                                     Length 372;
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                                                              Query Match 76.5%; Score 39; DB 3; Le Best Local Similarity 98.0%; Pred. No. 1.2e-05; Matches 50; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: HATADA, Yuji
APPLICANT: KOBAYASHI, Tohru
APPLICANT: KOBAYASHI, Tohru
APPLICANT: TSUMADORI, Masaki
TITLE OF INVENTION: Detergent Composition
FILE REFERENCE: 2173-0116P
CURRENT APPLICATION NUMBER: US/09/402,668
CURRENT FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: 9-091142 JAPAN
PRIOR PILING DATE: 1997-04-09
PRIOR FILING DATE: 1997-09-08
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-15700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature

LOCATION: (1)...(534)

OTHER INFORMATION: n = A,T,C or G
US-09-533-559-858
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KASAI, Miyuki
SHIKATA, Shitsuw
SUZUMATSU, Atsushi
KOIKE, Kenzo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Fusarium venenatum
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Best Local Similarity 73.84
Matches 31; Conservative
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LENGTH: 534
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APPLICANT:
APPLICANT:
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695 ATAGTGTCCGTACCTCTGATGTTCCTCGGTGTTTTGAGTTGCTGTGGTGTT 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 1722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Glazebrook, Jane
APPLICANT: Glazebrook, Jane
APPLICANT: Jirage, Dayadevi
APPLICANT: Jorele, Tina L
APPLICANT: Tootle, Tina L
APPLICANT: Food, Nan
APPLICANT: Feys, Bart
TITLE OF INVENTION: PAD4 COMPOSITIONS AND METHODS THEREFOR
FILE REFERENCE: 043503.0009
CURRENT APPLICATION NUMBER: US/09/434,840
CURRENT FILING DATE: 1999-11-04
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                     DB 3; Length 19412;
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CURRENT APPLICATION NUMBER: 05/9/434,840
CURRENT FILING DATE: 1999-11-04
EARLIER APPLICATION NUMBER: 09/190,733
                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.5%; Score 22.2;
64.7%; Pred. No. 59
                                                                                                                                                                           Score 23;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09434840; Patent No. 6620985; GENERAL INFORMATION: APPLICANT: Glazebrook, Jane APPLICANT: Jirage, Dayadevi APPLICANT: Tocle, Tina Li APPLICANT: Zhou, Nan APPLICANT: Eeys, Bart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09434840 Patent No. 6620985 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Arabidopsis thaliana
                                                                                                                                                                           45.1%;
                                                                                                                                                                     Query Match
Best Local Similarity 68.19
Matches 32; Conservative
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Matches 33; Conservative
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LOCATION: (36)..(1616)
                                                         ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17094
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
US-09-434-840-1/c
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US-09-434-840-3/c
SEQ ID NO 17094
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LENGTH: 1722
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Sequence 17094, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
FOLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION DUMBER: 60/241,755

PRIOR PELLING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

WINHBER OF SEQ ID NOS: 207012

SOFTWARE: FASESEQ for Windows Version 4.0
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Pred. No. 19;
0; Mismatches 9; Indels
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; Sequence 6972, Application US/09533559
; Patent No. 69028M
; GENERAL INFORMATION:
    APPLICANT: Mandy M. Berka
; APPLICANT: Mandy M. Berka
; APPLICANT: Bandy M. Rey
; APPLICANT: Defirey R.Shuster
APPLICANT: Defirey R.Shuster
; APPLICANT: Defire Blarke Olsen
; APPLICANT: Peter Blarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
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; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FARLIER FILING DATE: 1999-03-22
; EARLIER FILING DATE: 1999-03-22
; MUMBER OF SEQ ID NOS: 7860
; SGO ID NO 6972
LENGTH: 682
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                                                                                                                                                                                                                                                                                             15 CTIGATGCICCICGCIGICTIGATTIGGACCGGIGCT
                        NAME/KEY: misc feature
LOCATION: (1)...(573)
OTHER INFORMATION: n = A,T,C or G
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OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                        Query Match
Best Local Similarity 75.7%;
Matches 28; Conservative
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                                                                                             ; OTHER INFORMA
US-09-854-133-468
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US-09-434-640-62/c

is Sequence 62, Application US/09434840

is Sequence 62, Application US/09434840

j Patent No. 6620985

i GENERAL INFORMATION:

j APPLICANT: Glazebrook, Jane

j APPLICANT: Tootle, Tina L

APPLICANT: Tootle, Tina L

APPLICANT: Tootle, Tina L

APPLICANT: PAPLICANT: PAD4 COMPOSITIONS AND METHODS THEREFOR

ITITLE OF INVENTION: PAD4 COMPOSITIONS AND METHODS THEREFOR

FILE REFERENCE: 043503.0009

CURRENT FILING DATE: 1999-11-04

EARLIER APPLICATION NUMBER: 09/190,733

EARLIER PILING DATE: 1999-11-12

NUMBER OF SEQ ID NOS: 85

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 62

LENGTH: 1731

TYPE: NAN
                                                                                                       DB 3; Length 1722;
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                                                                                                  Query Match 43.5%; Score 22.2; DB 3; Length 1 Best Local Similarity 64.7%; Pred. No. 59; Matches 33; Conservative 0; Mismatches 18; Indels
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Pred. No. 59;
0; Mismatches 18; Indels
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ORGANISM: Arabidopsis thaliana
FEATURE:
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Best Local Similarity 64.7%;
Matches 33; Conservative
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)..(1064)
US-09-434-840-3
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; LOCATION: (1)..(1548)
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Search completed: May 9, 2006, 13:15:25 Job time: 19.3 secs

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Sequence 3 Sequence 3 Sequence 3

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US-10-653-047-6572
US-10-425-114-17271
US-10-767-701-15792
US-10-242-535A-46681
US-10-085-783A-46681
US-10-085-783A-56962
US-10-085-783A-56962
US-10-938-842A-1937
US-09-938-842A-1937
US-09-770-445-126
US-10-770-789-20
US-10-770-789-20
US-10-770-789-20
US-10-972-135A-19
US-10-972-135A-19
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US-10-972-135A-19
US-10-972-135A-19
US-10-972-135A-19
US-10-978-1374-1374
US-09-938-842A-1374
US-10-357-930-21184
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1626
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 137..454
NAME/KEY: sig_peptide
LOCATION: 137..187
                                  US-09-731-872-24
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Sequence 12, Appli
Sequence 16, Appl
Sequence 1704, Appl
Sequence 27, Appl
Sequence 27, Appl
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Sequence 110, App
Sequence 317, App
Sequence 3, Appli
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Sequence 21218, A
Sequence 6875, Ap
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                                                                                                            9, 2006, 12:56:11 ; Search time 135.6 Seconds (without alignments) 3110.164 Million cell updates/sec
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Sequence 19, P
Sequence 19, P
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1: /cgm2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
2: /cgm2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
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4: /cgm2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
5: /cgm2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
6: /cgm2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
7: /cgm2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
8: /cgm2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
9: /cgm2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
10: /cgm2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
            GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-876-997-24
US-10-643-836-24
US-09-731-872-19
US-09-876-997-19
US-10-643-836-19
US-10-643-836-19
US-10-104-047-1704
US-10-104-047-1704
US-10-798-512-7
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US-10-798-93-6875
US-10-719-993-6875
US-10-653-047-858
US-10-633-047-858
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US-10-243-552-110
US-10-347-614-7
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US-09-738-973-468
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Maximum Match 100%
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                                                                              - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Perfect score:
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No.
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Sequence 24, Application US/09731872

Sequence 24, Application US/09731872

Patent No. USZ0020102604A1

Patent No. USZ0020102604A1

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Dumos Milne Edwards, Jean Baptiste

APPLICANT: Bougueleret, Lydie

APPLICANT: Bougueleret, Lydie

TITLE OF INVENTION: FULL-ENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS

FILE REFERENCE: 78.U33.REG

CURRENT APPLICATION NUMBER: US/09/731,872

CURRENT FILING DATE: 1999-12-08

PRIOR APPLICATION NUMBER: US 60/169,629

PRIOR APPLICATION NUMBER: US 60/187,470

PRIOR PRIOR DATE: 1999-12-08

PRIOR PILING DATE: 1200-03-06

NUMBER OF SEQ ID NOS: 482

SOFTWARE: Patent.pm

LENGTH: 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 51; DB 3; Length 470; Best Local Similarity 100.0%; Pred. No. 2.7e-10; Matches 51; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTHER INFORMATION: Von Heijne matrix OTHER INFORMATION: score 10.7019149919754; OTHER INFORMATION: seq VLMLLAVLIWTGA/EN US-09-731-872-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24, Application US/09876997
Publication No. US20030152921A1
GENERAL INFORMATION:
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Gaps

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Sequence 19, Application US/09731872
; Sequence 19, Application US/09731872
; Bettent No. US20020102604A1
; GENERAL INFORMATION:
    APPLICANT: Unames Millne Edwards, Jean Baptiste
    APPLICANT: Unames Millne Edwards, Jean Baptiste
    APPLICANT: Bougueleret, Lydie
    APPLICANT: Bougueleret, Lydie
    APPLICANT: Ubbert, Severin
    TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
    TITLE OF INVENTION: UNMER: US 009/731,872
    CURRENT APPLICATION NUMBER: US 60/169,629
    PRIOR FILING DATE: 1999-12-08
    PRIOR FILING DATE: 2000-03-06
    NUMBER OF SEQ ID NOS: 482
    SOFTWARE: Patent.pm
    SOFTWARE: Patent.pm
    SEQ ID NO 19
    SEQ ID NO 19
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Sequence 19, Application US/09876997

Publication No. US2000152921A1

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Bougueleret, Lydie

APPLICANT: Boudert, Severin

TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS

FILE REFERENCE: 78.US4.CIP

CURRENT APPLICATION NUMBER: US/09/876,997

CURRENT FILING DATE: 2000-10-06

PRIOR FILING DATE: 2000-12-07

PRIOR APPLICATION NUMBER: US 60/169,629

PRIOR FILING DATE: 1999-12-08

NUMBER OF SEQ ID NOS: 482

SOFTWARE: Patent.pm

SEQ ID NO 19

LENGTH: 691

TYPE: DNA
                                                                                                                                                            137 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT 187
                                                                                                                          1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTTTGATTTGGACCGGTGCT 51
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Query Match 100.0%; Score 51; DB 9; Length 470; Best Local Similarity 100.0%; Pred. No. 2.7e-10; Matches 51; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 691;
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100.0%; Score 51; DB 3; I
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 51; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: SCORE 10.7019149919754
OTHER INFORMATION: Seq VLMLLAVLIWTGA/EN
US-09-731-872-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 42..515
NAME/KEY: 8ig_peptide
LOCATION: 42..92
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NAME/KEY: CDS
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Publication No. US20050096458A1

GENERAL INFORMATION:
Publication No. US20050096458A1

GENERAL INFORMATION:
APPLICANT: Bougueleret, Lydan Baptiste
APPLICANT: Bougueleret, Lydan Baptiste
APPLICANT: Jobert, Severin
ITLE OP INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78. US3. REG
CURRENT APPLICATION NUMBER: US/10/643,836
CURRENT FILING DATE: 2003-08-19
PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR FILING DATE: 1999-12-08
PRIOR FILING DATE: 2000-03-06
NUMBER OF SEQ ID NOS: 482
SOFTWARE: Patent.pm
SOFTWARE: Patent.pm
SOFTWARE: DATE
TYPE: DNA
                         APPLICANT: BOUGULETE, LYGIE
APPLICANT: BOUGULETE, LYGIE
APPLICANT: BOUGULETE, LYGIE
APPLICANT: JOBERT, SEVERIN
TITLE OF INVENTION FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78 US4 CIP
CURRENT APPLICATION NUMBER: US 0/9731,872
PRIOR PILING DATE: 2000-12-07
PRIOR PPLICATION NUMBER: US 60/187,470
PRIOR PLILING DATE: 2000-03-06
PRIOR PLILING DATE: 1999-12-08
PRIOR PLILING DATE: 1999-12-08
PRIOR PLILING DATE: 1999-12-08
PRIOR PLILING DATE: PROPERTY OF SECTION NUMBER: US 60/169,629
PRIOR PLILING DATE: PROPERTY OF SECTION NUMBER: US 60/169,629
PRIOR PLILING DATE: PROPERTY OF SECTION NUMBER: US 60/169,629
PRIOR PLILING DATE: PROPERTY OF SECTION NUMBER: US 60/169,629
PRIOR PLILING DATE: PROPERTY OF SECTION NUMBER: US 60/169,629
PRIOR PLILING DATE: PROPERTY OF SECTION NUMBER: US 60/169,629
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100.0%; Score 51; DB 3; I
Best Local Similarity 100.0%; Pred. No. 2.7e-10;
Matches 51; Conservative 0; Mismatches 0;
   APPLICANT: Dumas Milne Edwards, Jean Baptiste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: sig peptide
LOCATION: 137..187
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: secre 10.7019149919754
OTHER INFORMATION: seq VLMLLAVLIWTGA/EN
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OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: BECORE 10.7019149919754
OTHER INFORMATION: BEG VIMILAVLIWIGA/EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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NAME/KEY: sig_peptide
LOCATION: 137..187
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LOCATION: 137..454
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LOCATION: 137..454
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US-10-643-836-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 24
LENGTH: 470
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APPLICANT: YUE, HENLY; YAO, Monique G.
APPLICANT: ISON, Craig H.; LU, Yan
APPLICANT: ISON, Craig H.; LU, Yan
APPLICANT: WARREN, Baridget A.; ELLIOTT, Vicki S.
APPLICANT: WARREN, Baridget A.; ELLIOTT, Vicki S.
APPLICANT: TXU, Yuming; GIETZEN, Kimberly J.
APPLICANT: TXU, Yuming; GIETZEN, Kimberly J.
APPLICANT: TXU, Yuming; GIETZEN, Kimberly J.
APPLICANT: TANG, Toom Y.; LAL, Preeti G.
APPLICANT: TANG, Toom Y.; KHARE, Reena
APPLICANT: TRAN, Uyen K.; KHARE, Reena
APPLICANT: CHAMLA, Warinder K.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
TILE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
TILE REFERENCE: PF-0903 USN
CURRENT FILING DATE: 2002-08-08
PRIOR FILING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PELING DATE: 2001-02-09
PRIOR PELING DATE: 2001-03-08
PRIOR PELING DATE: 2001-03-08
PRIOR PELING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
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                            APPLICANT: Bihain, Bernard
TITLE OF INVENTION: GSSP3 Polynucleotides and Polypeptides and Uses Thereof
FILE REFERENCE: G-102US03RER: US/10/467,046
CURRENT APPLICATION NUMBER: US/10/467,046
CURRENT FILING DATE: 2003-08-01
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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100.0%; Score 51; DB 8; Length 1337;
Best Local Similarity 100.0%; Pred. No. 3.4e-10;
Matches 51; Conservative 0; Mismatches 0; Indels
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Pred. No. 3.5e-10;
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; OTHER INFORMATION: Incyte ID No: 5284076CB1
US-10-467-535-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 16, Application US/10467535; Publication No. US20040146970A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: sig_peptide
; LOCATION: (104)..(526)
US-10-467-046-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: (53)..(103)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                              LENGTH: 1337
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                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
APPLICANT: Johnes Milne Edwards, Jean Baptiste
APPLICANT: Johnes Milne Edwards
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REPERENCE: 78.US3.REG
CURRENT APPLICATION NUMBER: US/10/643,836
CURRENT APPLICATION NUMBER: US/09/731,872
PRIOR FILING DATE: 2000-12-07
PRIOR FILING DATE: 1999-12-08
PRIOR FILING DATE: 1999-12-08
PRIOR FILING DATE: 2000-03-06
NUMBER OF SEQ ID NOS: 482
SOFTWARE: Patent.pm
SEQ ID NO 19
LENGTH 691
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                                                                                                                                                                                                                                                                                                                                              Length 691;
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100.0%; Score 51; DB 3; I
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 51; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 2.9e-10;
tive 0; Mismatches 0;
                                                                                                                                                                             OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 10.7019149919754
OTHER OFFORMATION: seq VLMLLAVLIWTGA/EN
US-09-876-997-19
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OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: 8core 10.7019149919754
OTHER INFORMATION: 8eq VLMLLAVLIWHGA/EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19, Application US/10643836
Publication No. US20050096458A1
GENERAL INFORMATION:
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; Sequence 2, Application US/10467046
; Sequence 2, Publication No. US20040235709A1
; GENERAL INFORMATION:
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APPLICANT: Ebbets-Reed, Dana
APPLICANT: Chicca, Barbara A.
APPLICANT: Chicca, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 100.4
Matches 51, Conservative
                         FEATURE:
NAME/KEY: CDS
LOCATION: 42..515
NAME/KEY: 819_peptide
LOCATION: 42..92
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: 42..92
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LOCATION: 42..515
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NAME/KEY: misc feature
LOCATION: (1398)..(1398)
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NAME/KEY: SITE
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US-10-472-533-175
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LENGTH: 1898
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  0; Gaps
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                                                                 29 AIGGCGTIAGAAGICTIGAIGCICCTCGCTGTCTIGATTIGGACCGGTGCT 79
                                           1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGGATTTGGACCGGTGCT 51
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Sequence 1704, Application US/10104047

Publication No. US2003026392A1

GENERAL INFORMATION:

FAPLICANT: HELLIX RESEARCH INSTITUTE

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/10/104,047

CURRENT FILING DATE: 2002-03-25

PRIOR FILING DATE: 2002-03-25

PRIOR FILING DATE: 2002-03-25

NUMBER OF SEQ ID NOS: 4096

SOFTWARE: Patentin Ver. 2.1

LENTH: 1492
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  0; Indels
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100.0%; Score 51; DB 5; L
Best Local Similarity 100.0%; Pred. No. 3.7e-10;
Matches 51; Conservative 0; Mismatches 0;
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Sequence 27, Application US/10050704

Publication No. US20030050442A1

GERERAL INFORMATION:

GERERAL INFORMATION:

TITLE OF INVENTION:

FILE REFERENCE: PZ039P1

CURRENT APPLICATION NUMBER: US/10/050,704

CURRENT FILING DATE: 2002-01-18

PRIOR APPLICATION NUMBER: 09/684,524

PRIOR PILING DATE: 2000-10-10

FRIOR PELICATION NUMBER: 60/128,693

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-06

PRIOR PILING DATE: 1999-04-06

PRIOR PILING DATE: 1999-04-06

SRICH PRIOR PILING DATE: 1999-04-06

NUMBER OF SEQ ID NOS: 344

SOFTWARE: PATENTIN VERNER: 60/130,991

PRIOR PILING DATE: 1999-04-26

NUMBER OF SEQ ID NOS: 344

LENGTH: 1898
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1428)
COTHER INFORMATION: n equals a,t,g, or c
US-10-050-704-27
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
  51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CORGANISM: Homo sapiens
US-10-104-047-1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                          -10-104-047-1704
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  Matches
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15 Arcecerraciaeterrearecreerererrearrrearece
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100.0%; Score 51; DB 7; Length 18
Best Local Similarity 100.0%; Pred. No. 3.7e-10;
Matches 51; Conservative 0; Mismatches 0; Indels
                                                                                                                                                          Sequence 27, Application US/10798512
Fublication No. US20040152164A1
GENERAL INFORMATION:
APPLICARY: Ruben et al.
TITLE OF INVENTION: 62 Human Secreted Proteins
FILE REFRENCE: PS039P1
CURRENT APPLICATION NUMBER: US/10/798,512
CURRENT FILING DATE: 2000-10-10
FRIOR APPLICATION NUMBER: PCT/US00/08979
FRIOR FILING DATE: 2000-10-10
FRIOR FILING DATE: 2000-10-10
FRIOR FILING DATE: 1999-04-06
FRIOR FILING DATE: 1999-04-09
FRIOR FILING DATE: 1999-04-06
FRIOR FILING DATE: 1999-04-06
FRIOR FILING DATE: 1999-04-06
NUMBER OF SEQ. ID NOS: 344
SOSTWARE: Patentin Ver. 2.0
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Publication No. US20050197285A1

GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFRENCE: PS906FT
CURRENT FILING DATE: 2003-09-20

PRIOR FILING DATE: 2001-11-13

PRIOR FILING DATE: 2001-11-13

PRIOR FILING DATE: 2001-11-19

PRIOR FILING DATE: 2001-07-19

PRIOR APPLICATION NUMBER: US 60/306,171

PRIOR FILING DATE: 2001-07-19

PRIOR APPLICATION NUMBER: US 60/207,340

PRIOR PILING DATE: 2001-07-19

PRIOR FILING DATE: 2001-07-19

SOFTWARE: PALENTING DATE: 2001-07-19
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NAME/KEY: SITE
LOCATION: (1428)
OTHER INFORMATION: n equals a,t,g, or c
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Gaps
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Sequence 21218, Application US/09925065A

Publication No. US20050228172A9

GENERAL INPORMATION:
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR PELING DATE: 2000-11-24

PRIOR PELING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR PELING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-36

PRIOR FILING DATE: 2001-01-6

PRIOR FILING DATE: 2001-01-6

PRIOR FILING DATE: 2001-01-6

PRIOR FILING DATE: 2001-01-6

NUMBER OF SEQ ID NOS: 957066

SOFTWARE: PRASESEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT 51
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100.0%; Pred. No. 5.3e-10;
.ive 0; Mismatches 0; Indels
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NAME/KEY: misc feature

LOCATION: (9942)...(9942)

OTHER INFERMATION: n is a, c, g, or t
US-10-467-046-1
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LOCATION: (8293)
OTHER INFORMATION: n is a,
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LOCATION: (8334)..(8336)
OTHER INFORMATION: n is a,
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OTHER INFORMATION: n is a,
                                                                   NAME/KEY: misc feature
LOCATION: (8197)..(8197)
OTHER INFORMATION: n is a,
                             OTHER INFORMATION: n is a,
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Matches 35, Conservative
         LOCATION: (7347)..(7348)
                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
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; ORGANISM: Homo sapiens
US-09-925-065A-21218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-925-065A-21218/c
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US-10-719-993-6875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 21218
L'ENGTH: 526
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; Publication No. US20040235709A1
; GENERAL INFORMATION:
; APPLICANT: Salter-Cid, Luisa
; APPLICANT: Chicca, Barbara A.
; APPLICANT: Chicca, Dana
; APPLICANT: Chicca, Ohn
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: GSSP3 Polymucleotides and Polypeptides and Uses Thereof
; TITLE OF INVENTION: USPSP3 Polymucleotides
; CURRENT APPLICATION NUMBER: US/10/467,046
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/266,156
; NUMBER OF SEQ ID NOS: 3
; SOFFWARE: Patentin version 3.0
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                                                                                                                                                  Query Match
100.0%; Score 51; DB 9; Length 1898;
Best Local Similarity 100.0%; Pred. No. 3.7e-10;
Matches 51; Conservative 0; Mismatches 0; Indels
                                        NAME/KEY: misc feature
J. LOCATION: (1428)... (1428)
J. OTHER INFORMATION: n equals a,t,g, or c
US-10-472-533-175
OTHER INFORMATION: n equals a,t,g, or c
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OTHER INFORMATION: n is a, c, g,
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LOCATION: (2986)..(2986)
OTHER INFORMATION: n is a, c,
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LOCATION: (3847)..(3848)
OTHER INFORMATION: n is a,
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LOCATION: (3879)..(3879)
OTHER INFORMATION: n is a,
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LOCATION: (4105)...(4105)
OTHER INFORMATION: n is a,
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LOCATION: (4107)..(4109
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NAME/KEY: misc_feature
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ORGANISM: Homo sapiens
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LOCATION: 2387...2501
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LOCATION: 6649...6747
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LOCATION: 8907...9774
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LENGTH: 10115
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US-10-467-046-1
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Sequence 6875, Application US/10719993
Publication No. US20040265849A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 6875
LENGTH: 74648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    839 TGGTCTTGGGAAICTTTAAGCTCCTCTCAGTTTTGACATGGCCAGGTG 886
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                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CORGANISM: Homo sapiens
US-10-719-993-6875
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Sequence 106, App Sequence 806364, Sequence 742070, Sequence 375274,

Sequence 375233, Sequence 28636, Sequence 28637, Sequence 296631, Sequence 375275, Sequence 375275, Sequence 64489, A Sequence 64489, A Sequence 673082, Sequence 673083, Sequence 71644, A Sequence 71645, A Sequence 71645, A Sequence 786293, Sequence 786293,

US-09-925-065A-298636 US-09-925-065A-298636 US-09-925-065A-298636 US-09-925-065A-298636 US-09-925-065A-298686 US-09-925-065A-64489 US-09-925-065A-64489 US-09-925-065A-71644 US-09-925-065A-71644 US-09-925-065A-71645 US-09-925-065A-71645 US-09-925-065A-71645 US-09-925-065A-71645 US-09-925-065A-71645 US-09-925-065A-71645 US-09-925-065A-71645 US-09-925-065A-71645 US-09-925-065A-71646 US-09-925-065A-71645 US-09-925-065A-71645 US-09-925-065A-71645 US-10-301-480-172884 US-10-301-480-172884 US-10-301-480-172884 US-10-301-480-1768616

Sequence 650301

US-10-750-623-50706 US-10-995-561-13227

ALIGNMENTS

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317876
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ORGANISM: Homo sapiens
 US-10-475-075-564
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SEQ ID NO 564
LENGTH: 497
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                               Sequence 122455,
Sequence 735864,
Sequence 453, App
Sequence 317, App
Sequence 69, Appl
Sequence 552778,
Sequence 116187,
Sequence 151, App
Sequence 456973,
Sequence 456973,
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Sequence 563, App
Sequence 1704, Ap
Sequence 21218, A
                                                                                                             (without alignments)
1978.089 Million cell updates/sec
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| SIDS5/ptodata/1/pubpna/USO8 NEW PUB.seq:*
| SIDS5/ptodata/1/pubpna/USO8 NEW PUB.seq:*
| SIDS5/ptodata/1/pubpna/USO7 NEW PUB.seq:*
| SIDS5/ptodata/1/pubpna/USO7 NEW PUB.seq:*
| SIDS5/ptodata/1/pubpna/USO8 NEW PUB.seq:*
| SIDS5/ptodata/1/pubpna/USO9 NEW PUB.seq:*
| SIDS5/ptodata/1/pubpna/USO9 NEW PUB.seq:*
| SIDS5/ptodata/1/pubpna/USO9 NEW PUB.seq:*
| SIDS5/ptodata/1/pubpna/USO9 NEW PUB.seq:*
| SIDS5/ptodata/1/pubpna/USO0 NEW PUB.seq:**
                                                                                              May 9, 2006, 13:13:06; Search time 105 Seconds
            GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-301-480-122455

US-10-311-937-453

US-10-511-937-453

US-10-513-937-453

US-10-10-312-317

US-10-301-480-52778

US-10-301-480-1166187

US-10-301-480-1166187

US-10-301-480-1166187

US-10-301-480-1166187

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US-10-301-480-1166187

US-10-301-480-1166187
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US-10-475-075-563
US-11-072-512-1704
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51
1 atggcgttagaagtcttgat.....
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Maximum Match 100%
Listing first 45 summaries
                                                                  nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Match Length
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647.5
643.9
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Perfect score:
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No.
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APPLICANT: Bejanin, Stephane
APPLICANT: Bejanin, Stephane
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Jobert, Severin
APPLICANT: Giordano, Jean-Yves
TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins
FILE REPERBENCE: G-081U803PTC
CURRENT APPLICATION NUMBER: US/10/475,075
CURRENT FILING DATE: 2003-10-17
PRIOR PILING DATE: 2001-04-18
PRIOR FILING APE: 2001-04-18
SUPPRIOR FILING APE: 2001-04-18
SUPPRIOR FILING DATE: 2001-04-18
SUPPRIOR FILING DATE: 2001-04-18
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100.0%; Pred. No. 8.3e-11;
ive 0; Mismatches 0;
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FEATURE:
NAME/KEY: sig_peptide
LOCATION: 52..102
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 10.6999998092651
OTHER INFORMATION: seq VLMLLAVLIWTGA/EN
; Sequence 564, Application US/10475075; Publication No. US20060053498A1; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 51; Conservative
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Sequence 122455, Application US/10301480
; Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms; TITLE OF INVENTION: in the Human Genome
; FILE REPERENCE: 108827.137
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APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US 60/350,978
PRIOR APPLICATION NUMBER: US 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER: OF SEQ ID NOS: 4096
SEQ ID NO 1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21218, Application US/09925065A Publication No. US20040181048A1
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Best Local Similarity 70.0
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-21218
                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
US-11-072-512-1704
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APPLICANT: Tanaka, Hiroaki
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Dumas Milne Edwards, Jean-Yee
APPLICANT: Glordano, Jean-Yee
TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins
FILE REFERENCE: G-081US03PCT
CURRENT APPLICATION NUMBER: US/10/475,075
PRIOR PPLICATION NUMBER: PCT/IB01/00914
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 918
SOFTWARE: Patent.pm
SEQ ID NO 563
LENGTH: 500
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       1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 72..122
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 10.6999998092651
OTHER INFORMATION: seq VLMLLAVLIWTGA/EN
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Publication No. US20060029945A1
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// OTHER INFORMATION: n = a, g, c or t
US-10-475-075-563
                                                                                                                                                                Sequence 563, Application US/10475075
Publication No. US20060053498A1
GENERAL INFORMATION:
APPLICANT: Bejanin, Stephane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: 1SOGAI, TAKAO
APPLICANT: SUGIXAMA, TOMOXASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISONO, JUN-ICHI
APPLICANT: HOO, YUKI
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OTSUKA, MOTOYUKI
NAGAHARI, KENJI
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SEKI, NAOHIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTSUKA, KAORU
NAGAI, KEIICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIE, RYOTARO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens
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LOCATION: 72..122
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LOCATION: 72..500
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NAME/KEY: Unsure
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                                                                                                                                             US-10-475-075-563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 4156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 CTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
6
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Pred. No. 9.7;
0; Mismatches 8;
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CURRENT APPLICATION NOWEL #11/072,512
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.4%; Pred. ....tive 0; Mismatches
                   APPLICATION NUMBER: PCT/US2003/012946
      PRIOR APPLICATION NUMBER: PCT/US2003/01294,
PRIOR PILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-012-20
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PATENTIN VERSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 317, Application US/11072512; Publication No. US20060029945A1; GENERAL INFORMATION: APPLICANT: ISOGAI, TAKAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
NAGAHARI, KENJI
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OTSUKI, TETSUJI
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YAMAMOTO, JUN-ICHI
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RYOTARO
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Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WAKAMATSU, AI
SATO, HIROYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTSUKA, KAORU
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                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-11-072-512-317
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
US-10-893-483-49/c
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                                                                                                                                                                                                                                                                     SEQ ID NO 453
LENGTH: 4156
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 10827.1137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR PILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SEQ ID NO 735864
LENGTH: 526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 12; Length 526
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APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: METHODS AND MONITORING TRANSPLANT REJECTION
TITLE PEPERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
                                                                                                                                                                                                                                                                                                                                                                                                                                                51.0%; Score 26; DB 11; Length 52 70.0%; Pred. No. 1.3; tive 0; Mismatches 15; Indels
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70.0%; Pred. No. 1.3;
iive 0; Mismatches
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR PILING DATE: 2002-08-09
PRIOR APPLICATION WUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FRSESEQ for Windows Version 4.0
SEQ ID NO 122455
LENGTH: 526
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Publication No. US20060088836A1
GENERAL INCORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
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Woodward, Robert
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Best Local Similarity 70.0°
Matches 35, Conservative
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Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapien
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US-10-301-480-735864
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APPLICANT:
APPLICANT:
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; ORGANISM: Homo sapiens
US-10-505-928-151
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US-10-301-480-1166187
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APPLICANT: Wang, David G.

TITLE OF INVENTION: In the Human Genome
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108927.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-00
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FREEEEQ for Windows Version 4.0
SEQ ID NO 552778
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Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
CURRENT FILINO NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US/10/215,598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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                                                                                         APPLICANT: Blatzer, Josef
APPLICANT: Blatzer, Josef
APPLICANT: Schooten, Wim van
TITLE OF INVENTION: Humanized Immunoglobulin Loci
FILE REFERENCE: 39691-0007A
CURRENT APPLICATION NUMBER: US/10/893,483
PRIOR APPLICATION NUMBER: 60/487,733
PRIOR FILING DATE: 2003-07-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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Pred. No. 41;
                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 460
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 552778, Application US/10301480
Publication No. US20060057564A1
Sequence 49, Application US/10893483
Publication No. US20060026696A1
GENERAL INFORMATION:
APPLICANT: Buelow, Reland
                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Oryctolagus cuniculus
US-10-893-483-49
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Best Local Similarity 66.7%;
Matches 32; Conservative
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Best Local Similarity 76.3%;
Matches 29; Conservative
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; ORGANISM: Homo sapien
US-10-301-480-552778
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Publication No. US20040181048A1

SEQUENCE ASSOCIATION:
GREEKL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome;
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT APPLICATION NUMBER: US 60/243,096

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR FILING DATE: 2000-11-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 9570608

SOFTWARE: FRASESQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 151, Application US/10505928
Publication No. US20060088532A1
GENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research et al.
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28667/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
                                                                                                                                                                                                                                                                                                      Score 22.4; DB 12;
Pred. No. 41;
0; Mismatches 16;
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66.7%; Pred. No. 86;
:ive 0; Mismatches
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 741
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Best Local Similarity 66.7%;
Matches 32; Conservative (
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Best Local Similarity 66.7%
Matches 32, Conservative
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SOFTWARE: Patentin 3.2
SEQ ID NO 151
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353 TAGAGGTCTTGAAGCTCCTCCTCTGTAGAAGTGG 319
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Publication No. US20060057564A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms

TITLE OF INVENTION: in the Human Genome

CURRENT PELICATION NUMBER: US/10/301,480

CURRENT FILING DATE: 2002-11-21

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1128341

LENGTH: 635
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Publication No. US20060057564A1
GENERAL INPORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: In the Human Genome
TITLE APPLICATION WHERE: US/10/301,480
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT APPLICATION NUMBER: US 10/215,598
PRIOR PILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOUTHARE: FRAEESEQ FOR Windows Version 4.0
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43.5%; Score 22.2; DB 7; Length 625;
Best Local Similarity 77.1%; Pred. No. 49;
Matches 27; Conservative 0; Mismatches 8; Indels (
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43.5%; Score 22.2; DE
Best Local Similarity 77.1%; Pred. No. 49;
Matches 27; Conservative 0; Mismatches
                    TYPE: DNA
CORGANISM: Homo sapiens
US-09-925-065A-456973
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; ORGANISM: Homo sapien
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; ORGANISM: Homo sapien
US-10-301-480-1128341
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CO960964 Pe15c12.y
CQ144937 PUIKSOSTD
CW516351 OP BROO4
CW516351 OP BROO4
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco R1; 1st strand cDNA
was prepared; Site 1: Not 1; John Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
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information can be
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CK2481997 POLI 76 A
CK2481997 POLI 76 A
CK348182 BET008024
CK370178 170005999
AA707067 zj28a07.8
BEZ683112 BEZ881182
BEZ68311 601194810
CK370177 170005319
BEC68118 170006001
CK980458 CK980458
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
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1 (bases 1 to 331)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NATional Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Barl: ggapbs-r@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMANDA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 395 Scd Brzor: 0.00
Seq primer: -40ml3 fwd. BT from Amersham.
Location/Qualifiers
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VERSION
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CF819479 EST808176
CF816222 EST693604
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BB008763 BB008763
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3787.526 Million cell updates/sec
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              GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd
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Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGACGCCGAGGCGCGAATG-AT (30) BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo, CA)."
(Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTYT3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                       BE972717 516 bp mRNA linear BST 04-OCT-2000 601652136F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935288 5',
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM777 row: h column: 09
High quality sequence stop: 505.
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1 (bases 1 to 516)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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/mol_type="mRNA"
/db_xref="teaxon:9606"
/db_sref="IMAGE:3935288"
/lab host="DH108 (T1 phage-resistant)"
/clone_lib="NIH_MGC_82"
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I Similarity 100.0%; Pred. No. 2.4e-08;
51; Conservative 0; Mismatches 0;
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BE972717.1 GI:10586053
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Best Local Similarity 100.
Matches 51, Conservative
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Matches 51; Conserv
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RESULT 3

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753 bp mRNA linear EST 16-SEP-2002
AGENCOURT_10278669 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6592356
5', mENA sequence.
BUS61351
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BI463012 626 bp mRNA linear EST 21-AUG-2001
603204535F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5270384 5',
                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

cloud through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LiAM11682 row: e column: 09
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarihini,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 753)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Location/Qualifiers
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/db_xref="taxon:9606"
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/lab_host="DH10B"
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us-10-664-025-43_copy_53_103.rst

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Homo sapiens
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BG772527.1 GI:14083180

EST.2527.1 GI:14083180
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: egabbe-remail.nih.gov
Tissue Procurement: CLONYECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
Clone distribution: MGC clone distribution information
Clone distribution: MGC clone distribution information
clone distribution: MGC clone distribution information
thtp://image.lnl.gov
Plate: LLCM2815 row: g column: 12
High quality sequence stop: 442.
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIREN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Location/Qualifiers
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1 (bases 1 to 776)
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KEYWORDS
SOURCE
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BG772527
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/clone_lib="NIH_MGC_97"
/clone="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamH; Site_2: Sall-xhol (gtcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size-2: kb and normalized to ROF 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein a NIH_MGC Library.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B1459538 778 bp mRNA linear EST 21-AUG-2001
603200545F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5266642 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGKI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

TOSHIYUki and Piero Carninci (RIKEN)

TOSHIYUki and Piero Carninci (RIKEN)

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hominidae, Homo.

1 (bases 1 to 778)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                      th 100.0%; Score 51; DB 2; Length 776; Similarity 100.0%; Pred. No. 2.7e-08; 51; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 674.
Location/Qualifiers
                        /clone="IMAGE:4837612"
/lab_host="DH108"
xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a NIH MGC Library."
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B1459538.1 GI:15250194
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Hominidae; Homo.
                                                                             Homo sapiens
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                   3X118111.1
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               VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
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KEYWORDS
SOURCE
ORGANISM
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/tissue_type="medulla"
/tissue_type="medulla"
/lab host="DHIDB"
/clone lib="NIH MGC L19"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                               BIS20154 119 HOMO SAPIES CDNA CLORE IMAGE:5163455 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LibrANI1465 row: m column: 24
High quality sequence stop: 851.
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                             Gaps
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                                                                                                                                    191 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT 241
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                                                                                                               1 AIGGCGITAGAAGICTIGAIGCICCICGCIGICTIGAITIGGACCGGIGCI
                                   Length 778;
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                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                 100.0%; Score 51; DB 3; I
100.0%; Pred. No. 2.7e-08;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                         BI520154
BI520154.1 GI:15344946
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                          Hominidae; Homo.
1 (bases 1 to 878)
                                   Query Match
Best Local Similarity 100.
Matches 51; Conservative
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                                                                                                                                                                                                                                                                                         mRNA sequence.
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Best Local S
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ORGANISM
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JOURNAL
COMMENT
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KEYWORDS
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Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Econed into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            598 bp mRNA linear EST 17-DEC-2003
H3059H12-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
H3059H12 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B"
/clone lib="Soares testis NHT"
/note="Vector: pTyT3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not 1; Site_2: Eco RI; lst strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free from RZPD; contact RZD; contact RZDD (chone@rzpd.de) for further information. Seq primer: M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                   1 (Diases incomp.)

2 (Diases incomp.)

2 (Diases incomp.)

3 (Diases incomp.)

4 (Diases incomp.)

5 (Diases incomp.)

6 (Diases incomp.)

6 (Diases incomp.)

7 (Diases incomp.)

8 (Diases incomp.)

9 (Diases incomp.)

9 (Diases incomp.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.rzpd.cd.clonecadas/cgi.
bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Fex: +49 30 32639 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="IMAGP998D122574 ; IMAGE:1030619"
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/db_xref="taxon:9606"
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Mus musculus
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GI:27881212
                                                                 sapiens (human)
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Scaurognath; Murzidea; Murzinae; Mus.
Scaurognath; Murzidea; Murzinae; Mus.
Nikaidon; O. Sauto, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K., Frazer, K.S., Gasterland, T.A.,
Fletcher, C.F., Forrest, R., Frazer, K.S., Gasterland, T.A.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, B.L., Konagaya, A.,
Kawaji, H., Kawasawa, Y., Kedierski, R.M., King, B.L., Konagaya, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
Fetrovsky, N., Pillai, R., Pontius, J.U., Oli, D., Ramachandran, S.,
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Tasdale, R.D., Tomita, M.,
Verado, R., Van, Margere, C., Semple, C.A., Setou, M., Shimada, K.,
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
Saltana, R., Takenaka, Y., Taylor, M.S., Taylor, M.S., Taylor, M.S., Taylor, M.S., Carhinci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Arakawa, T., Bultary, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Genome Sequences Mann. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
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Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Adachi,J., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itob,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohasto,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Direct Submission
                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
                                                                                                                                 Sciurognathi, Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Yoshihide Hayashizaki
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/clone is among a rearrayed set of 15,247 Clones from 11
clone is among a rearrayed set of 15,247 Clones from 11
embryo cDNA libraries (including preimplantation stage
embryos from unfertilized egg to blastocyst, embryonic
part of E7.5 embryos, extraembryonic part of E7.5
embryos, and E1.5 female mesonephros/gonad) and one
newborn ovary CDNA library. Average insert size 1.5 kb.
All source libraries are cloned unidirectionally with
Oligo(dT)-Not primers. References include: (1)
Genome-wide expression profiling of mid-gestation
placenta and embryo using a 15,000 mouse development al
CDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97:
9127-9122; (2) Large-scale cDNA analysis reveals phased
gene expression patterns during preimplantation mouse
develolpment, 2000, Development, 127: 173-1749; (3)
Genome-wide mapping of unselected transcripts from
extraembryonic tissue of 7.5-day mouse embryos reveals
enrichment in the t-complex and under-representation on
the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
                                                                                                                                                                                                                                                                                                                                                                Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
National Institute on Aging/National Institutes of Health
1333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@1gsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details.
Seq primer: -21M13 Reverse
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BY731676 RIKEN full-length enriched, 2 days pregnant adult female ovary Mus musculus cDNA clone E330031A07 5', mRNA sequence.
                               Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X.,
Grahovac,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,H.,
Wood,W.H. III, Becker,K.G. and Ko,M.S.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA
                                                                                                                                             Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
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                                                                                                                                                                                                                                                                                                          On Jan 26, 2001 this sequence version replaced gi:12563570.
Other_ESTs: H3059H12-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/mol_type="mRNA"
/strain="CSPL/GJ"
/db_xref="niasG?:H3059H12-5"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 598 POLYA=No.
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EST.
Mus musculus (house mouse)
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/mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="Plate=1058 Col=17 Row=D"
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GSS.
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Homo sapiens
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Class: BAC ends
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AQ743481
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862 bp mRNA linear EST 06-AUG-2004
AGENCOURT 30258260 NIH MGC_257 Mus musculus cDNA clone
IMAGE:30931566 5', mRNA sequence.
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I (Dasse 1 to 862)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm.0A07 Betheada, MD 20892

Email: Cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Kathleen Horner, Stanford University

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

High quality sequence stop: 654.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
                                                                                                                                                                                                                                                                                          /note="Site 1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                         /tissue_type="ovary"
/dev_stage="2 days pregnant adult"
/lab_nost="DH10B"
/clone lib="RIKEN full-length enriched, 2 days pregnant
adult female ovary"
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/clone="IMAGE:30931566"
/lab_host="DH10B_TonA"
   xref="taxon:10090"
db_xref="taxon:100"
|clone="E330031A07"
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CO810251.1 GI:51028724
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Best Local Similarity
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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
/clone lib="NIH MGC 257"

/note="Organ: oocyte; Vector: pExpress-1; Site_1: EccRV;
Site_2: NotI; cDNA was primed using oligo-dT primer:
5'-pGACTACTACACGCGACGCCCCC(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >0.5 kb
resulted in an average insert size of 1.0kb. This is a
normalized library (primary library is NIH MGC_256) and
was constructed by Express Genomics (Frederick, MD). Note:
this is a NIH_MGC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae; Homo.

1 (bases 1 to 834)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,

Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="RPCI-11 Human Male BAC Library"
//clone lib="Wector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor and partially disested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ743481
HS_5482_B1_B09_SP6_RPCI-11 Human Male_BAC_Library Homo sapiens
genomic_clone_Plate=1058_Col=17_Row=D, genomic_survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Cocidioides posadasii
Cocidioides posadasii
SM Coccidioides posadasii
Coccidioides posadasii
Coccidioides posadasii
Sukaryota; Fundi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides
I (bases I to 738)
S Gardner,M.J. and Cole,G.T.
Gardner,M.J. and Cole,G.T.
Analysis of gene expression in Coccidioides posadasii mycelia and spherules via expressed sequence tags
Unpublished (2003)
Unpublished (2003)
Contact: Gardner MJ
The Institute for Genomic Research
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 9208
                                                                                                                                                                   Submitted (102-100-1001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbeedger.riken.go.jp, URL.http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 01-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   738 bp mRNA linear EST 01-APR-200 EST689341 Coccidioides posadasii saprobic phase cDNA library, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                  Unpublished

2 (bases 1 to 621)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanbe, H. and Sakaki, Y.
Direct Submission
          Taylor, T.D., Yada, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 52.2%; Score 26.6; DB 10; Length 621; 1 Similarity 76.2%; Pred. No. 41; 32; Conservative 0; Mismatches 10; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254 TGGNGGTCGATGTCTTGATGATCCTGGCTGTGGGGATTTGCA 295
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/mol_type="mRNA"
/strain="C735"
    Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library RPCI-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Pan troglodytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic_DNA"
/db_xref="taxon:9598"
/clone="RP43-016P02.TJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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: EcoRI
: EcoRI.
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Seq primer: M13 Reverse
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                                                                                                                                                                                                                                                                                                                                                              Sequencing: TJ
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R.Site 2
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CF811959/c
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                                                                                                                                                                                                                             CC815351 859 bp DNA linear GSS 16-JUL-2003
ZAWBBC0521C24r ZAWBBc Zea mays genomic clone ZAWBBC0521C24 3',
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                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 859)
Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C., Sequencing of the maize genome at PGIR (2003b)
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSS 09-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBBc0521C24"
/lab host="E. coli DH10B"
/clone_lib="ZMMBBc"
/note="Vector: pTARBAC1.3; Site_1: BamHI; Site_2: BamHI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Pan troglodytes DNA, clone: RP43-016P02.TJ, genomic survey
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                                                                                                       231 TGGCGCCCGATGTCTTGATGATCCTGGCTGTGGGGATTTGCATCAGT 277
      DB 9; Length 834;
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                                             Indels
                                                                                   2 TGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
7ea: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.5%; Score 26.8; DB 9;
73.9%; Pred. No. 36;
iive 0; Mismatches 12;
  Score 27.8; DE Pred. No. 15; 0; Mismatches
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Location/Qualifiers
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                                                                                                                                                                                                                                                                      genomic survey sequence.
CC815351
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Ouery Match
Best Local Similarity 74.5%;
Matches 35; Conservative
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/db xref="taxon:199306"
/clone="CIBA142"
/dev tagge="baprobic phase (mycelia)"
/dav stagge="saprobic phase (mycelia)"
/lab_host="E. coli DH10B, Tl phage resistant"
/clone lib="Coccidioides posadasii saprobic phase cDNA
library, greater than 4kb"
/note="vector: pExpress l; Site_1: Not I; Site_2: Eco RV;
Coccidioides posadasii saprobic phase cDNA library, size
fractionated cDNA > 4 kb"
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Search completed: May 9, 2006, 14:40:01 Job time : 635 secs

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                                     Aabj8337

Aabj8337

Abg 79646

Add14149

Abm85595

Abm852953

Adx40751

Adx40751

Adx40751

Adx40751

Adx51908

Adx24002

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ADC74338
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gene expression by rectifying mutations or deletions in a patient's gene expression by rectifying mutations or deletions in a patient's genome that affect the activity of GNNSET or by supplementing the patients own production of GENNSET polypeptides. Conversely, antisense nucleic acid molecules may be administered to down regulate GENNSET expression by binding with the cells' own genes and preventing their expression. The sense and antisense nucleic acids may also be used as DNA probes in diagnostic assays to detect to duratitate the presence of similar nucleic acid sequences in samples, and hence to determine which patients may be used of restorative therapy. The GENNSET polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators (agoniers and antagonists) of GENNSET polypeptide expression and activity. The present sequence is a GENNSET polypeptide of
                                                                                 potentially secreted proteins. The nucleic acids and the polypeptides they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GENSET gene expression. For example, they be used to treat disorders associated with decreased GENSET
                                                                 encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Giordano J;
                                                               invention relates to full length GENSET human nucleic acids
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diseases, and for diagnosis of those diseases.
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                                 Claim 21; Page 806; 921pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 106 AA;
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New GENSET polynucleotides and polypeptides, useful for treating heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, CNS, cardiovascular or gastrointestinal effects of the

WPI; 2003-075548/07.

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The present invention relates to novel GENSET polynucleotides (ABZ36404-ABZ56911) encoding polypeptides (ABP75963-ABP76368). The polynucleotides and polypeptides are useful in screening and diagnostic assays for abnormal GENSET expression and/or biological activity. They are also useful for screening of compounds for treating or preventing GENSET-related disorders, such as heavy metal toxicity, cancer, inflammatory diseases, immume disorders, and the neuromuscular, central nervous system (CNS), cardiovascular or gastrointestinal effects of the toxicity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatic; antiinflammatory; nootropic; neuroprotective; cardiant; gastrointestinal; gene therapy; GRNET; heavy metal toxicity; cancer; inflammatory disease; immune disorder; neuromuscular; toxicity; central nervous system; cardiovascular; gastrointestinal.
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                                 Claim 14; Page 680; 735pp; English.
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The invention interacts to tuil femilia man included according potentially secreted proteins. The nucleic acids and the polypeptides they encode may be used in the prevention, treatment and diagnosts of diseases associated with inappropriate GRNSET gene expression. For example, they be used to treat disorders associated with decreased GENSET gene expression by rectifying mutations or deletions in a patient's gene expression by rectifying mutations or deletions in a patient's gene expression by rectifying mutations or deletions in a patient's patients own production of GENSET polypeptides. Conversely, antisense nucleic acid molecules may be administered to down regulate GENSET carpression. The sense and antisense nucleic acids may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence to determine which suffice may be in need of restorative therapy. The GENSET polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of GENSET polypeptide of expression and activity. The present sequence is a GENSET polypeptide
diseases, immune disorders, and the neuromuscular, central nervous system (CNS), cardiovascular or gastrointestinal effects of the toxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to full length GENSET human nucleic acids encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-367870/38.
N-PSDB; AAH64743.
                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                     Sequence 148 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200142451-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                       Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                 AAG89140;
                                                                                                                                                                              Query Match:
                                                                                                           Pred. No.:
                                                                                                                                                                                                                                                                                                                                             RESULT 4
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                                                                                                                            Score:
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Human; cell growth; differentiation; death; CGDD; cancer; cell proliferative disorder; arteriosclerosis; atherosclerosis; cirhosis; hepatitis; paroxysmal nocturnal haemoglobinuria; psoriasis; polycythaemia vera; primary thromobocytopaenia; developmental disorder; renal tubular acidosis; anaemia; mental retardation; epilepsy; AIDS; neurological disorder; Alzheimer disease; Parkinson's disease; asthma; reproductive disorder; infertility; autoimmune disorder; gout; allergy; inflammatory disorder; acquired immunodeficiency syndrome; uveltis; autoimmune thyroiditis; contact dermatitis; Crohn's disease; infection; diabetes mellitus; glomerulonephritis; irritable bowel syndrome; multiple sclerosis; osteoparthritis; pancreatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baughn MR;
Burford N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated polypeptide comprising CGDD1-12 (cell growth, differentiation and death), a naturally occurring amino acid sequence at least 90% identical to CGDD, a biologically active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human proteins associated with cell growth, differentiation and death, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), cancer, atherosclerosis or hepatitis.
                                                                                                                                                                                                  21
                                                                                                                                                                                                              ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yao MG, Ison CH, Lu Y, Warren BA, Elliott VS,
Xu Y, Gietzen KJ, Tang TY, Lal PG, Duggan BM,
Richardson TW, Tran UK, Khare R, Walia NK;
                                                  158
17
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                                                                                                                                                           US-10-664-025-43_COPY_53_103 (1-51) x AAG89140 (1-158)
                                                                  Matches:
Conservative:
Mismatches:
                                                  Length:
                                                                                                               Indels:
                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                            ABG97353 standard; protein; 158 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 146; 181pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              Human CGDD4, INCYTE 5284076CD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-FEB-2001; 2001US-0268111P.
23-FEB-2001; 2001US-0271175P.
08-MAR-2001; 2001US-0274503P.
09-MAR-2001; 2001US-0274552P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-FEB-2002; 2002WO-US003715
                                                  0.000172
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100.0%
88.0%
                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rheumatoid arthritis.
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N-PSDB; ABS78646.
                                                                                                Best Local Similarity:
Sequence 158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200272830-A2.
                                                                               Percent Similarity:
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                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                              16-DEC-2002
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                                                                                                                                                                                                                                                                                                                              ABG97353;
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Lu DAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yue H,
                                                                                                               Query Match:
                                                 Pred. No.:
                                                                                                                                                                                                                                                            RESULT 5
                                                                                                                                                                                                                                                                                ABG97353
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01-FEB-2002; 2002WO-IB001333.

08-AUG-2002.

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Liegument. Or an immunogenic Iraquent. Also included are the polymucleotides encoding CGDD1-12, a recombinant polymucleotides encoding CGDD1-12, a recombinant polymucleotide.

Comprising a promoter sequence operably linked to the CGDD comprising the recombinant polymucleotide, a cell transformed with the recombinant polymucleotide, an anti-car transgenic organism comprising the recombinant polymucleotide, an anti-cCGDD antibody, screening for compounds which bind to/modulate or are compounds antipolymucleotide and a preventing disorders associated with aberrant expression of CGDD, polymucleotide microarray. The polypeptides, polymucleotides associated with aberrant expression of CGDD, particularly cell proliferative (e.g. arteriosclerosis, atherosclerosis, particularly cell proliferative (e.g. arteriosclerosis, atherosclerosis, particularly the polypeptides, and proper content disorders (e.g. Alzheimer disease, Parkinson's disease or disorders (e.g. renal tubular acidosis, anaemia or mental retardation), neurological disorders (e.g. Alzheimer disease, Parkinson's disease or centerfy productive disorders (e.g. infertility or a distrubtion in the menstrual cycle), or autoimmune/inflammatory disorders (e.g. Alzheimer disease, asthma, autoimmune context dermatitis, crohn's disease, disbetes mellitus, crohrad, polymuclament, and polymuclament, fungal, parasitic, procasal or helminthic cuesting in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid crepresents a compounds on the expression of nucleic acid and amino acid crepresents a components and proper and compounds on the expression of nucleic acid and emino acid crepresents a component and components of proper and components of proper and components and context descented with CGDD. The present sequence
   fragment or an immunogenic fragment. Also included are the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGDD protein
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Sequence 158 AA;

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158
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             Matches:
Conservative:
Mismatches:
       Length:
                                     Indels:
                                             Gaps:
       0.000172
             81.00
100.0%
                                    88.0%
                              Best Local Similarity:
                      Percent Similarity:
Alignment Scores:
                                     Query Match:
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US-10-664-025-43_COPY_53_103 (1-51) x ABG97353 (1-158)

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51
1 ATGCCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT
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ABG31324 standard; protein; 158 AA. 05-NOV-2002 (first entry) Human GSSP3 polypeptide. ABG31324; RESULT 6 ABG3132

Human; GSSP3; circulating blood glucose level, insulin sensitivity; body mass; serum glucose regulation; body weight loss; obesity; metabolic-related disorder; impaired glucose tolerance; stroke; insulin resistance; hyperlipidaemia; atherosclerosis; heart disease; hypertension; syndrome C; type I diabetes; type II diabetes; microangiopathy; retinopathy; neuropathy; nephropathy, ocular lesion; polycystic ovarian syndrome; acanthosis nigrican; leprechaunism; lipoatrophy; physical performance; exercise; dyslexia; schizophrenia; attention-deficit disorder; hyperactivity disorder; psychiatric disorder.

Homo sapiens

18. .158 /label= Mature_GSSP3_polypeptide 17
 label= Signal_peptide Peptide Protein

Location/Qualifiers

WO200260466-A2

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The present invention relates to the isolation of human GSSP3

polypeptide, and polynucleotide sequences that encode it. The GSSP3

polypeptide reduces circulating blood glucose levels, increases insulin

polypeptide reduces body mass. The GSSP3 polypeptide and

compliantly, and/or reduces body mass. The GSSP3 polypeptide and

compositionism, body weight loss, and prevention of body weight gain.

Compositions comprising GSSP3 polypeptides are useful for controlling

blood glucose levels, for treating metabolic-related diseases or

chood glucose levels, for treating metabolic-related diseases or

disorders (e.g. obesity, impaired glucose tolerance, insulin resistance,

ymdrome C, type I or II diabetes, diabetes related complications,

or syndrome C, type I or II diabetes, diabetes related complications,

microangiopathy, retinopathy, neuropathy, nephropathy, polycystic ovarian

canthosis nigricans, leprechaumism and lipoatrophy). The polypeptides

are also useful to improve physical performance during work or exercise,

are also useful to improve physical performance during work or exercise,

are also useful to improve physical performance during work or exercise,

can to treat dyslexia, attention-deficit disorder, attention-

deficit/Myperactivity disorder, and psychiatric disorders such as

schizophrenia. The present sequence represents human GSSP3 polypeptide
                                                                                                                                                                                                                                                                                                                                                      Reducing circulating glucose levels or increasing insulin sensitivity, useful for reducing body mass or preventing body weight gain, comprises administering composition comprising GSSP3 polypeptide.
                                                                                                                                                                                                       Chicca J, Yen-Potin F;
                                                                                                                                                                                                       Bour BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 96-97; 97pp; English.
                                                                                                                                                                                                       Salter-Cid L, Ebbets-Reed D,
                                                                                                  02-FEB-2001; 2001US-0266156P.
                                                                                                                                                                                                                                                                                 WPI; 2002-608487/65.
                                                                                                                                                                                                                                                                                                            N-PSDB; ABK90053.
                                                                                                                                                    (GEST ) GENSET
                                                                                                                                                                                                                                    Bihain B;
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Sequence 158 AA;

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158
17
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             Matches:
Conservative:
Mismatches:
Indels:
      0.000172
             81.00
100.0%
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88.0%
                               Best Local Similarity:
Query Match:
                       Percent Similarity:
Alignment Scores:
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US-10-664-025-43_COPY_53_103 (1-51) x ABG31324 (1-158)

21 1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT g 8

ABR47931 standard; protein; 158 AA ABR47931

RESULT 7

12-JUN-2003 (first entry)

ABR47931;

Human secreted protein, SEQ ID 822.

Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic; vulnerary; antiinflammatory; nootropic; neuroprotective; antiparkinsonian; gene therapy; human; cardiovascular disorder.

Homo sapiens.

WO200295010-A2

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immune disorder; inflammation; infection; wound healing; drug screening; chromosome identification; chromosome mapping; cytostatic; antiinflammatory; immunosuppressive; vulnerary; gene therapy.
                                                                                                                                                                                                                                 21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
                                                                                                                                                                                               19-MAR-2002; 2002WO-US008276.
                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.000172
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                                                                                                                                                                                                                                                                                                                                                      Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-029900/02
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABZ71354
                                                                                                                    WO200276488-A1
                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                           03-OCT-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADB91675;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB91675
      g
                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to novel human secreted proteins (ABR47633-ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins and their coding sequences are useful for the preparation of a diagnostic or pharmaccutical composition for diagnosing or treating a cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary arrhythmia, tachycardia, cardiac arrest, coronary arrhythmia, tachycardia, cardiac arrest, coronary arreatiosclerosis and myocardial ischaemia), neural disorders, immune gastrointestinal disorders, pulmonary disorders, renal disorders, proliferative disorders pulmonary disorders, renal disorders, proliferative disorders and/or cancerous diseases and conditions, for wound healing and epithelial cell proliferation, to treat inflammation or preventing neural damage which occurs in neuronal disorders or neurodegenerative conditions such as Alzheimer's disease and Parkinson's disease, to enhance bone and periodontal regeneration and aid in tissue transplants or bone grafts, to prevent skin ading or hair loss, to extrans the prevent and differentiation of haematopoietic cells and bone manned before transplants or combination with other cyckines, to marrow for enhance procombination with other cyckines, to maintain and and periodontal regeneration of maintain and and periodontal regeneration of maintain and and periodon with other cyckines, to maintain and and periodon with other cyckines, to maintain and and periodon with other cyckines, to maintain and periodon with other cyckines, to maintain and and periodon with other cyckines, to maintain and periodon with other cyckines, to maintain and and periodon with other cyckines, to maintain and periodon with other cyckines, to maintain and periodon and and periodon with other cyckines, to maintain and periodon and and periodon with other cyckines, to maintain and periodon and and perio
                                                                                                                                                                                                                                                                    Novel human secreted proteins, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating cardiovascular disorders such as arrhythmia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organs before transplantation or for supporting cell culture of primary tissues, to increase or decrease differentiation or proliferation of embryonic stem cells, or to modulate mammalian characteristics or metabolism. Note: The sequence data for this patent was published in electronic format and is available from WIPO at they, wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, secreted protein, digestive disorder, gastrointestinal disorder, mouth, oesophagus, stomach, small intestine, large intestine, liver, biliary tract, pancreas, cancer, tumour, hyperproliferative disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human gene 165 encoded secreted protein HTELS08, SEQ ID NO:464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTTGGACCGGTGCT
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                  Claim 13; SEQ ID NO 822; 1881pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
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                                                                        21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
                                      19-MAR-2002; 2002WO-US009785
                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                             Rosen CA, Ruben SM;
                                                                                                                                                                                                                                 WPI; 2003-129429/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 158 AA;
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Best Local Similari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
  28-NOV-2002
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ABZ71190-ABZ71478 represent cDNAs corresponding to 178 human secreted protein genes, and ABP00011-ABP00299 represent the proteins they encode. Drotein genes, and ABP00011-ABP00299 represent the proteins they encode. CC protein genemic fragments. The invention also encompasses antibodies specific for the secreted proteins, and recombinant concerted proteins, and modulators of proteins. The secreted proteins, nucleic acids encoding them, antibodies or antibody fragments specific for the secreted proteins, and modulators of protein activity are useful for diagnosing, treating, ameliorating or preventing diseases are useful for diagnosing, treating, ameliorating or preventing cigestive disorders. Such conditions include disorders of the mouth, coesophagus, stomach, small intestine, large intestine, liver, biliary tract and pancreas, and include cancers of these organs and tissues. The coesophagus and their nucleic acids may also be used in the creatment of immune disorders, and to promote wound healing. Nucleic acids proper invention may be used for chromosome identification, chromosome coeff the invention may be used for chromosome identification, chromosome coeff the invention may be used for chromosome identification, chromosome coeff the invention may be used for chromosome identification, and samples, as hybridisation probes, and as molecular weight amarkers. The present sequence represents a human secreted protein of the
New human secreted proteins and nucleic acids, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating e.g. gastrointestinal diseases and disorders, or cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetAlaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAla 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
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                                                                                                                                                                                    Claim 13; Page 1048; 1216pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ż
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transcription-related protein; osteoporosis; neurological disease;
                cancer; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADC74338
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                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated nucleic acid molecules ADB91065-
ADB91448 and ADB91835-ADB91911 encoding human secreted proteins ADB91449-
ADB91344. ABAO disclosed is a recombinant vector comprising
the recombinant vector. The polypeptide of the invention is useful in
identifying a binding partner by contacting the polypeptide with a
claentifying a binding partner by contacting the polypeptide with a
claentifying a binding partner by contacting the polypeptide with a
claentifying a binding partner by contacting the polypeptide with a
claentifying a binding partner by contacting the polypeptide with a
claentifying a binding partner by contacting the polypeptide. Polymelectide
antibody or its fragment, agonist or antagonist are useful for preparing
a pharmaceutical composition for diagnosing or treating diabetes or
conditions related to diabetes. The present sequence is that of the human
immunoglobulin Fc portion used to generate fusion proteins, increasing
the stability of the fused protein as compared to the secreted protein
conju. Note: The sequence data for this patent did not form part of the
printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                           Nucleic acid encoding a human secreted protein is useful in diagnosing or treating diabetes or conditions related to diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration; cell regeneration; membrane protein; signal transduction-related protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetAlaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAla 17
                                        Secreted protein; gene therapy; antidiabetic; diabetes; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT
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17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human protein encoded by clone TESTI20282420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels:
                                                                                                                                                                                                                                                                                                                                                  Claim 3; SEQ ID NO 621; 1537pp; English
             Human secreted protein #SEQ ID 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB65520 standard; protein; 158 AA
                                                                                                                                                                                     19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                              19-MAR-2002; 2002WO-US008124
                                                                                                                                                                         21-MAR-2001; 2001US-0277340P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.000172
81.00
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88.0%
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                                                                                                                                                                                                                                                       Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                WPI; 2003-229407/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 158 AA;
                                                                                          WO2003004622-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                    16-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADB65520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB65520
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The invention discloses a polynuclectide comprising a sequence selected from 1970 fully defined nuclectide sequences which encode novel colypeptides. Also claimed is a polypeptide encoded by the polynuclectide or pebtide or tits partial peptide, an antibody binding to the polypeptide or peptide of the polynuclectide, immunologically assaying the polypeptide or peptide or text of the polynuclectide by contacting the polypeptide or peptide or with the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polynuclectide in an expressible manner and an antisense polynuclectide. The oligomuclectide is useful as a primer for synthesising the polynuclectide in an expressible manner and an antisense polynuclectides and encoded for the formation of the polynuclectides and encoded genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell cranscription-related proteins, signal transduction-related proteins, cranscription-related proteins, disease-related proteins and genes cancer, tumours. The cDNA may be used to regulate concing them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours. The cDNA may be used to regulate sequence data for this patent is not represented in the printed protein between the printed proteins parter of specification, but is based on sequence information supplied by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
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                                                                                                                                                                                                                                                                                                                                                                     (HELI-) HELIX RES INST.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page; 222pp; English
                                                                                                                                                                                                                                                               05-NOV-2001; 2001JP-00379298.
25-JAN-2002; 2002US-00350978.
                                                                                                                                                                                             28-MAR-2002; 2002EP-00007401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.000172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as targets of gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.00
100.0%
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88.0%
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Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-450961/43.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ADB63550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Homo sapiens.
                                                           EP1308459-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                              07-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
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21

1 ATGCCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT

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AAB38337 standard; protein; 159

AAB38337

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The invention relates to a novel human secreted polypeptide comprising a defined sequence given in the specification. The polypeptide, nucleic acid molecule, antibody, agonist or antiagonist of the invention may be useful for preparing a composition for diagonosing or treating a haemopoletic or haematologic disorder such as anaemia, autoimmune disorders such as rheumatold arthritis, inflammation, Grave's disease, disorders con a rheumatold arthritis, inflammation, Grave's disease, neurodegenerative disorders including Parkinson's disease and Alzheimer's cases, wounds and hyperproliferative disorders including atherosclerosis or cancer, as well as bacterial, viral, fungal or parasitic infections. The polypeptide may also be used during gene therapy procedures and for identifying a binding partner by contacting the polypeptide with a binding partner and determining whether the binding partner increases or decreases the activity of the polypeptide.
                                                                                                                                                        antianaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid; antidabetic; immunosuppressive; dermatological; nephrotropic; antidatericis immunosuppressive; dermatological; nephrotropic; antibacterial; virucide; fungicide; antiparastic; antiarteriosclerotic; vulnerary; cytostatic; haemopoietic; haematologic; anaemia; autoimmune disorder; haematologic; anaemia; autoimmune disorder; rheumatoid arthritis; inflammation; Grave's disease; diabetes; systemic lupus erythematosus; glomerulonephritis; neurodegenerative; Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis; cancer; bacterial; viral; fungal; parastic infection; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human secreted polypeptide for diagnosing, preventing or treating hematopoietic or hematologic disorders (e.g. anemia), autoimmune disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 16; SEQ ID NO 971; 2272pp; English.
                                                                                                                      Human secreted protein - SEQ ID 971,
ADC74338 standard; protein; 158 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUL-2001; 2001US-0306171P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAR-2002; 2002WO-US008277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAR-2001; 2001US-0277340P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-430516/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders (e.g. di
atherosclerosis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ADC73723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003038063-A2
                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                             01-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-MAY-2003
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                                     ADC74338
                                                                                                                                                                                                                                                                                                                                           human.
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Shi Y; Birse CE;

Rosen CA, Soppet DR, Florence KA, Moore PA,

i J, Komatsoulis GA, Olsen HS, Ebner R,

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Young PE; Ruben SM, Lafleur

WPI; 2000-647418/62.

99US-0128693P. 99US-0130991P.

09-APR-1999; 26-APR-1999;

(HUMA-) HUMAN GENOME SCI INC

06-APR-2000; 2000WO-US008979.

WO200061623-A1

19-0CT-2000

Homo sapiens.

cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective; nootropic; antibacterial; virucide; fungicide; opthalmalogical; human; vulnerary; gene therapy; infection; secreted protein.

Immunosuppressive; antiarthritic; antirheumatic; antiproliferative;

Human secreted protein encoded by gene 17 clone HTELS08.

(first entry)

31-JAN-2001

AAB38337;

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Sequences AAB38321-B3839 represent the amino acid sequences of 62 human secreted proteins encoded by the genes AAC69512-C69587. The genes and proteins are useful for preventing, amediating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) autoimmune diseases e.g. rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms of the breast or liver; (c) cardiovascular disorders e.g. cardiac arrest; (d) cerebrovascular disorders e.g. cerebral isofomis; (e) angiogenesis; (f) nervous system disorders e.g. creebral isofomis; (e) angiogenesis; (f) nervous system disorders e.g. creebral isofomis and infections caused by bacteria, viruses and fungi; and (h) ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, com aintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid molecules encoding 62 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 608-609; 716pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.000173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
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158 0 0 0 0

Matches: Conservative: Mismatches: Indels:

100.0% 100.0% 88.0% 81.00

Percent Similarity: Best Local Similarity:

Best Local S. Query Match:

Length:

0.000172

Alignment Scores:

US-10-664-025-43_COPY_53_103 (1-51) x ADC74338 (1-158)

(first entry)

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Human, splice variant, tumour-involved gene; TIG;
pharmaceutical composition; cancer; diagnostic; tumour; gene therapy;
endothelial cell; cell differentiation; cell proliferation; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acid sequence, which is an alternative splicing variant tumor involved genes, useful for detecting cancer, predisposition to cancer, for evaluating cancer state and in gene therapy for treating
                                                                                          Tumour involved gene (TIG) splice variant protein, NV-27.
ABG79696 standard; protein; 624 AA.
                                                                                                                                                                                                                                                                                               13-MAR-2001; 2001US-00805020.
                                                                                                                                                                                                                                                                                                                            14-MAR-2000; 2000IL-00135402
16-MAY-2000; 2000IL-00136154
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Levine Z, David A,
                                                                                                                                                                                                                                                                                                                                                                                                                         (BERN/) BERNSTEIN J.
                                                                                                                                                                                                                                                                                                                                                                           (LEVI/) LEVINE Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ABS65226
                                                                                                                                                                                                                                  US2002086384-A1.
                                                                                                                                                                                                      Homo sapiens.
                                                           15-NOV-2002
                                                                                                                                                                        gene therapy
                                                                                                                                                                                                                                                                 04-JUL-2002.
                              ABG79696;
                                                                                                                                                                                                                                                                                                                                                                                          (DAVI/)
                                                                                                                                                                                                                                                                                                                                                                                                            (ROMA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer.
 AAW1445-52 are the protein products of the car genes (carA-H) which are involved in the biosynthesis of carbapenem, an antibiotic which acts as a beta-lactamase inhibitor. The car biosynthetic genes are regulated by the carR gene product (AAW14444), a positive activator of the biosynthetic genes which functions in trans. The car genes can be used to identify homologous genes in bacteria and fungi, while products of the genes may be used to raise antibodies used to detect clones (in a Streptomyces library) that express cross-reactive protein. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful
                                                                                                                                                                                                                                                               carbapenem; carR; carB; carC; carD; carE; carF; carG; carH;
biosynthesis; antibiotic; beta-lactamase inhibitor; regulatory.
            New genes encoding enzymes involved in carbapenem biosynthesis for isolating other carbapenem synthesising genes and producing carbapenem in heterologous organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Holden MTG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sebaihia M, Cox ARJ, H
Williams P, Stewart GSAB;
                                                                                                         AAW14446 standard; protein; 250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 4; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          95WO-GB001125
                                                                                                                                                                                                                                                                                                                                                                                                                                      94GB-00010142
                                                                                                                                                                    (revised)
(revised)
(first entry)
                                                                                                                                                                                                                                                                                                              Pectobacterium carotovorum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmond GPC, Mcgowan SJ,
Porter LE, Bycroft BW, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYWA-) UNIV WARWICK.
(UYNO-) UNIV NOTTINGHAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-020587/02.
                                                                                                                                                                                                                                  CarB gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAT09700.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                       20-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmond GPC,
                                                                                                                                                                    16-OCT-2003
25-MAR-2003
17-MAY-1997
                                                                                                                                                                                                                                                                                                                                           WO9532294-A1
                                                                                                                                                                                                                                                                                                                                                                                                          18-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
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                                                                                                                                         AAW14446;
                                                                                            AAW14446
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Bernstein J;

Romano C,

DAVID A. ROMANO C.

2002-635679/68.

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The invention discloses isolated human nucleic acid alternative splicing variants that are all tumour-involved genes (TIG8). The nucleic acids and collypeptides are useful for determining the level of a nucleic acid or polypeptide in a biological sample, for detecting a variant nucleic acid or polypeptide sequences in a biological sample for variant mucleic acid or polypeptide sequences in a biological sample and for determining the ratio between the level of variant sequence in a first biological sample and the level of the original sequence from which composition comprising a carrier and the nucleic acid is useful for composition comprising a carrier and the nucleic acid, is useful for composition comprising a carrier and the nucleic acid, is useful for increasing or decreasing the level of the encoded protein. The nucleic acids are also useful for dagnostic purposes, especially for detecting cancer or a predisposition to cancer, for evaluating the state or aggressiveness of cancer disease, in basic research, for understanding the physiological function of the original TIG, in targeting or developing pharmaceuticals, for distinguishing various stages in the life cycle of the same type of cells which may be helpful for the development of pharmaceuticals for various cancer stages in which cell cycle of pharmaceuticals for various cancer stages in which cell cycle of the rate in product and modulating its activity and for modulating endothelial differentiation and proliferation, as vell as to modulating the paragraph of the variant product and modulation, we are near to make the control of the variant product and modulation, we are near to make the control of the variant product and modulation is accompanied in the variant product and modulation, we are the control of the variant product and modulation, we are the control of the variant product and modulation, we are as to an accompanied.
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Claim 4; Page 94-95; 180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 624 AA;
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0 0 0 0 0 0

76.4 47.00 100.0% 80.0% 51.1%

Local Similarity:

Query Match:

Percent Similarity:

Indels: Gaps:

Length: Matches: Conservative: Mismatches: US-10-664-025-43_COPY_53_103 (1-51) x AAW14446 (1-250)

9 AGAAGICITGAIGCICCICGCIGICITGAI 38

RESULT 14 ABG79696

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Length:

79.3

Alignment Scores:

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The present invention describes a predictor set comprising a plurality of polynucleotides or polypeptides whose expression pattern is predictive of polynucleotides or polypeptides whose expression pattern is predictive of the response of cells to treatment with a compound that modulates protein tyrosine kinase activity or members of the protein tyrosine kinase cathway. Also described: (1) predicting whether a compound is capable of modulating the activity of cells, comprising obtaining a sample of cells, cerelating the activity of the cells; (2) a plurality of markers, and correlating the expression of the markers to the compound's ability to modulate the activity of the cells; (2) a plurality of cell lines for correlate with compound sensitivity or resistance of cells associated correlate with a disease state; and (3) identifying polynucleotides and correlate with a disease state, comprising subjecting the plurality of associated with a disease state, comprising subjecting the plurality of cell lines to one or more compounds ensitivity or resistance of cells associated with a disease state by using the collynucleotides or polypeptides that predict the sensitivity or resistance of cells associated with a disease state by using the corresistance of cells associated with a disease state by using the expression pattern of the microarray. The polynucleotides and colpapelides have cytostatic activities, and can be used in gene therapy. The polynucleotides and polypeptides are useful in predicting drug cativity of compounds that interact with potein tyrosine kinase pathways. These may be used in determining drug sensitivity in patients to allow the development of individualized
                                                                                                                                                                                                                                                                                                                                                                                                                                           predictor set; protein tyrosine kinase activity modulator; protein tyrosine kinase; cytostatic; gene therapy; drug sensitivity; genetic profile; cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides and polypeptides for predicting the activity of compounds that interact with protein tyrosine kinases and/or protein tyrosine kinase pathways.
                                                                                                                                                                                 51 AGCACCGGTCCAAATCAAGACAGCGAGGAGCATCAAGAC 13
    0 4 M O O
                                                                                                                  US-10-664-025-43_COPY_53_103 (1-51) x ABG79696 (1-624)
                  Conservative:
Mismatches:
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    Matches:
                                                          Indels:
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                                                                                                                                                                                                                                                                               ADD14149 standard; protein; 633
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51.1%
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N-PSDB; ADD14751.
              Percent Similarity:
Best Local Similarity:
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                                                        Query Match:
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CC genetic profiles which aid in treating diseases and disorders (e.g. cancer) based on patient response at a molecular level. The present CC sequence is used in the exemplification of the present invention.

XX

SQ Sequence 633 AA;

Alignment Scores:

Perc. No.:

Score:

Percent Similarity:

T6.94

Conservative:

Percent Similarity:

T6.94

Conservative:

Best Local Similarity:

T6.94

Conservative:

T6.95

Conservative:

T6.96

Conservative:

T6.97

Conservative:

T6.97

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T6.97

Conservative:

T6.96

Conservative:

T6.97

Conservative:

T6.98

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Search completed: May 9, 2006, 10:04:46 Job time : 13.1 secs

US-10-664-025-43_COPY_53_103 (1-51) x ADD14149 (1-633)

8 8

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Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

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166, App.
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17927, A
26326, A
14283, A
17452, A
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15523, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-621-976-523

Sequence 5223, Application US/09621976

Fatent No. 6639063

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Jobert, S.

APPLICANT: Glordano, J.Y.

ITILE OF INVENTION: ESTS and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2

FILE REFERENCE: GENSET.054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SEQ ID NO 5223

LENGTH: 106
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US-10-290-579A-165
US-09-290-579A-248
US-09-120-579A-248
US-09-270-767-32256
US-09-200-125-1
US-08-08-10-10-34
US-09-09-10-125-1
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US-09-055-69-34
US-09-055-534-148-34
US-09-661-468-34
US-09-661-468-34
US-10-290-578-166
US-10-290-578-166
US-10-290-578-168
US-10-290-578-168
US-09-30-578-168
US-09-30-578-168
US-09-252-991A-17927
US-09-252-991A-17927
US-09-252-991A-17927
US-09-252-991A-17452
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US-09-253-911-842A-4
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Matches:
Conservative:
Mismatches:
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228
80
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ORGANISM: Homo sapiens
 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , LUCATION: -17..-1
US-09-621-976-5223
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   FEATURE:
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Query Match:
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-MODEL=frame+ n2p.model -DEV=xlp
-Q-fabseyABSSWEB spool/10110664025/runat 08052006 173459 28431/app_guery.fasta_1
-Q-fabsexPabsSWEB spool/10110664025/runat 08052006 173459 28431/app_guery.fasta_1
-DB=Issued_Patents_AA -QEMT=fasta n=SUFFIX=n2p.rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=Dits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=AB -DOCALIGN=200 -THR SCORE=pot -THR MX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMI=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abse02p -USER=US10664025_GCGN 1 1 101 @runat 08052006 173459 28431
-NCPU=6 -ICPU=3 -NO MMAP -NEG SCORES=0 -WAIT -DSPBECCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5223, Ap Sequence 5222, Ap Sequence 5222, Ap Sequence 4, Appli Sequence 10511, A Sequence 23223, A Sequence 23224, A Sequence 2, Appli Sequence 2, Appli
                                                                                                                                    (without alignments)
1621.715 Million cell updates/sec
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                                                                                                                                                                                                                        atggcgttagaagtcttgat......tcttgatttggaccggtgct
                                                                                                               May 9, 2006, 10:08:38 ; Search time 0.78 Seconds
            GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-09-621-976-3903
US-09-621-976-3903
US-10-104-047-5222
US-08-737-825-4
US-09-549-016-10511
US-09-252-911A-23223
US-09-252-911A-23254
US-08-764-343-4
US-08-764-343-4
US-08-764-343-4
US-08-767-579-2
US-09-252-991A-20495
                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                  572060 seqs, 82675679 residues
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92
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Match Length
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Database

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Result No.

1 MetAlaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAla 17

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RESULT 4
US-10-104-047-3674
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Sequence 5222, Application US/09621976

Patent No. 6639063

Patent No. 6639063

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Glordano, J.Y.

TITLE REFERENCE: GENGET. 054PR2

CURRENT FILICHON NUMBER: US/09/621,976

CURRENT FILICHO DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 5222

LENGTH: 158
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0
                                                                APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: PATENT. DM
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Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
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              Sequence 3903, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
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88.0%
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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Query Match:
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; NAME/KEY: SIGNAL
; LOCATION: -17..-1
US-09-621-976-3903
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; LOCATION: -17...1
US-09-621-976-5222
 -09-621-976-3903
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Pred. No.:
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LENGTH: 153
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APPLICANT: SEBAHILA, MOHAMMED
APPLICANT: COX, ANTHONY RICHARD JOHN
APPLICANT: COX, ANTHONY RICHARD JOHN
APPLICANT: HOLDEN, MATTHEW THOWAS GEOFFREY
APPLICANT: PORTER, LAUREN BILZABETH
APPLICANT: WILLIAMS, PAUL
APPLICANT: WILLIAMS, PAUL
APPLICANT: WILLIAMS, PAUL
APPLICANT: STEWART, CORDON SIDNEY ANDERSON BIRNIE
TITLE OF INVENTION: GENES INVOLVED IN THE BIOSYNTHETIC PATHWAY OF CARBAPENEM
NUMBER OF SEQUENCES: 12
CORRESPONDENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-664-025-43_COPY_53_103 (1-51) x US-10-104-047-3674 (1-158)
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                                                                 APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. 6943241e1 full length cDNA
TITLE OF INVENTION: No. 6943241e1
TILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
PRIOR APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD97
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/737,825
FILING DATE: 03-UTM-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1009-0105P
; Sequence 3674, Application US/10104047; Patent No. 6943241; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08737825
Patent No. 5871922
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 100
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               6.09e-06
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SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                           SEQ ID NO 3674
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Sequence 23224, Application US/09252991A
; Sequence 2324, Application US/09252991A
; Sequence 2324, Application US/09252991A
; Batent No. 6551795
; GENERAL INFORMATION:
    TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22254
           APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196-136
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23223
LENGTH: 209
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Matches:
Conservative:
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GENERAL INFORMATION:
APPLICANT: Londos, Constantine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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46.00
92.3%
61.5%
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46.00
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61.5%
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Best Local Similarity:
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Best Local Similarity:
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US-09-252-991A-23254
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US-08-132-649-2
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Patent No. 6812339

GENERAL INFORMATION:
FAPELICANT: VENTER, J. Craig et al.
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION WINBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOUTHARD: PSESEE FASTESE FASTES FASTESE FASTESE FASTES FASTE
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Conservative:
Mismatches:
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US-09-252-991A-23223
; Sequence 23223, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Erwinia carotovora
TELEPHONE: (703) 205-8000
TELEAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: Amino acid
TYPE: Amino acid
TYPE: Amino acids
TYPE: Amino aci
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Best Local Similarity:
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Best Local Similarity:
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; ORGANISM: Human
US-09-949-016-10511
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DB:
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DB:
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                                                                                                                     ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/132,649
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL ADIPOCYTE-SPECIFIC
TITLE OF INVENTION: DIFFERENTIATION-RELATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 GTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGAC 44
APPLICANT: Greenberg, Andrew S.
APPLICANT: Kimmel, Alan R.
APPLICANT: Egan, John J.
TITLE OF INVENTION: CLONING OF PERILIPIN PROTEINS NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
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Matches:
Conservative:
Mismatches:
Indels:
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CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 15280-145-1
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-9600
TELEPRONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
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OPERATING SYSTEM: DOS
SOFTWARE: FRASEQ Version 1.5
CURRENT APPLICATION DATA:
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amino acid
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MEDIUM TYPE: Diskette
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Best Local Similarity:
Query Match:
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US-10-664-025-43_COPY_53_103 (1-51) x US-08-764-343-4 (1-517)
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,579
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Conservative:
Mismatches:
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APPLICATION NUMBER: US/08/764,343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: GBTTCHT-WACKOWSKI, EUGEI
REGISTRATION NUMBER: 37,30
REFERENCE/DOCKET NUMBER: 1528
TELECOMMUNICATION INFORMATION:
TELERAX: (415) 543-5600
TELERAX: (415) 543-5600
INFORMATION FOR SEQ ID NO: 2:
                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
STRANDENESS: single
                 FILING DATE: Filed Herewith PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.9
45.00
69.2$
69.2$
                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY: GenBank
CLONE: 1172433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
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US-08-767-579-2
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RESULT 15
US-09-132-5855
US-09-132-5855
; Sequence 5855, Application US/09328352
; Sequence 5855, Application US/09328352
; GENERAL INFORMATION:
; APPLICANT: GAIT L. Breton et al.
; APPLICANT: GAIT L. Breton et al.
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REPERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hahn, Beatrice
APPLICANT: Hahn, Beatrice
APPLICANT: Gao, Feng
APPLICANT: Gao, Feng
APPLICANT: Shaw, George
TITLE OF INVENTION: CLONES AND SEQUENCES FOR NON-SUBTYPE B ISOLATES OF HUMAN
TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS TYPE 1
FILE REFERENCE: D6287D
CURRENT FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: US 09/184,418
PRIOR APPLICATION NUMBER: US 09/184,418
SHOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 270
                                                                                                                                                                                                                                                                                                                                                                                                  US-10-664-025-43_COPY_53_103 (1-51) x US-10-290-579A-165 (1-33)
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Indels:
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US-10-290-579A-248
                                                                                                                                                                                OTHER INFORMATION: isolate=94IN476.104; gene=vpu
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    CURRENT FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: US 09/184,418
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 270
SEQ ID NO 165
LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 248, Application US/10290579A; Patent No. 6897301; GENERAL INFORMATION:
                                                                                                                       TYPE: PRT
ORGANISM: artificial sequence
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44.00
85.7
50.0
47.8
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Query Match:
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US-10-290-579A-165
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; Sequence 20455, Application US/09252991A
; Sequence 20455, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC CAID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT PELING DATE: 1999-02-18
; PRIOR FILING DATE: 1999-02-18
; PRIOR PELING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20495
; LINCTH: 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (15), (28), (61)
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-20495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hahn, Beatrice
APPLICANT: Gao, Feng
APPLICANT: Gao, Feng
APPLICANT: Gao, Feng
TITLE OF INVENTION: CLONES AND SEQUENCES FOR NON-SUBTYPE B ISOLATES OF HUMAN
TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS TYPE 1
FILE REFERENCE: D6287D
CURRENT APPLICATION NUMBER: US/10/290,579A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-664-025-43_COPY_53_103 (1-51) x US-09-252-991A-20495 (1-658)
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Patent No. 6897301
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
                  i LENGTH: 517 amino acide

i TYPE: amino acid

TOPOLOGY: linear

i MOLECULE TYPE: protein

US-08-767-579-2
                                                                                                                                                          16.9
45.00
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SEQUENCE CHARACTERISTICS
LENGTH: 517 amino acid
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; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5855
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5855
Alignment Scores: 44.00 Matches: 7
Score: 44.00 Matches: 7
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Best Local Similarity: 53.8$ Mismatches: 0
Query Match: 2
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Best Local Similarity: 53.8$ Indels: 0
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Best Local Similarity: 53.8$ Indels: 0
Conservative: 6
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Best Local Similarity: 11 Mismatches: 0
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Best Local Similarity: 11 Mismatches: 0
Conservative: 6
Best Local Similarity: 12 Mismatches: 0
Conservative: 6
Best Local Similarity: 12 Mismatches: 0
Conservative: 6
Best Local Similarity: 13.00
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464, App 251583, 206002, 63, Appl 1800, Ap 175, App

Sequence

Sequence Sequence Sequence 48396, A 48396, A 48396, A 71786, A 66911, A 1175, A 5790, Appl 90, Appl 91, Appl 185, Appl 185, Appl 1860, A 259901, 259901, 259901,

US-10-425-115-251583 US-10-425-115-206002 US-10-087-195-1800 US-10-087-192-1800 US-10-144-599-161519 US-10-424-599-161519 US-10-424-599-161519 US-10-425-114-48396 US-10-425-114-48396 US-10-425-114-69311 US-10-369-493-8151 US-10-369-493-8151 US-10-369-493-8151 US-10-464-368-91 US-10-464-368-91 US-10-464-368-91 US-10-464-368-91 US-10-464-368-91 US-10-464-368-91 US-10-464-368-91 US-10-464-368-91 US-10-455-115-25991 US-10-425-115-25997 US-10-425-115-25997 US-10-425-115-25997 US-10-425-115-25997 US-10-425-115-25997 US-10-425-115-25997 US-10-425-115-25997 US-10-425-115-25997 US-10-115-268-82 US-10-111-904-82 US-10-113-904-82 US-10-113-904-82 US-10-113-918-82 US-10-1175-918-82

Sequence Seq

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ALIGNMENTS

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RESULT 1
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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                                                                              May 9, 2006, 10:09:27 ; Search time 1.81 Seconds
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
        GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                       protein search, using frame_plus_n2p model
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Maximum DB seq length: 200000000
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Ygapop 10.0 , Yi
Fgapop 6.0 , Fi
Delop 6.0 , D
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JOURNALL DATE OF A PROPERTY OF A PRICANT: DUMBER SEVERTH HUMAN CDNAB ENCODING POTENTIALLY SECRETED PROTEINS TILE OF INVENTION: FULL ENGINE OF A PROPERTY A PRICATION NUMBER: US 60/169,629

FRICE REFERENCE: 78.083.REG

CURRENT FILING DATE: 1995-12-08

FRICH APPLICATION NUMBER: US 60/169,629

FRICH APPLICATION NUMBER: US 60/187,470

FRICH APPLICATION NUMBER: US 60/187,470
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ORGANISM: Homo sapiens
FEATURE:
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; LOCATION: -17...-1
US-09-731-872-265
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Sequence 265, App Sequence 265, App Sequence 266, App Sequence 260, App Sequence 113, App Sequence 113, App Sequence 4, Appli Sequence 113, Appli Sequence 113, Appli Sequence 3, Appli Sequence 260, Appli

US-09-731-872-265 US-09-876-997-265 US-10-643-836-265 US-09-731-872-260 US-10-050-704-113 US-10-467-555-4 US-10-768-113 US-10-768-113 US-10-643-836-260

106 106 106 1158 1158 1158 1158 1158

888.0 888.0 888.0 888.0 888.0 888.0 888.0

81 81 81 81 81 81 81 81 81

12643978611

Description

SUMMARIES

DB

Query Match Length

Result No. 21

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USE OB TAIL 872-260

| Sequence 260, Application US/09731872
| Sequence 260, Application US/09731872
| Sequence 260, Application US/09731872
| Patent No. US20020102604A1
| Patent No. US20020102604A1
| Patent No. US20020102604A1
| APPLICANT: Dumas Milne Edwards, Jean Baptiste
| APPLICANT: Dumas Milne Edwards, Jean Baptiste
| APPLICANT: Jobert, Severin
| TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
| FILE REFERENCE: 78.US.09/731,872
| CURRENT FAPLICATION NUMBER: US 60/169,629
| PRIOR APPLICATION NUMBER: US 60/169,629
| PRIOR APPLICATION NUMBER: US 60/187,470
| PRIOR PILING DATE: 2000-03-06
| WUMBER OF SEO ID NOS: 482
| SOFTWARE: Patent.pm
| SEO ID NO 260
| LENGTH: 158
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Publication No. US20030152921A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Bougueleret, Lydie
APPLICANT: Jobert, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78.US4.CIP
CURRENT APPLICATION NUMBER: US/09/876,997
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/731,872
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FEATURE:
NAME/KEY: SIGNAL
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                                                                                                                                                                                                               Sequence 265, Application US/09876997

Sequence 265, Application WS. US2030152921A1

GENERAL INFORMATION:

JENERAL INFORMATION:

APPLICANT: Duman Milne Edwards, Jean Baptiste

APPLICANT: Duman Milne Edwards, Jean Baptiste

APPLICANT: Dobert, Severin

TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS

FILE REFERENCE: 78.US4.CIP

CURRENT APPLICATION NUMBER: US/09/876,997

CURRENT FILING DATE: 2000-12-07

PRIOR APPLICATION NUMBER: US 60/187,470

PRIOR APPLICATION NUMBER: US 60/169,629

PRIOR APPLICATION NUMBER: US 60/169,629

PRIOR APPLICATION NUMBER: US 60/169,629

NUMBER OF SEQ ID NOS: 482

SEQ ID NO 265

LENGTH 1.106
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| Bublication No. US20050096458A1 |
| CENERAL INFORMATION: US20050096458A1 |
| GENERAL INFORMATION: DECEMBER OF THE CONTINUE OF THE CONTINUE OF THE CONTION: THE CONTINUE OF THE CONTIN
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US-10-664-025-43_COPY_53_103 (1-51) x US-09-731-872-265 (1-106)
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Matches:
Conservative:
Mismatches:
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity:
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LOCATION: -17...-1
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Alignment Scores:
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Matches:
Conservative:
Mismatches:
Indels:
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TITLE OF INVENTION: 62 Human Secreted Proteins
FILE REFERBKCE: PZ039P1
CURRENT APPLICATION NUMBER: US/10/050,704
CURRENT APPLICATION NUMBER: 09/684,524
PRIOR PELING DATE: 2000-10-10
PRIOR PELING DATE: 2000-10-10
PRIOR PELING DATE: 2000-10-10
PRIOR PLING DATE: 1200-04-06
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
PRIOR PILING DATE: 1999-04-26
PRIOR PILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 344
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 13
LENGTH: 158
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Matches:
Conservative:
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Indels:
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PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR PLING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 482
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US-10-104-047-3674
; Sequence 3674, Application US/10104047
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Publication No. US20030050442A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local Similarity:
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Best Local Similarity:
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; NAME/KEY: SIGNAL
; LOCATION: -17..-1
US-09-876-997-260
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LENGTH: 158
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GENERAL INFORMATION:

APPLICANT: YUE, Henry; YAO, Monique G.
APPLICANT: 150N, Craig H.; LU, Yan
APPLICANT: 150N, Craig H.; LU, Yan
APPLICANT: BAUGEN, Mariah R.; ELLOTT, Vicki S.
APPLICANT: WARREN, Baridget A.; ELLOTT, Vicki S.
APPLICANT: TYON, Yuming; GIETZEN, Kimberly J.
APPLICANT: TYON, Yuming; GIETZEN, Kimberly J.
APPLICANT: TYON, TY, LUL, Preeti G.
APPLICANT: TANG, TOW Y.; LAL, Preeti G.
APPLICANT: LU, Dyung Aina M.; RICHARDSON, Thomas W.
APPLICANT: LU, Dyung Aina M.; RICHARDSON, Thomas W.
APPLICANT: CHAWLA, Marinder K.; KHARE, Reena
APPLICANT: CHAWLA, Marinder K.;
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
FILE REPERBUES: PROJOG USN
CURRENT PILING DATE: 2003 USN
CURRENT PAPLICATION NUMBER: US (0/268,111
PRIOR PELLOATION NUMBER: US (0/211,175
PRIOR PELLOATION NUMBER: US (0/211,175
PRIOR APPLICATION NUMBER: US (0/271,533
PRIOR APPLICATION NUMBER: US (0/271,175
PRIOR APPLICATION NUMBER: US (0/271,533
PRIOR APPLICATION NUMBER: US (0/274,503)
PRIOR PILING DATE: 2001-03-09
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; GENERAL INFORMATION:
; APPLICANT: HELLIX RESEARCH INSTITUTE
; TITLE OF INVENTION:
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT APPLICATION NUMBER:
; PRIOR PILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3674
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Mismatches:
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OTHER INFORMATION: Incyte ID No: 5284076CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 4, Application US/10467535; Publication No. US20040146970A1; GENERAL INFORMATION:
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SOFTWARE: PERL Program
SEQ ID NO 4
LENGTH: 158
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; ORGANISM: Homo sapiens
US-10-104-047-3674
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Length:

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Publication No. US20040235709A1

GENERAL INFORMATION:

APPLICANT: Salter-Cid, Luisa

APPLICANT: Chicca, Barbara A.

APPLICANT: Chicca, John

APPLICANT: Chicca,
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Mismatches:
Indels:
                                    Conservative:
Mismatches:
Indels:
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SEQUENCE 113, Application US/10798512
SEQUENCE 113, Application US/10798512
SEQUENCE 113, Application US/10798512
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: 62 Human Secreted Proteins
FILE SEPERENCE: PZO39P1
CURRENT APPLICATION NUMBER: US/10/798,512
CURRENT FILING DATE: 2004-03-12
PRIOR APPLICATION NUMBER: US/09/684,524
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-06
PRIOR FILING DATE: 1999-04-06
PRIOR FILING DATE: 1999-04-06
SEQ ID NOS: 344
SOFTWARE: PATCHING UNCE: 1582
SEQ ID NOS: 344
SEQ ID NOS: 344
   Matches:
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CORGANISM: Homo sapiens
US-10-798-512-113
                         Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-467-046-3
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US-10-643-836-260

US-10-643-836-260

Sequence 260, Application US/10643836

Publication No. US20050096458A1

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Dumas Wilne Edwards, Jean Baptiste
APPLICANT: Dumas Wilne Edwards, Jean Baptiste
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Dobert, Severin
FILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR FILING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR FILING DATE: 12000-03-06
NUMBER OF SEQ ID NOS: 482
SEQ ID NO 260
LENGTH: 158
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                                                                                                                                                                                                                                                                                                                      (1-158)
                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
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Mismatches:
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; Publication No. US20050197285A1
; GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Human Secreted Proteins
; TILE REFERENCE: PS906PCT
CURRENT APPLICATION NUMBER: US/10/472,533
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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ORGANISM: Homo sapiens
                                                           ; NAME/KEY: SIGNAL
; LOCATION: (1)..(17)
US-10-467-046-3
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Best Local Similarity:
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Best Local Similarity:
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US-10-643-836-260
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Pred. No.:
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DB:
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 206002
LENGTH: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-664-025-43_COPY_53_103 (1-51) x US-10-425-115-206002 (1-110)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-805-020-63

// Sequence 63, Application US/09805020

/ Publication No. US20020086384A1

/ GENERAL IMPORMATION:

/ TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES

/ FILE REFERENCE: 2786-0168P

/ CURRENT APPLICATION NUMBER: US/09/805,020

/ CURRENT FILING DATE: 2001-03-13

/ SEQ ID NO SS 27

/ SEQ ID NO 63

/ PERSONNER: PATENT VET.
                                                                                                                                                                                                                                   , OTHER INFORMATION: Clone ID: MRT4577_119456C.1.pep
US-10-425-115-206002
                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
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Job time : 10.05 secs
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Best Local Similarity:
                                                                                                                                                                                       TYPE: PRT
ORGANISM: Zea mays
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Publication No. US20040214272A1
General INFORMATION:
GARRAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: APPLICANT: About Xinua
APPLICANT: APPLICANT: About Xinua
APPLICANT: APPLICANT: About Xinua
APPLICANT: APPLICANTON: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 251583
                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT 51
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Matches:
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CURRENT FILING DATE: 2003-09-20
PRIOR APPLICATION NUMBER: US 60/331,287
PRIOR FILING DATE: 2001-10-13
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 650
SOFTWARE: Patentin Ver. 2.0
LENGTH: 158
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-10-425-115-251583
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Sequence:

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Sequence 787, Application US/10475075
; Beublication No. US20060053498A1
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Glordano, Jean-Yves
; TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins
; TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins
; TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: PCT/IB01/00914
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 918
; SOFTWARE: Patent.pm
; SEQ ID NO 787
 Sequence 1859, Ap Sequence 1860, Ap Sequence 8671, Ap Sequence 8671, Ap Sequence 82, Appl Sequence 82, Appl Sequence 82, Appl Sequence 117803, Appl Sequence 117803, Appl Sequence 17804, Appl Sequence 17804, Appl Sequence 1918, Appl Sequence 1918, Appl Sequence 1918, Appl Sequence 1918, Appl Sequence 169, Appl Sequence 169, Appl Sequence 17776, Appl Sequence 17776, Appl Sequence 10, Appl Sequence 10, Appl Sequence 11, Appl Sequence 119, Appl Seq
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US-10-501-035-313
US-11-126-313-34
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US-10-453-372-178
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 TYPE: PRT
ORGANISM: Homo sapiens
 ; NAME/KEY: SIGNAL
; LOCATION: -17..-1
US-10-475-075-787
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-DB=Published Applications AA New -QFMT=fastan -SUPFIX=n2p.rapbn -MINMATCH=0.1
-LOOPCL=0 -LOŌPEXT=0 -UNITS=bIts -START=1 -END=-1 -MATRIX=blosum62
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Sequence 788, App
Sequence 3374, Ap
Sequence 1234, App
Sequence 1234, App
                                                                                                       (without alignments)
1336.144 Million cell updates/sec
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1: \SIDS5/ptodata/1/pubpaa/US08 NEW PUB.pepl:*

2: \SIDS5/ptodata/1/pubpaa/US06 NEW PUB.pep:*

3: \SIDS5/ptodata/1/pubpaa/US07 NEW PUB.pep:*

4: \SIDS5/ptodata/1/pubpaa/US07 NEW PUB.pep:*

5: \SIDS5/ptodata/1/pubpaa/US08 NEW PUB.pep:*

6: \SIDS5/ptodata/1/pubpaa/US09 NEW PUB.pep:*

7: \SIDS5/ptodata/1/pubpaa/US09 NEW PUB.pep:*

8: \SIDS5/ptodata/1/pubpaa/US09 NEW PUB.pep:*

9: \SIDS5/ptodata/1/pubpaa/US09 NEW PUB.pep:*

9: \SIDS5/ptodata/1/pubpaa/US09 NEW PUB.pep:*
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           GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-475-075-787
US-10-475-075-788
US-11-072-512-3674
US-10-501-035-338
US-10-784-004-1234
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Result 8

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OTSUKA, MOTOYUKI
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Best Local Similarity:
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Pred. No.:
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US-10-475-788

US-10-475-788

Sequence 788, Application US/10475075

Publication No. US2006005349841

GENERAL INFORMATION:

APPLICANT: Bejanin, Stephane

APPLICANT: Dumas Milne Edwards, Jean-Baptiste

APPLICANT: Jobert, Severin

MUMBER OF SEQ ID NOS: 918

SEQ ID NO 788

LENGTH: 148

TYPE: PRT

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Publication No. US20060029945A1
GENERAL INFORMATION:
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APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISONO, YUUKO
APPLICANT: HOO, YUKI
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NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
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                 Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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) LOCATION: -17...-1
US-10-475-075-788
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APPLICANT:
APPLICANT:
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Sequence 338, Application US/10501035
Publication No. US20060046249A1
Sequence 338, Application US/10501035
Publication No. US20060046249A1
GENERAL INFORMATION:
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASI
TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
FILE REPERENCE: DO185 PCT
CURRENT APPLICATION NUMBER: US/10/501,035
CURRENT PILING DATE: 2004-07-09
PRIOR FILING DATE: 2004-01-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetAlaLeuGluValLeuMetLeuLeuLeuAlaValLeuIleTrpThrGlyAla 17
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Matches:
Conservative:
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Matches:
Conservative:
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Indels:
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Indels:
APPLICANT: NAGAHARI, KENJI

APPLICANT: MASUHO, YASUHIKO

TITLE REPERENCE: 084335-0191

CURRENT APPLICATION NUMBER: US/11/072,512

CURRENT APPLICATION NUMBER: US 60/350,978

PRIOR APPLICATION NUMBER: US 60/350,978

PRIOR APPLICATION NUMBER: US 60/350,978

PRIOR APPLICATION NUMBER: JP 2001-379298

PRIOR FILING DATE: 2001-11-05

NUMBER OF SEQ ID NOS: 4096

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3674
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8.210-784-004-1234
; Sequence 1234, Application US/10784004
; Publication No. US20060084066A1
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SOFWARE: Patentin version 3.2
SEQ ID NO 338
LENGTH: 633
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81.00
100.0%
100.0%
88.0%
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47.00
76.9%
69.2%
51.1%
                                                                                                                                                                                                                                                                                                         TYPE: PRT
CORGANISM: Homo sapiens
US-11-072-512-3674
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US-10-501-035-338
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Best Local Similarity:
Query Match:
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1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGT 48
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
GENERAL INFORMATION:
APPLICANT: Blogen Idec
ITTLE OF INVENTION: Surrogate Markers of Pain
FILE REFERENCE: 08201.6029-00000
CURRENT APPLICATION NUMBER: US/10/784,004
CURRENT FILING DATE: 2004-02-20
NUMBER OF SEQ ID NOS: 1251
SOFTWARE: Patentin version 3.2
SEQ ID NO 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WS-UL-16

Sequence 1859, Application US/11264096

Sequence 1859, Application US/11264096

Publication No. US20060084794A1

GENERAL INFOMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Abbumin Fusion Proteins

FILE REFERENCE: PF546D1

CURRENT APPLICATION NUMBER: US/11/264,096

CURRENT APPLICATION NUMBER: 09/833,245

PRIOR APPLICATION NUMBER: 60/229, 358

PRIOR FILING DATE: 2000-04-12

PRIOR FILING DATE: 2000-04-12

PRIOR FILING DATE: 2000-04-12

PRIOR APPLICATION NUMBER: 60/256, 931

PRIOR APPLICATION NUMBER: 60/199, 384

PRIOR APPLICATION NUMBER: 60/199, 384

PRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 2267

SEQ ID NO 1859
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Publication No. US20060084794A1
GENERAL INFORMATION:
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76.9$
69.2$
51.1$
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81.2$
50.0$
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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; ORGANISM: human
US-10-784-004-1234
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US-11-264-096-1860
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Pred. No.:
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Pred. No.:
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Sequence 8673, Application US/11096568A
| Publication No. US20060048240A1
| GENERAL INFORMATION:
| TITLE OF INVENTION: Therby
| TITLE OF INVENTION: Therby
| FILE REFERENCE: 2750-1592PUS2
| CURRENT APPLICATION NUMBER: US/11/096,568A
| SEQ ID NOS: 34471
| SEQ ID NO 8673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 LeuAlaPhePheSerLeuValLeuIleSerValLeuLeuTrpThrGly 28
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
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Mismatches:
Indels:
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF54601
GURRENT APPLICATION NUMBER: US/11/264,096
GURRENT FILING DATE: 2005-11-02
PRIOR APPLICATION NUMBER: 09/833,245
PRIOR FILING DATE: 2010-04-12
PRIOR PPLICATION NUMBER: 60/229, 358
PRIOR PPLICATION NUMBER: 60/256, 931
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ 1D NOS: 2267
SOFTWARE: PATENTIN OF SEQ 1D NOS: 2267
SOFTWARE: DATE : 2005
SEQ 1D NOS: 2267
SEQ 1D NO 1860
SUMPLY SEQ 1D NOS: 2267
SEQ 1D NO 1860
SUMPLY SEQ 1D NOS: 2267
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; OTHER INFORMATION: Ceres Seq. ID no. 13589015
US-11-096-568A-8673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Triticum aestivum
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81.2%
50.0%
48.9%
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75.0%
58.3%
48.9%
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; ORGANISM: Homo sapiens
US-11-264-096-1860
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Best Local Similarity:
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Best Local Similarity:
Query Match:
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US-11-096-568A-8673
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US-11-096-568A-8672
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APPLICANT: Kapur, Vivek and Gebhart, Connie J.

APPLICANT: Kapur, Vivek and Gebhart, Connie J.

TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES

TITLE OF INVENTION: PROM LAWSONIA INTRACELLULARIS AND METHODS OF USING

FILE REFERENCE: 09531-128011

CURRENT APPLICATION NUMBER: US/11/098,686

CURRENT PILING DATE: 2005-04-04

PRIOR PILING DATE: 2005-10-01

PRIOR PILING DATE: 2003-10-01

PRIOR PILING DATE: 2002-10-04

NUMBER OF SEQ ID NOS: 11433

SOFTWARE: PRESEQ for Windows Version 4.0

SEQ ID NO 10809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P333001C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
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Mismatches:
Indels:
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Matches:
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PRIOR FILING DATE: 1997-06-18
PRIOR PELING DATE: 1997-06-18
PRIOR PEPLICATION NUMBER: 60/05974
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/059115
PRIOR PELING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059117
PRIOR PILING DATE: 1997-09-17
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; Sequence 82, Application US/10131826A
; Publication No. US20050245730A1
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
                                                                                                                                                                                                                                                                                                                                                                             Lawsonia intracellularis
               US20060024696A1
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Watanabe, Colin K
Wood, William
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Filvaroff, Ellen
Gao, Wei-Qiang
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Gurney, Austin L.
Sherwood, Steven
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45.00
85.7%
42.9%
48.9%
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Best Local Similarity:
Query Match:
                                     GENERAL INFORMATION:
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM:
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APPLICANT:
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APPLICANT:
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APPLICANT:
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Sequence 8672, Application US/11096568A
Publication No. U520060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 8672
LENGTH: 126
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| Sequence 8671, Application US/11096568A
| Sequence 8671, Application US/11096568A
| Publication No. US20060048240A1
| GENERAL INFORMATION:
| APPLICANT: Alexandrov, Nickolai et al.
| TITLE OF INVENTION: Therby
| TITLE OF INVENTION: Therby
| FILE REFERENCE: 2750-15928US2
| CURRENT APPLICATION NUMBER: US/11/096,568A
| CURRENT FILING DATE: 2005-04-01
| NUMBER OF SEQ ID NOS: 34471
| SEQ ID NO 8671
| LENGTH: 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-664-025-43\_COPY\_53\_103 (1-51) x US-11-096-568A-8672 (1-126)
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115 GlyProAsnGlnGluAspGluSerGluGlnAspTyr 126
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Matches:
Conservative:
Mismatches:
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Mismatches:
Indels:
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: LOCATION: (1)..(131)

: OTHER INFORMATION: Ceres Seq. ID no. 13589013

US-11-096-568A-8671
                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
NACATION: (1). (126)
OTHER INFORMATION: Ceres Seq. ID no. 13589014
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Matches:
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US-11-098-686-10809
; Sequence 10809, Application US/11098686
                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Triticum aestivum
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75.0%
58.3%
48.9%
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RIC149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 550 SEQ ID NO 82 LENGTH: 406
                                                                                                                                                                                                                                                                                                                             US-10-664-025-43_COPY_53_103 (1-51) x US-10-973-115B-82 (1-406)
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Matches:
Conservative:
Mismatches:
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PRIOR APPLICATION NUMBER: 60/049911
PRIOR PILING DATE: 1997-06-18
PRIOR PILING DATE: 1997-06-18
PRIOR PILING DATE: 1997-08-26
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059117
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
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PRIOR PILING DATE: 1997-09-17
PRIOR PRILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/05958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 82, Application US/10137873A Publication No. US20060084138A1 GENERAL INFORMATION:
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Goddard, Audrey
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Wood, William
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Filvaroff, Ellen
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64.3%
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                                                  TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
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; ORGANISM: How
US-10-137-873A-82
                          LENGTH: 406
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SARE
TITLE OF INVENTION: SAME
TITLE OF INVENTION: SAME
TITLE OF INVENTION: SAME
FILE REFERENCE: 39870-3330R1C30C1
CURRENT APPLICATION NUMBER: US/10/973,115B
CURRENT PILING DATE: 2004-10-22
PRIOR APPLICATION NUMBER: US 10/145,747
PRIOR APPLICATION NUMBER: US 10/028,072
PRIOR FILING DATE: 2000-12-01
PRIOR FILING DATE: 2000-12-01
PRIOR PILING DATE: 2000-12-01
PRIOR FILING DATE: 2000-06-16
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-03-05
PRIOR FILING DATE: 1999-03-05
PRIOR FILING DATE: 1999-03-05
FRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR PILING DATE: 1997-09-18
PRIOR PLING DATE: 1997-09-18
PRIOR PLING DATE: 1997-09-19
PRIOR PLING DATE: 1997-09-19
PRIOR PRING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
FEMONT
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Matches:
Conservative:
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Tumas, Daniel
Watanabe, Colin K.
Wood, William I.
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Filvaroff, Ellen
Gao, Wei-Quiang
Gerritsen, Mary E.
Goddard, Audrey
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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TYPE: PRT
ORGANISM: Homo Sapien
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Best Local Similarity:
Query Match:
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APPLICANT: DeForge, Laura
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Laura
APPLICANT: Desnoyers, Laura
APPLICANT: General Filvance Andrey
APPLICANT: Gederad, Andrey
APPLICANT: Gedevach, Paul J
APPLICANT: Grewart, Fimothy A
APPLICANT: Stewart, Fimothy A
APPLICANT: Stewart, Fimothy A
APPLICANT: Stewart, Fimothy A
APPLICANT: Stewart, Fimothy A
APPLICANT: Matanabe, Colin K
APPLICANT: Matanabe, Colin K
APPLICANT: Anany, Zemin
APPLICANT: Anany Saniel
APPLICANT: Wood, William
APPLICANT: Matanabe, Colin K
APPLICANT: Matanabe, Colin K
APPLICANT: Mood, William
APPLICANT: Mood, William
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Matches:
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Matches:
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Publication No. US20060084139A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Search completed: May 9, 2006, 10:11:25 Job time : 3.65 secs

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hypothetical protein MTH378 - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: H69148
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Ciu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func.
A;Title: Complete genome sequence of Methanobacterium translation not shown
A;Reference number: A68000; MUID:98037514; PMID:9371463
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-334 cMTH>
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-MODEL=frame+ n2p.model -DEV=xlh
-Q= Abss/ABSWEBE spool/US10664025/runat 08052006 173455 28373/app query.fasta_1
-Q= Abss/ABSWEB spool/US10664025/runat 08052006 173455 28373/app query.fasta_1
-DB=PIR -QFMT=fastan -SUFPIX=n2p.rpr -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX-Eblosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UOTFWT=pto -NORM=ext -HEAPSIXE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss07
-USER=USI0664025_@CGN 1 1 35 -GTUNAT 0 -17455_28373 -NCPU=6 -ICPU=3
-NO WMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                          OM nucleic - protein search, using frame_plus_n2p model
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Maximum Match 100%
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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1: pirl:*
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	hypothetical prote conserved hypothet S-adenosylmethioni homoserine dehydro hypothetical prote	nitrogen fixation FixI protein - Rhi FixII copper trans nitrogen fixation	nitrogen fixation LDL receptor precu hypothetical prote deoxyxylulose 5-ph hypothetical prote conserved hypothet X/Y protein - mous	multidrugestilux t complement recepto threonine-serine p threonine-serine p threonine-serine p hypothetical prote	complement regulat protein F3F19.15 [hypothetical prote probable flavoprot
2 T01671 2 S06409 2 T28742 2 G85850 2 F64981	2 F91006 2 D71256 2 C82697 2 S74407	AC3448 C32052 C95344 AG2764		C70025 443519 BVECTC C85973 D91128	. JC2054 E86265 T08930 S74576
81 81 165 203 203	203 278 347 693	757 27 27 27 27 27 27 27 27 27 27 27 27 27	763 2 879 1 399 2 133 2 250 2	256 444 444 443 112 22 22 22 22	522 2 522 2 571 2 594 2
4446.7.7.94 7.094 7.094 7.094	7. 94 7. 94 7. 94 7. 94 7. 94	7.94 7.94 7.94 7.94		4455.7 4455.7 455.7 7.7 7.7 7.7	45.7 45.7 45.7
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ALIGNMENTS

8 8 8 8 0 0 0 0 4 4 Matches: Conservative: Mismatches: Length: 4.99 50.00 86.7 53.3 54.3

US-10-664-025-43_COPY_53_103 (1-51) x H69148 (1-334)

Indels:

GCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGT 48

~ RESULT S17804

hypothetical prote Nel-homolog protei ferredoxin 2[4Fe-4

T47478 T10756 FECLCE r08826

47.8 47.8 46.7

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conserved hypothet secretory carrier

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46.00
90.0<del>$</del>
80.0<del>$</del>
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Best Local Similarity:
Query Match:
DB:
    A;Residues: 1-710 <BEV>
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No.:
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               C.Species: Rhodobacter capsulatus
C.Species: Rhodobacter capsulatus
C.Sacesaion: S17804
R.Sacesaion: S17804
R.Sacion: S17804
R.Surke, D.H.; Alberti, M.; Armstrong, G.A.; Hearst, J.E.
submitted to the EMBL Data Library, November 1991
A.Description: The complete nucleotide sequence of the 46 kb photosynthesis gene cluster
A.Reference number: S17803
A.Reference number: S17804
A.Rocession: S17804
A.Rocession: S17804
A.Rocession: 1-274 <EMB>
A.Residues: 1-274 <EMB>
A.Residues: 1-274 <EMB>
A.Cross-references: UNIPROT: P26158; UNIPARC: UPI000013BE4E; EMBL: Z11165; NID: 946097; PIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A36353
Mon repair protein XRCC1 - human
C;Species: Howo sapiens (man)
C;Species: Howo sapiens (man)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 05-Oct-2004
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 05-Oct-2004
C;Accession: A3653
R;Thompson, L.H.; Brookman, K.W.; Jones, N.J.; Allen, S.A.; Carrano, A.V.
Mol. Cell. Biol. 10, 6160-6111, 1990
A;Title: Molecular cloning of the human XRCC1 gene, which corrects defective DNA strand
A;Reference number: A36353; MUID:91061722; PMID:2247054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Accession: A36353
A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-633 <THO>
A, Cross-references: UNIPROT: P18887; UNIPARC:UP10000139020; GB:M36089; NID:G340396; PIDN:
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C;Species: Arabidopsis thaliana (Gouse-ear cress)
C;Date: 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13458
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; I submitted to the Protein Sequence Database, July 1999
A;Reference number: Z17587
A;Accession: T13458
A;Molecule type: DNA
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Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
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hypothetical protein 274 - Rhodobacter capsulatus
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A;Map position: 19q13.2-19q13.2
C;Superfamily: DNA-repair protein XRCC1
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Pred. No.:
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A;Cross-references: UNIPROT:Q9SU46; UNIPARC:UPI000009FF34; EMBL:AL109619; GSPDB:GN00062, A;Experimental source: cultivar Columbia; BAC clone T19F6 C;Genetics: A;Gene: ArSP:T19F6.90 A;Map position: 4 A;Introns: 73/3; 158/3; 200/2; 215/2; 242/3; 265/3; 329/3; 351/3; 374/3; 467/2; 508/1; 5
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A; Residues: 1-22, VV, 24-26, GG, 28-60, KK, 62-143, PV, 145-155, VK, 157-177, HV, 179-185, AE'
A; Residues: 1-22, VV, 24-26, GG, 28-60, VK, 62-143, PV, 145-155, VK, 157-177, HV, 179-185, A; Cross-references: UNTRARC: UPPIO0000280E4; GB: 219521; NID: 9286378; PIDN: CAA79581.1; PID:
A; Experimental source: strain BALB/C, adult male liver
C; Comment: This transmembrane glycoprotein binds LDL, the major cholesterol-carrying lip
nd complexes must first clueter into clathrin-coated pits.
C; Cyuperfamily: LDL receptor; EGF homology; LDL receptor ligand-binding repeat homology cLDL:
F; 22-862/Pomain: LDL receptor ligand-binding repeat homology cLDL:
F; 27-862/Pomain: LDL receptor ligand-binding repeat homology cLDL:
F; 68-104/Pomain: LDL receptor ligand-binding repeat homology cLDL:
F; 199-134/Pomain: LDL receptor ligand-binding repeat homology cLDL:
F; 199-23/Pomain: LDL receptor ligand-binding repeat homology cLDL:
F; 190-439/Domain: LDL receptor ligand-binding repeat homology cLDL:
F; 190-439/Domain: LDL receptor WWID-containing repeat homology cWW:
F; 190-439/Domain: LDL receptor WWID-containing repeat homology cWW:
F; 190-528/Domain: LDL receptor WWID-containing repeat homology cWW:
F; 190-157/Domain: LDL receptor WWID-containing repeat homology cWW:
F; 190-190/Domain: LDL receptor WWID-containing repeat hom
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(f.Species: Mus musculus (house mouse)
(f.Species: Mus musculus (house mouse)
(f.Species: Mus musculus)
(f.Species: Mus musculus)
(f.Species: Mus musculus)
(f.Species: Musculus)
(f.Species:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;791-812/Domain: transmembrane #status predicted <TMM>F;813-862/Domain: intracellular #status predicted <INT>F;827-831/Region: coated-pit mediated internalization signal
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clustered O-linked oligosaccharides
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Matches:
Conservative:
Mismatches:
Indels:
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perilipin A - rat
CiSpecies: Rattus norvegicus (Norway rat)
CiSpecies: Rattus norvegicus (Norway rat)
CiSpecies: Rattus norvegicus (Norway rat)
CiSpecies: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
CiAccession: A49413
RiGrenberg, A.S.; Egan, J.J.; Wek, S.A.; Moos Jr., M.C.; Londos, C.; Kimmel, A.R.
RiGrenberg, A.S.; Egan, J.J.; Wek, S.A.; Moos Jr., M.C.; Londos, C.; Kimmel, A.R.
A; Fritle: Isolation of cDNAs for perilipins A and B: sequence and expression of lipid dr.
A; Reference number: A49413
A; Accession: A49413
A; Accession: A49413
A; Status: preliminary
A; Molecule type: mRNA; protein
A; Residues: 1-517 cGRE.
A; Residues: 1-517 cGRE.
A; Cross-references: UNIPROT:P43884; UNIPARC:UPI0000131BF7; GB:L26043; NID:g457373; PIDN
A; Experimental source: adipocytes
A; Note: sequence extracted from NCBI backbone (NCBIN:14105), NCBIP:141051)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable ATP-binding component of ABC transporter PA4223 [imported] - Pseudomonas aerug
C;Species: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                            UNIPARC:UPI0000074A70; EMBL:AL110477; NID:e1542121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein Y113G7B.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 09-Jul-2004
C;Accession: T26440
R;Lernard, N.
Submitted to the EMBL Data Library, September 1999
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                           A;Accession: T26440
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-309 <WIL>
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A;Experimental source: clone Y113G7B
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Best Local Similarity:
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F;839-851/Region: basolateral targeting signal
F;97,273,462/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;319-330,326-339,341-353,359-369,365-378,380-393,667-682,678-697,699-712/Disulfide bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable membrane protein YGL149w - yeast (Saccharomyces cerevisiae)
NyAlternate names: hypothetical protein G1895
CySpecies Saccharomyces cerevisiae
CyBecies Saccharomyces cerevisiae
CyBate: 10-Apr-1996 #sequence revision 19-Apr-1996 #text_change 09-Jul-2004
CyAccession: S60434; S64163; $\frac{2}{3}\frac{2}{4}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2}{3}\frac{2
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R,James, C.M.; Indge, K.J.; Oliver, S.G.
submitted to the Protein Sequence Database, May 1996
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Cross-references: UNIPARC:UP1000013B104; EMBL:272672; NID:g1322733; PID:e243769; PID:g
Experimental source: strain S288C
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A;Status: nucleic acid sequence not shown
A;Status: 1-101 -/JMA
A;Rossiduse: 1-101 -/JMA
A;Cross-references: UNIPROT:P53116; UNIPARC:UPI000013B104; EMBL:Z48618
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1995
R;Volckaert, G:, Voet, M:, Verhasselt, P.; Defoor, E.
Bubmitted to the Protein Sequence Database, May 1996
A;Reference number: S64153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGC 50
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C;Genetics:
A;Coss-references: $GD:$0003117
A;Map position: 7L
C;Superfamily: $accharomyces cerevisiae probable membrane }C;Keywords: transmembrane protein
F;1-17/Domain: transmembrane #status predicted <TML>F;21-37/Domain: transmembrane #status predicted <TML>
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;1-17/Domain: transmembrane #status predicted <TMl>
;21-37/Domain: transmembrane #status predicted <TM2>
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50.0%
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A;Molecule type: DNA
A;Residues: 1-101 <VOL>
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Best Local Similarity:
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C;Species: Homo sapiens (man)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
R;Minfield, S.L.; Tayebi, N.; Martin, B.M.; Ginns, E.I.; Sidransky, E.
Genome Res. 7, 1020-1026, 1997
Genome Res. 7, 1020-1026, 1997
A;Title: Identification of three additional genes contiguous to the glucocerebrosidase LA;Reference number: 216482; MUDE:97474796; PMID:9331372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C,Accession: T47478
R;Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Lemcke, K Bubmitted to the Protein Sequence Database, February 2000
A;Reference number: Z24467
A;Accession: T47478
                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-347 <WIN>
A;Cross-references: UNIPROT:014828; UNIPARC:UPI00001696B1; EMBL:AF023268; NID:92564910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F18N11.140 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr.2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-690 <10R>
A;Residues: 1-690 <10R>
A;Cross-references: UNIPROT:Q9M3E0; UNIPARC:UPI00000AA555; EMBL:AL132953
A;Experimental source: cultivar Columbia; BAC clone F18N11
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A;Note: F18N11.140
C;Superfamily: Arabidopsis thaliana hypothetical protein F18N11.140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Introns: 22/3; 48/3; 89/3; 130/1; 173/1; 226/2; 260/2; 299/3
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                                                                                                                                                                         secretory carrier membrane protein homolog propin1 - human
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C;Species: Bacillus subtils

C;Species: Bacillus

R;Species: C;Species

R;Species: C;Species

C;Species: C;Species

A;Authors: Poulger, D; Fritz, C; Fujita, M; Fujita, Y; Fuma, S; Galizzi, A; Galler

iech, J; Harwood, C.R; Henauc, A; Jubert, H; Holaspel, S; Hosono, S; Hulto, M; F.

Koetter, P; Koningstein, G; Krogh, S; Kumano, M; Kurita, K; Japhidus, A; Lauler, J; Lazarevic, V; Lee, S.M; Levine, A; Liu, H; Masuda, S; Mauthors: Lauber, J; Lazarevic, V; Lee, S.M; S.H; Parro, V; Pohl, T.M; Portectale

Y, M; Ogawa, K; Ogiwara, A; Oudega, B; Rose, M; Sadie, Y; Sacio, T; Scanlon, A; Authors: Schleich, S; Schroeter, R; Scoffone, F; Sediguchi, J; Sekowska, A; Seror, akeuchi, M; Tamakoshi, A; Tanaka, T; Terpstra, P; Tognoni, A; Tosato, V; Uchiyama, A; Atthores: Schleich, B; Wight, A; Yamano, K; Yasta, K; Yoshida, R; A; Atthores: Voshikawa, H; P; Zumstein, B; Yoshikawa, H; Danchin, A, A; Atthores: Voshikawa, H; P; Zumstein, B; Yoshikawa, H; Danchin, A, A; Atthores: DNA

A; Residues: Drose: DNA

A; Residues: DSS

A; Rose, M; Rivoles, C; Rocha, B; Mills; 9384377

A; Rose-references: UNIPROT: O06487; UNIPARC: UPI00000606F; GB: Z99107; GB: AL009126; NID: A; Genetics:
C; Genetics:
C; Section: Pfoli
                                C;Accession: A83118

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor, A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                 A;Accession: A83118
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-570 <STO>
A;Cross-references: UNIPROT:Q9HWG6; UNIPARC:UPI0000C6EB7; GB:AE004839; GB:AE004091; NIC
C;Genetics:
A;Gene: PA4223
        Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
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Mismatches:
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Conservative:
Mismatches:
Indels:
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C;Superfamily: membrane sulfatase, HI1246 type
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A; Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isc A; Reference number: 214389; MUID:86245056; PMID:2424612 A; Accession: T01671 A; Accession: T01671 A; Accession: T01671 A; Anolecule type: mRNA A; Residues: 1-81 ALL A; Residues: 1-81 ALL A; Residues: 1-81 ALL A; Cross-references: UNIPARC:UPI000017865F; EMBL:K03456; NID:9328018 C; Superfamily: HIV-1 vpu protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGGCGTTAGAAGICTTGATGCTCCTCGCTGTCTTGATTTGGACC 45
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43.00
86.7<del>$</del>
40.0<del>$</del>
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                                                                        C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10756
R;Kuroda, S.; Tokunaga, C.; Kiyohara, Y.; Konishi, H.; Matsuhashi, S.; Kikkawa, U.
submitted to the EMBL Data Library, November 1998
A;Bescription: Protein kinase C-binding protein.
A;Reference number: Z17122
A;Reference number: Z17122
A;Accession: T10756
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Melecule type: mRNA
A;Melecule type: MRNA
A;Mesidues: 1-810 <KUR.>
A;Cross-references: UNIPROT:Q62919; UNIPARC:UPI000012FF2B; EMBL:U48246; NID:g3851179; PI
A;Experimental source: strain Sprague-Dawley, brain
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 20-Jun-2000
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TUBMed=14702039; DOI=10.1038/ng1285;

TUBMed=14702039; DOI=10.1038/ng1285;

TUBMed=14702039; DOI=10.1038/ng1285;

TUBMED T., SUZUKI Y., Nishikawa T., Chubahara T., Tanaka T., Ishii S., Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., A Yamanoto J.-I., Satto K., Kawai Y., Isono Y., Nakamura Y., Nakamura Y., Murakami K., Yasuda T., Kaku Y., Kodaira H., Kondo H., Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Shiratori A., Sudo H., Hosoiri T., Yamashita H., Kimata M., Sato K., Tanikawa M., Sano K., Tanikawa M., Hiraoka S., Chiba Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Rimata M., Matanabe S., Coo Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Nomura Y., Matsunawa H., Ichihara T., Shiohata N., Sano S., Nomiyama H., Satoh N., Takami S., Terashima Y., Sano S., Sonikawa Y., Matanabe K., Kumagai A., Takemoto M., Kawakami B., Makagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Hishigaki H., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Pulimori Y., Komiyama H., Tashiro M., Tashingami A., Fuliwa T., A Namadaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Rujimori Y., Komiyama K., Pujimori K., Hirao M., Ohmori Y., Kumada K., Pujimori K., Fuliwabata A., Hishigami A., Hishigami A., Hishigami A., Hikabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Ono T., Yamada A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Akabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Ono T., Yamada A., Hikiji T., Noguchi S., Itoh T., Shigeta K., Senba T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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054MC23 ASPEU

04MC23 ASPEU

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06ADS6 9HIV1

04PUS8 9HIV1

04PUS8 9HIV1

04SFP2 9HIV1

04SFP2 9HIV1

07SFP2 9HIV1

07
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Q8G6X3_B1FLO
Q4SQC4_TETNG
Q66JFO_XEBNTR
Q4SMK4_TETNG
Q4Q635_LETNA
Q82FLI_STRAW
Q82FLI_STRAW
Q8RWU9_ARATH
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01-0CT-2002 (TrEMBLrel. 22, Last seq
01-0CT-2002 (TrEMBLrel. 22, Last ann
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Homo sapiens (Human).
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-Q=/abss/ABSSWEB_spool/US10664025/runat_08052006_173450_28308/app_query.fasta_1
-Q=/abss/ABSSWEB_spool/US10664025/runat_08052006_173450_28308/app_query.fasta_1
-Q=/abss/ABSSWEB_spool/US126_12p.rup_MINAATGH=0.1 -LOOPEXX=0
-UNITS=bits -START=1 -BND=-1 -MATRIX=100 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -TANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -BND=-1 -MATRIX=0 -MAXLEN=200000000 -HOST=abss07
-USFR-US10664025_GCGN 1 1 266_Gwruat_0805206_173450_28308 -NCUE=6 -ICPU=3
-NO MWAP -NEG SCORES=0 -WAIT -DSPBIOCE*100 -LOONGLOG -DBV TIMEOUT=120
-WARN TIMEOUT=10 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP==7
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                  GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                           using frame_plus_n2p model
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Q4FZG8_MOUSE
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Q5N0H7_SYNP6
Q5CN74_CRYHO
Q29172_FIG
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Maximum DB seq length: 200000000
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Ygapop 10.0 , Y
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Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A bopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A brapleton M., Soares M.B., Bonaldon M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Widin T.B., Tooshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Widin T.B., Tooshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Brownstein M.J., Widin T.B., Tooshiyuki S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Schemutz J., Myers R.M.,
B Charteffield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
B Cherration and initial analysis of more than 15,000 full-length human
          Togashi T., Oyama M., Hata H., Watanabe M., Komateu T., Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.; "Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                   21
                                                                                                                                                                                                                                                                                                                                                   1 MetAlaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAla 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
                                                                                                                                                                                                                                                                                                                                   1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTTGGACCGGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                    Nat. Genet. 36:40-45(2004).
EMBL, AKO93517; BAC04191.1; -; mRNA.
Engembl; ENSG00000149507; Homo sapiens.
SEQUENCE 158 AA; 17942 MW; EEB43D70A8A391E8 CRC64;
                                                                                                                                                                                                                                                                                                    US-10-664-025-43_COPY_53_103 (1-51) x Q8N9U6_HUMAN (1-158)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein FLJ36198.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Matches:
Conservative:
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QBGWS3 HUMAN PRELIMINARY;
QBGWS3;
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Director MGC Project;
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NIH MGC Project;
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MEDLINE-2238257; Pubmed-12477932; DOI=10.1073/pnas.242603899;
X Structure Structure.

A Structure R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
X Aluschul S.F., Zeoberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A ltschul S.F., Zeoberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A pokins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Marusina R., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratene P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahesley R.W., Touchman J.W., Screen E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,
Schnetchield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
Schnetch A., Schein J.E., Jones S.J.M., Marra M.A.,
Schnetch A., Schein J.E., Jones S.J.M., Marra M.A.,
Schnetch A., Schein J.E., Jones S.J.M., Marra M.A.,
Schnetch A.,
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC099498; AAH99498.1; -; mRNA.
Hypothetical protein.
SEQUENCE 164 AA; 18849 WW; 49ADE19216BE8606 CRC64;
                                                                              Hypothetical protein.
SEQUENCE 158 AA; 17971 MW; EEB43D6FBBAB81FF CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
14-Pothetical protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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EMBL; BC048121; AAH48121.1; -; mRNA.
EMBL; BC036256; AAH36256.1; -; mRNA.
Ensembl; ENSG0000149507; Homo sapiens.
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                                                                                                                   Homoserine dehydrogenase.
Name=thrA; OrderedLocusNames=syc2003 c;
Synechococcus sp. (strain PCC 6301) (Anacystis nidulans).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Tachia sadinata (Beef tapeworm).
Eukaryota, Metazoa; Platyhelminthes; Cestoda; Eucestoda; Cyclophyllidea; Taeniidae; Taeniida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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                                                            US-10-664-025-43_COPY_53_103 (1-51) x Q4FZG8_MOUSE (1-164)
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
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                                                                                                                                                                                                                                                                                                             174 AA
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                                                                                                                                                                                                                                                                                                             PRT;
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InterPro; IPR003961; FN III.
SMART; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 AA; 18702 MW;
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Q8T8D7;
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Best Local Similarity:
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Garate T.;
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Xu P., Widner G., Wang Y., Ozaki L.S., Alves J.M., Serrano M.G.,
Puiu D., Manque P., Akiyoshi D., Mackey A.J., Pearson W.R., Dear P.H.,
Bankler A.T., Peterson D.L., Abrahamsen M.S., Kapur V., Tzipori S.,
                                                                                                                                                                                                                                                                                                                                                                                                      47
                                                                                                                                                                                                                                                                                                                                                                                                                     40 GlyValArgSerLeuAspLysProArgSerValAspIleSerArg 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cryptosporidium hominis.
Eukaryota, Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
                                                                                                                                                                                                                                                                                                                                                                                                    GGCGTTAGAAGTCTTGATGCTCCTCGTGTCTTGATTTGGACCGG
                                                                                                                                                                           432 AA; 45628 MW; 3FE3A02F84FD75B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The genome of Cryptosporidium hominis.";
Nature 431:1107-1112(2004).
BEBL; AAEL0100015; ESD551.1; -; Genomic_DNA.
SEQUENCE 132 AA; 14733 MW; 8721106746EIIFSF CRC64;
                                                                                                                                                                                                                                                                                                                                                             US-10-664-025-43_COPY_53_103 (1-51) x Q5N0H7_SYNP6 (1-432)
                                                                                                                                                                                                                                US-10-664-025-43_COPY_53_103 (1-51) x Q5CN74_CRYHO (1-132)
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Conservative:
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Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTCCAAATCAAGACAGCGAGGAGCATCAAGAC 13
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InterPro; IPR002912; ACT.
InterPro; IPR005106; Hmsr dh_NAD_bind.
InterPro; IPR001142; Homoser_dehydrog.
Pfam; PF00142; ACT; 1.
Pfam; PF00142; ACT; 1.
ProDom; PF001447; NAD_binding_3; 1.
ProDom; PF001244; Acolac synthsm; 1.
PROSITE; PS01042; HOMOSER_DHGENASE; 1.
Complete proteome.
SEQUENCE 432 AA; 45628 WW; 3FE3A02F84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
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(TrEMBLrel. 01, I
(TrEMBLrel. 26, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 PIG

029172 PIG PRELIMINARY;

029172;

01-NOV-1996 (TEMBLEEL 01,

01-NOV-1996 (TEMBLEEL 01,

01-NOV-1996 (TEMBLEEL 01,

01-NOV-1996 (TEMBLEEL 26,

NAME-OOF (TEMBLEEL 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QSCN74_CRYHO PRELIMINARY;
QSCN74;
                                                                                                                                                                                                                                  3.54
53.00
80.0%
66.7%
57.6%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.65
51.00
90.9$
81.8$
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                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                              Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CG4090-PA.
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Delta H;
MEDLINE=98037514; PubMed=9371463;
MEDLINE=98037514; PubMed=9371463;
MEDLINE=98037514; PubMed=9371463;
MEDLINE=98037514; PubMed=9371463;
Aldredge T., Bashizzadeh R., Blakely D., Cook R., Gilbert K.,
Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
"Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics.";
                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                TISSUE-Small intestine;

BDLINE-36327607; PubMed-8672129; DOI=10.1007/s003359900153;

Winterce 9A.K., Fredholm M., Davies W.;
"Evaluation and characterization of a porcine small intestine cDNA library: analysis of 839 clones ";

Mamm. Genome 7:509-517 (1996).

EMBL, F15058; CAA23315.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol. 179:7135-7155(1997).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the UPF0104 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 CACCGGTCCAAATCAAGACAGCGAGGAGCATCAAGACTTCTA 8
                                                                                                                                                                                                                                                               9361 MW; 448BF6A549FE4AE4 CRC64;
                                                                                                                                                                                                                                                                                                                  00239
                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-664-025-43_COPY_53_103 (1-51) x Q29172_PIG (1-79)
                                                                                                                                                                                                                                                                                                                                                Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                   Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Hypothetical UPF0104 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                334 AA
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Matches:
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Pfam; PF03706; UPF0104; 1.
TIGRFAMB; TIGR00374; Cons_hypoth374; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methanobacterium thermoautotrophicum.
                                                                                                                                                                                                                                                                                                                  111.3
50.00
85.7%
64.3%
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                                                                                                  NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                               79
79 AA;
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Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
                                                              NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
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026478;
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RA Arroya J., Barriman M., Anderson M.J., Wortman J., Kim H.Stanley.,
RA Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
RA Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
Ravoya P., Collina M., Collina M., Collean R., Davies R., Dyer P.S.,
Radorova N., Fedorova N., Fedorlyum T.V., Fischer R.,
Roddman G.H., Gomi K., Giffith.Jones S., Gallilam R., Hass B.,
Rodlana G.H., Gomi K., Giffith.Jones S., Gallilam R., Hass B.,
Radorova H., Kltamoto K., Kobayashi T., Kulkarni R.,
Radoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
RA Monyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
Rabbinowitsch E., Rawlins N., Rajandream M.-A., Sandrea M. Price C., Pritchard B.L., Quail M. A.,
Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
Rabbinowitsch E., Rawlins N., Rajandreas M. A., Sandrez M., Price C., Galzberg K., Squares S.,
Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares S.,
Sanchez-Ferrero J., Yurner G., Vazquez de Aldana C.R., Weidman J. W.,
Machida M., Hall N., Barrell B., Denning D.W.;
Machida M., Hall N., Barrell B., Denning D.W.;
Rapengillus funigatus.";
Rapergillus funigatus.";
REBL/Genbank/DDBJ databases
C. Ermitced (MAY-2005) to the EMBL/GenBank/DDBJ databases
C. Ermitched (MAY-2005) to the EMBL/GenBank/DDBJ entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OŘFNames=Afu4g14790;
Aspergillus fumigatus Af293.
Bukaryota; Pumig Ascomycota; Pezizomycotina; Eurotiomycetes;
Burotiales; Trichocomacese; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                            48
                                                                                                                                                                                                                                                                                                                                                                                           25
Hypothetical protein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                           4 GCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGT
                                                                                                                                                                                                                                                                                                                                                                              Potential.
46D280EC683CB611 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary data.

--- SIMILARITY: Belongs to the cytochrome P450 family.
BEMBL, AAHFO1000005; EAL89316.1; -; Genomic_DNA.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR00128; EAL80316.1;
InterPro; IPR001865; Ribosomal_S2.
Pfam; PF00067; p450; 1.
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4
6
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Last annotation update)
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Matches:
Conservative:
Mismatches:
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                                 Potential.
Potential.
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Potential.
Potential.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
               27
53
140
162
238
267
267
297
320
36959 M
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50.00
86.7<del>$</del>
53.3$
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Complete proteome; H
TRANSMEM 7
TRANSMEM 33
TRANSMEM 120 1
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                               33
120
142
218
247
277
                                                                                                                                                                                                                                        Percent Similarity:
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SEQUENCE
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DB:
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9
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Pred. No.:

SABBB

RESULT 10 Q5ASI7

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Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
Bichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
Sucgang R., Bertinan M., Song J., Olsen R., Szafranski K., Xu Q.,
Ruggal B., Kummerfeld S., Madera M., Konfoortov B.A., Rivero F.,
Bankier A.T., Lehmann R., Hamlin N., Davies R., Gauder P., Pey P.,
Rathornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
Rerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
Rathorher P., Desany B., Just E., Morio T., Rost R., Churcher C.,
Rathory D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
Hauser H., James K., Quiles M., Mohan M.B. Saito T. Buchrieser C.,
Wardroper A., Felder M., Thangavelu M., Johnson D., Knights A.,
Loulseged H., Mungall K., Oliver K., Price C., Quail M.A.,
Urushihara H., Hernandez J., Rabbinowitsch E., Steffen D., Sanders M.,
Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox B.C.,
Milliams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
Whether M. Marker D., Mohan M.B., Kay R.R.,
Walliams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
Whather M. Marker D., Mohan M.B., Kay R.R.,
Walliams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
Walliams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
Walliams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
Walliams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
Walliams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
Walliams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
Walliams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
                                                                                                                            GGTCCAAATCAAGAC-----AGCGAGGAGCATCAAGACTTCTAACGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 0:0-0(2005).
-1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS-10-664-025-43_COPY_53_103 (1-51) x Q5ASI7_EMENI (1-1152)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .l protein.
674 AA; 77632 MW; 920A285423EC59BD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                    Dictyostelium discoideum (Slime mold).
Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                        13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein.
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Last sequence update)
Last annotation update)
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AAFI01000124; EAL64570.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                                                Q54N72_DICDI PRELIMINARY;
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QGRK14;
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49.00
81.2%
56.2%
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                                                                                                                                                                                                                                                                                                                                                                                               ORFNames=DDB0186513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
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Best Local Similarity:
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Arachchi H.M., Baarna N., Bastien V., Bloom T., Boguslavkiy L.,
Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
Diaz J.S., Dodge S., Dodgey K., Dorris L., Elknia T., Engels R.,
Brickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
Agfe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
Mathews C., Maucelli E., McCarthy M., Meldrim J., Meneus L.,
Mihova T., Menga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
Nicola C., Deterson K., Phunkhang P., Pierre N., Purcell S.,
Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
Romin J., Schauer S., Schupback R., Seaman S., Severp P., Smirnov S.,
Ramas J., Tesfaye S., Theodore J., Topham K., Travers M.,
Valamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
Lander E.,
Lander E., Zimmer A., Zembek L., Zimmer A., Zody M.,
Lander E., Stander Phomann J., Zembek L., Zimmer A., Zody M.,
Lander E., Zimmer A., Zembek L., Zimmer A., Zody M.,
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Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aspergillus nidulans FGSC A4.
Eukaryota, Pungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, Emericella.
NCBI_TaxID=227321;
               PROSITE; PS00086; CYTOCHROME P450; UNKNOWN 1.
PROSITE; PS00962; RIBOSOMAL 52 1; UNKNOWN T.
Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase.
SEQUENCE 507 AA; 57810 MW; 16F1DE6E90612F32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               45
                                                                                                                                                                                                                                                                                                                                                                                                                     ACBEE3B1AFFECCDB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGAATTTGGACC
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10
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Last annotation update)
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Matches:
Conservative:
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Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QSASI7 EMENI PRELIMINARY;
QSASI7;
                                                                                                                                                                    12.5
50.00
86.7
53.3
54.3
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49.50
66.7$
55.6$
PRINTS; PR00385; P450
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                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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Best Local Similarit
Query Match:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22375625; PubMed=12487816; DOI=10.1089/088922202320886325;
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                                                                                                   SCOLE S.W., Zimmeran M.T., Rankin D.;
SCOLE S.W., Zimmeran M.T., Rankin D.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY496068; AAR88259.1; -; Genomic_RNA.
GO; GO:0008174; F:RNA methyltransferase activity; IEA.
GO; GO:0003723; F:RNA binding; IEA.
R GO; GO:0003724; F:RNA halicase activity; IEA.
R GO; GO:000396; F:RNA halicase activity; IEA.
GO; GO:000396; P:RNA directed RNA polymerase activity; IEA.
GO; GO:001997; P:VATA | Genome replication; IEA.
R GO; GO:001979; P:VATA | Genome replication; IEA.
R InterPro; IPR00566; Viral helicasel.
InterPro; IPR00566; Viral helicasel.
R Pfam; PP01460; Vmethyltransf; 1.
SEQUENCE 1098 AA; 124146 MW; 4FAIlDCID83D1347 CRC64;
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databases.
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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Viruses; Retroid viruses; Retroviridae; Lentivirus;
Primate lentivirus group.
NCBL_TaxID=11676;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Mismatches:
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Kim B., Phillips J.B., Lane J.R., Merling R.,
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ
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STRAIN=99UGB25647;
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                                           NCBI_TaxID=64958;
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Pred. No.:
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STRAIN=99UGK38855;
MEDLINE=22375625; PubMed=12487816; DOI=10.1089/088922202320886325;
Harris M.E., Serwadda D., Sewankambo N., Kim B., Kigozi G.,
Kiwanuka N., Phillips J.B., Wabwire F., Meehen M., Lutalo T.,
Lane J.R., Merling R., Gray R., Wawer M., Birx D.L., Robb M.L.,
McCucchan F.E.;
"Among 46 near full length HIV type 1 genome sequences from Rakai
District, Uganda, subtype D and AD recombinants predominate.";
AnDS Res. Hum. Retroviruses 18:1281-1290(2002).
                                                                                                                                          Serwadda S., Sewankambo N., Wabwire F., Kigozi G., Kiwanuka N.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
BMBL, AP484481, AAN73479-1; Genomic_DNA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0019076; P:viral release; IEA.
InterPro; IPR008187; Vpu.
InterPro; IPR008187; Vpu.
SEQUENCE 81 AA; 9322 MW; 98B7887582935D15 CRC64;
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databases.
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                              to the EMBL/GenBank/DDBJ databases
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the EMBL/GenBank/DDBJ databases
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Last annotation update)
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9HIV1 PRELIMINARY;
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48.00
86.7
53.3
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Harris M.E., Birx D.L.,
Submitted (FEB-2002) to
NUCLEOTIDE SEQUENCE.
STRAIN=99UGB25647;
Meehen M., Wawer M.;
Submitted (FEB-2002) t.
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NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
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                                                                                                                             STRAIN=99UGB25647;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
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01-OCT-2003
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NUCLEOTIDE SEQUENCE.
STRAIN=99UGK38855;
STRAIN=99UGK38855;
Serwadda S., Sewankambo N., Wabwire F., Kigozi G., Kiwanuka N.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AR484520; AAN73822.1; -, Genomic_DNA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0019076; P:viral release; IEA.
InterPro; IPR009187; Vpu_cyt.
InterPro; IPR009032; Vpu_cyt.
Pfam; PF00558; Vpu; 1.
SEQUENCE 81 AA; 9317 MW; 430257630240FDEC CRC64;
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Bacteriophage Mx8.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
P22-like viruses.
NCBI_TaxID=49964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.

YOUGETIAN P., Walthers D., Salmi D., Magrini V., Hartzell P.L.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF396866, AA84359.1; -; Genomic DNA.

SEQUENCE 199 AA; 22023 MW; F893907DZ8FD4DD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 CACCGGTCCAAATCAAGACAGCGAGGAGCATCAAGACTTCTAACGCCA 2
                                                                                                                                                                                                                                                                                                                                     STRAIN=99UGK38855;
Meehen M., Wawer M.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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Q94MU5,
Q94MU5,
Q1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
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Matches:
Conservative:
Mismatches:
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26 HisArgGinLysSerArgGinArgAspAlaThrArgArgArgTrpPro 41

Search completed: May 9, 2006, 10:09:14 Job time : 16.1 secs This Page Blank (uspfo)

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 512)
S Edwards, J.B.D.M., Jobert, S. and Glordano, J.E.
EST and encoded human protein.
L Patent: JP 2002010789-A 36 15-JAN-2002; GENSET CORP
OS Homo sapiens (human)
PN JP 2002010789-A/36
PD 15-JAN-2002
PP 07-AUG-2000 JP 200209989
PR 05-AUG-1999 US 60/147499
PR 05-AUG-1999 US 60/147499
PR JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI
AR414950 Sequence
AX91784 Sequence
BD119756 EST and e
AX884897 Sequence
AX894897 Sequence
AX970560 Sequence
CS072276 Sequence
AX574404 Sequence
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CQ780456 Sequence
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PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC C12N15/09, C12N2/10, C12N2/
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Location/Qualifiers
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JP 2002010789-A/36.
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                     GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                               293 AGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT 352
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                                                                                                AGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT 300
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                CTTACACCAGTTTCTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTATTGCTGAC
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/note="Von Heijne matrix score 10.699998092651
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Patent: EP 1104808-A 43 06-JUN-2001;
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Sequence 43 from Patent EP1104808.
AX969240
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                                                                                    53 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCTGAGAACCTC 112
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100.0%; Score 459; DB 6; Length 512; 100.0%; Pred. No. 2.8e-117; ive 0; Mismatches 0; Indels
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1 (bases 1 to 512)
Edwards.J.-B.D.M., Jobert,S. and Giordano,J.-Y.
EST's and encoded human proteins
Patent: US 6639063-A 43 28-OCT-2003;
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AR412406.1 GI:40167516
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/wol_type="genomic DNA"
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Oy 181 CGGATACATACGTATATGAGTTTATATATCTTGTTCGTGATTGTGGCATCAGGACA 240	361 CTTACACCAGTTTCTACTGAGATGAAATAGAATCGATCCTTTTATTGCTGAC	RESULT 4 CQ737424 LOCUS LOCUS LOCUS SEQUENCE 23358 from Patent W002068579. ACCESSION CQ737424 VERSION CQ737424.1 GI:42335713 KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human) Eukaryota; Metazoa; Chordata; Craniata; Futeleostomi;	Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo. 1	JOURNAL Patent: WO 02068579-A 23358 06-SEP-2002; PEATURES Location (NY) (US) FEATURES 1. 477 / organism="Homo sapiens" //mol_type="unassigned DNA" /db_xref="taxon:9606"	Query Match 98.7%; Score 453; DB 6; Length 477; Best Local Similarity 100.0%; Pred. No. 1.3e-115; Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Oy 1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGATTTGGACCGGTGCTGAGAACCTC 60	61 CATGRADATAGETTGCTCTCTGGACTGGTTGTCTCTGTTTGCGGTTTGCGGGTTGTTGCGGTTTGCGGGAAATTGCGGACTGGTTGCTGGTTGTTGCGGGTTGCTGGTTGTTGCGGGAAATTGCGGAAATTGCGGAAATTGCGGAATGAGGAATGGGGAAATTGCGGAAATTGCGGAATGGGGAATGGGGAATGGGGTTGCTGCGAAATTGCGGAATGGGGTTGCTGCGCTGCCCTGCCAAATTGCGGAATTGCGGAATGGGGTTGCTGCCTGC		Db 241 AGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACGAGCTGTACTTTACCCCAAGGAAT 300 Qy 301 ATAGATCATGAGCAAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGGG 360

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footom start = "unramed protein product" | Codom start = "CAP15667.1" | Codom start = "CAP15667.1" | Codom start = "CAP15667.1" | Cab xref="G1:40978038" | Camanatation="MALEVLMILAVLIWTGAENLHVKISCSLDWLMVSVIPVAESRNLYIPADELHLGMGCPRANHHTPVYSETYIVRDCGIRTRVVSETTLECTELFFPRNID HDPQBIHLGMGCPRANHTHPVYSETYIVRDCGIRTRAVSETLECTELFFPRNID | CAPACITAL = "CAPACITAL = "
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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/note="Von Heijne matrix score 10.699998092651
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Parent: EP 1104808-A 1362 06-JUN-2001;
Patent: FR)
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TITCAGACAACAGCAGAAGAGITAGGAITAITA 505
                                                                                                                  Sequence 1362 from Patent EP1104808. AX970559
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Unclassified.
1 (bases to 642)
Edwards, J.-B.D.M., Jobert, S. and Giordano, J.-Y.
EST's and encoded human proteins
Patent: US 6639063-A 1362 28-OCT-2003;
WOX;
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6639063.

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Sequence 1362 from patent US
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                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                                                                                                                     Chicca, J., Yen-Potin, F.
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Patent: WO 02060466-A 2 08-AUG-2002;
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104. .526
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AX574405
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                                                                           AX574405.1 GI:27551738
                                                                                                              Homo sapiens (human)
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                                        PAT 05-MAY-2005
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                              Dumas Milne Edwards,J.B., Bougueleret,L. and Jobert,S.
Full-length human cDNAs encoding potentially secreted proteins
Patent: WO 2010142451-A 19 14-JUN-2001;
Serono Genetics Institute S.A. (FR)
Location/Qualifiers
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42. .518
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                               Sequence 19 from Patent WO2001042451.
CS072271
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                                                                                      CS072271.1 GI:63089501
                                                                                                                         Homo sapiens (human)
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                                                                                                                                             Homo sapiens
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YIFADELHLGMGCPANRIHTYVYEFIYLVRDCGIRTRVVSEETLLFQTELYFTPRNID
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 42476002.
Location/Qualifiers
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shirak:

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 9430

Web site: http://www.shgc.stanford.edu

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov
         Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/db_xref="GeneID:219990"
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/db xref="taxon:9606"
/clone="MGC:43628 IMAGE:5270384"
/tissue type="Testis"
/clone lib="NIH MGC_97"
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/db_xref="GeneID:219990"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                 Vertebrata; Euteleostomi;
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Proteins associated with cell growth, differentiation, and death Patent: WO 02073810-A 16 19-SEP-2002; Inc. (US)
Location/Qualifiers
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Homo sapiens hypothetical protein FLU36198, mRNA (cDNA clone
MGC:43628 IMAGE:5270384), complete cds.
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Mammalla, Eutheria, Buarchontoglires, Primates, Catarrhini,
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100.0%; Pred. No. 1.2e-115;
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                                                                    AX600204.1 GI:28400246
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Best Local Similarity 100.0
Matches 453, Conservative
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/translation="MALEVIMILAVLIWTGAENLHVKISCSLDWLMYSVIPVAESRNL
YIFADELHLGWGCPANRIHTYVYEFIYLVRDCGIRTRVVSEETLLFQTELYFTPRNID
HDPQEIHLECSTSRKSVWLTPVSTENEIKLDPSPFIADFQTTAEELGLLSSSPNLL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 106 Row: j Column: 14
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 42476002.
Location/Qualifiers
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Submitted (04-MAR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
     Generation and initial analysis of more than 15,000 full-length
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                              human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/producl="hypothetical protein LOC219990"
/protein_id="AAH48121.1"
/db_xref="GI:2885618""
/db_xref="GI:28950"
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/db_Aref="taxon:9606"
/clone="MGC:57403 IMAGE:5266642"
/clone Tib="NHP MGC_97"
/lab_host="DH.0B"
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/db_xref="GeneID:219990"
186. .662
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Strauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altechul, S.F., Zeeberg, B., Buetcow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Boask, S.A., McEwan, P.J., McKarnan, K.C., Male, S.J., Guraratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.W., Sodersgren, E.J., Lu, X., Glbbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Kzzywinski, M.I., Shalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
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Homo sapiens hypothetical protein FLJ36198, mRNA (cDNA clone
MGC:57403 IMAGE:5266642), complete cds.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                  Length 1502;
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Pred. No. 1.2e-115;
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llarity 100.0%; Pred. No. 1.2
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Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
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                                   195 CGGATACATATCTATATGACTTTATATATATCTTGCTGGTTGTGGCATCAGGACA 254
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                                                                                                         ATAGATCATGAGCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGG 374
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                      AGGGTAGTTTCTGAGGAAACTCTCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT
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Helix Research Institute (JP); Research Association for
Biotechnology (JP)
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                                                                                                                                                                                                                                                                                                            TTTCAGACAACAGCAGAAGAGTTAGGATTATTA 453
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryoca, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                        486 ATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGG
                                                                                                                                                           546 CTTACACCAGTTTCTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTATTGCTGAC
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                                                                                                                                            TCTACTGAGAATGAAATTGGATCCTAGTCCTTTTATTGCTGAC
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                                 426 AGGGTAGTTTCTGAGGAAACTCCCTTTTTCAAACCGAGGTGTACTTTACCCCCAAGGAAT
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/note='n equals a,t,g, or c'.
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PN JP 200254371-A/26
PD 24-DEC-2002
PP 6-APR-2000 JP 2000611564
PR 09-APR-1999 US 60/128693,26-APR-1999 US 60/130991
Charles e birse,paul a mouret,kimberly a florence,steven m
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1 (bases 1 to 1898)
Brise, C.E., Mouret, P.A., Florence, K.A., Ruben, S.M., Romatsoulis, G.A., Ni, J., Ebner, R., W,D., Lafleur, G.Shi, Y., Soppet, D.R., Rosen, C.A. and Young, P.E. Patent: JP 2002543771-A 26 24-DEC-2002;
Human Genome Sciences Inc
                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                    TTTCAGACAACAGCAGAAGAGTTAGGATTATTA 453
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/organism="Homo sapiens"
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JP 2002543771-A/26.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity
Matches 453; Conserv
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E 3 (bases 1 to 1492)

S Isogai, T. and Yamamoto, J.

Direct Submission

Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Razusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(B-mail:genomics@hri.co.jp, Tel 81-438-52-3975, Fax:81-438-52-386)

NBDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Halix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5- & 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 CGGATACATACATATGTATATGAGTTTATATATCTTGTTCGTGATTGTGGCCATCAGGACA 240
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Job time : 3498.4 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARNUJJI7 1492 bp mRNA linear PRI 30-JAN-2004
Homo sapiens cDNA FLJ36198 fis, clone TESTI2028242, weakly similar
to Mus musculus EPCS26 mRNA.
                                                                                                                                                           CTTACACCAGITICTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTATTGCTGAC 420
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Oligo capping; fis (full insert sequence).
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Description		Aah64743 Human sec	Abk90053 DNA encod	_	Aac69528 Human sec	Acc50642 Human sec	Abz71354 Secreted		Adc73723 Human sec	Adb63550 Human cDN	Abz36691 Human GEN	Abz36690 Human GEN	Aah64748 Human sec	Adj12678 DNA fragm	Abk90052 Human GSS	Aak92136 Human cDN	Aak93954 Human cDN	Ad130381 5' end of	Ad128563 5' end of	Ade28662 Human NOV
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The invention relates to full length GENSET human nucleic acids encoding potentially secreted proteins. The nucleic acids and the polypeptides they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GENSET gene expression. For example, they be used to treat disorders associated with decreased GENSET

Claim 7; Page 579; 921pp; English.

22 90.2 19.7 1126 12 ADI31209 24 90.2 19.7 1131 14 ADI52669 25 90.2 19.7 1148 6 ABG92578 26 90.2 19.7 1148 6 ABG92578 27 90.2 19.7 1153 2 AAX55748 28 90.2 19.7 1153 2 AAX55748 29 90.2 19.7 1153 2 AAX65748 30 90.2 19.7 1187 3 AAA26978 31 89.2 19.4 646 12 ADI23826 33 81.4 17.7 697 10 ADI28864 33 81.4 17.7 697 10 ADI28866 34 17.8 17.6 386 2 AAY87718 37 66.6 14.5 420 10 ACF57662 38 47.8 10.4 1408 8 ABX60065 39 47.8 10.4 1408 8 ABX60065 39 47.8 10.4 1408 8 ABX60065 30 47.8 10.4 1408 8 ABX60065 31 45.4 9.9 1098 6 ABS703981 32 42.8 9.3 705 5 AAS91529	Ad131209 Full leng	Ady52669 Human fet	Aax51726 DNA encod	Abq92578 Human sec	Aav55748 Human sec	Abq92074 Human pol	Aaa26978 Human cor	Adc24643 Human cDN	Aak93399 Human cDN	Ad129826 5' end of	Ade28664 Human NOV	Adm93409 Human NOV	Aav87718 EST clone	Abl92990 Rat metas	Adno7781 Human mam	Acf57862 PLAC1 int	Aal37077 Human mus	Aal37075 Human mus	Abx60063 cDNA enco	Abx60065 cDNA enco	Adj30813 Human mus	Adj30815 Human mus	Abs70398 Human bon	Aas91529 DNA encod	
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ALIGNMENTS

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Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;
                                                                                                                                                                                                                                                                                         Full length GENSET human nucleic acids encoding potentially secreted proteins, useful in gene therapy and vaccination against a variety of diseases, and for diagnosis of those diseases.
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                                                                         Human secreted protein cDNA, SEQ ID NO: 19
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                 AAH64743 standard; cDNA; 691 BP.
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06-MAR-2000; 2000US-0187470P.
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P-PSDB; AAG89140.
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                                                                                                                       Homo sapiens.
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                                                                                                    GENSET; 88.
                                   AAH64743;
     AAH64743
ID AAH6
RESULT 1
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                  genome that affect the activity of GENSET or by supplementing the patients own production of GENSET polypeptides. Conversely, antisense nucleic acid molecules may be administered to down regulate GENSET expression by binding with the cells' own genes and preventing their expression. The sense and antisense nucleic acids may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence to determine which patients may be in need of restorative therapy. The GENSET polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of GENSET polypeptide expression and activity. The present sequence is a GENSET nucleic acid of
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98.7%; Score 453; DB 5; Le
Best Local Similarity 100.0%; Pred. No. 2.5e-132;
Matches 453; Conservative 0; Mismatches 0;
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gene; ds

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The present invention relates to the isolation of human GSSP3

CC polypeptide reduces circulating blood glucose levels, increases insulin

CC polypeptide reduces body mass. The GSSP3 polypeptide and

CC polypeptide reduces body mass. The GSSP3 polypeptide and

CC compositionty, and/or reduces body mass. The GSSP3 polypeptide and

CC compositions comprising GSSP3 polypeptides are useful for controlling

CC compositions comprising GSSP3 polypeptides are useful for controlling

CC plood glucose levels, for treating metabolic-related diseases or

CC disorders (e.g. obesity, impaired glucose tolerance, insulin resistance,

CC disorders (rype I or II diabetes, diabetes related complications,

CC hyperlipidaemias, atheroselerorais, heart disease, hypertension, stroke,

CC hyperlipidaemias, atheroseleropathy, nephropathy, polycystic ovarian

CC microangiopathy, retinopathy, neuropathy, nephropathy, polycystic ovarian

CC syndrome, ocular lesions, microangiopathic lesions, or syndromes such as

CC acanthosis nigricans, leprechaunism and lipoatrophy). The polypeptides

CC are also useful to improve physical performance during work or exercise,

and to treat dyslexia, attention-deficit disorder, attention-

CC deficit hyperacentivity disorder, and psychiatric disorders such as

CC schipper and contains and c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGATACATACATATATATGAGTTTATATATCTTGTTCGTGATTGTGGCATCAGGACA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reducing circulating glucose levels or increasing insulin sensitivity, useful for reducing body mass or preventing body weight gain, comprises administering composition comprising GSSP3 polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          schizophrenia. The present sequence encodes human GSSP3 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yen-Potin F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 453; DB 6; Le
Pred. No. 3.3e-132;
                                                                                                                                       "GSSP3 polypeptide"
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100.0%; Pred. No. 5...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bour BA,
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                                                              ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salter-Cid L, Ebbets-Reed D,
                                                                                                                                                                                                                                                                                                                                                                       01-FEB-2002; 2002WO-IB001333.
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Matches 453; Conservative
                                                                                         .529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GEST ) GENSET
                        Homo sapiens.
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                                                                                                                                                            sig_peptide
                                                                                                                                                                                                        mat_peptide
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sequence at least 90% identical to CGDD,
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AC AAC6
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                                                                                                               CTTACACCAGTITCTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTATTGCTGAC 420
                                                                                                                            CTTACACCAGTTTCTACTGAGAATGAAATAAAATTGGATCCTTGTTATTGCTGAC 472
                                                                                                                                                                                                                                                                                                                               Human; 88; gene; cell growth; differentiation; death; CGDD; cancer; cell proliferative disorder; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; paroxysmal necturnal haemoglobinuria; psoriasis; polycythaemia vera; primary thrombocytopaenia; developmental disorder; renal tubular acidosis; anaemia; mental retardation; epilepsy; AIDS; neurological disorder; Alzheimer disease; Parkinson's disease; asthma; inflammatory disorder; infertility; autoimmune disorder; gout; allergy; inflammatory disorder; acquired immunodeficiency syndrome; uveitis; autoimmune thyroiditis; contact dermatitis; Crohn's disease; infection; diabetes mellitus; glomerulonephritis; irritable bowel syndrome; multiple sclerosis; osteoarthritis; osteoporosis; pancreatitis;
                                                                              Baughn MR;
Burford N;
CGGATACATACATATGTATGAGTTTATATATCTTGTTGTGGTGATTGTGGGCATCAGGACA
                     AGGGTAGTTTCTGAGGAAACTCTCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT
                                 ATAGATCATGACCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated polypeptide comprising CGDD1-12 (cell growth, differentiation and death), a naturally occurring amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human proteins associated with cell growth, differentiation death, useful for diagnosing, treating or preventing autoimmune inflammatory disorders (e.g. AIDS, allergy or anemia), cancer, atheroscierosis or hepatitis.
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TY, Lal PG, Duggan BM,
Khare R, Walia NK;
                                                                                                                                                            TITCAGACAACAGCAGAAGAGITAGGAITATTA 453
                                                                                                                                                                         Human cDNA encoding, CGDD4, INCYTE 5284076CB1.
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n UK, Khare R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ison CH, Lu Y,
                                                                                                                                                                                                                                            ABS78646 standard; cDNA; 1480
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23-FEB-2001; 2001US-0271175P.
08-MAR-2001; 2001US-0274503P.
09-MAR-2001; 2001US-0274552P.
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Richardson TW,
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P-PSDB; ABG97353.
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Xu Y, G
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Lu DAM,
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comprising a promoter sequence operably linked to the CGDD
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comprising of cGDD or alter the expression of CGDD polymucleotide, an anti-
cGD polymucleotide microarray. The polypeptides, polymucleotide and a
cGDD polymucleotide microarray. The polypeptides, polymucleotide and a
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agonists and antagonists are useful for diagnosing, treating or
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cGDD polymucleotide microarray. The polypeptides, polymucleotides,
agonists and antagonists are useful for diagnosing, treating or
cGDD polymucleotide microarray. The polypeptides, polymucleotides,
cgnowenting disorders associated with aberrant expression of CGDD,
carrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia
cycle, particularly cell proliferative (e.g. arteriosclerosis, atheroaclerosis,
cirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia
cycle, gineral tubular acidosis, anaemia or mental retardation),
contact defense (e.g. affatishment of assease, diabetes mellitus,
cycle osteoporosis, primitable bowel syndrome, multiple sclerosis,
costeoarthritis, or viral, bacterial, fungal, parasitic, procazol or helminthic
cinfections. They are also useful in the assessment of the effects of
condense of proteins associated with CGDD. The present sequence encodes
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100.0%; Pred. No. 3.4e-132;
ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1480 BP; 463 A; 244 C; 265 G; 508 T; 0 U; 0 Other;
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Best Local Similarity 100.
Matches 453, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to the isolation of genes (AAC69512-C69587)

encoding 62 human secreted proteins (AAB38321-B38396). The genes can be used to generate fusion proteins by linking to the gene for the human immunoglobulin G FC portion (AAC69503) for increasing the stability of the fusion protein as compared to the human protein only. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, proteins, and prevention of: (a) autoimmune diseases e.g. cheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms of the breast or liver; (c) cardiovascular disorders e.g. cardiac arrest; (d) cerebrovascular disorders e.g. cardiac arrest; (d) cerebrovascular disorders e.g. cerebral isolations system disorders e.g. disease; (g) infections caused by bacteria, viruses and fung; and (h) ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging cell culture of primary tissues, to regenerate tissues and in chemotaxis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCTGAGAACCTC
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Birse CE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid molecules encoding 62 human secreted proteins for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Soppet DR,
Moore PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA, S
Florence KA,
                                          Human secreted protein gene 17 clone HTELS08.
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HS, Ebner
                                                                                                                                                                                                                                                                                   06-APR-2000; 2000WO-US008979.
                                                                                                                                                                                                                                                                                                                        99US-0128693P.
                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-647418/62.
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26-APR-1999;
     31-JAN-2001
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The present invention relates to novel human secreted proteins (ABR47633-ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins and their coding sequences are useful for the preparation of a diagnostic or pharmaceutical composition for diagnosing or treating a cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest coronary arrestosclerosis and myocardial ischaemia), neural disorders, immune arteriosclerosis and myocardial ischaemia), neural disorders, immune system disorders, pulmonary disorders, renal disorders, for proliferative disorders and/or cancerous diseases and conditions, for wound healing and epithelial cell proliferation, to treat inflammation or infection, for treating thrombosis and arteriosclerosis, for treating or preventing neural damage which occurs in neuronal disorders or neurodegenerative conditions such as Alzheimer's disease and Parkinson's disease, to enhance bone and periodontal regeneration and aid in tissue transplants or bone grafts, to prevent skin aging or hair loss, to
                                                                                                                                                                           360
AGGGTAGTTTCTGAGGAAACTCTCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT 300
                                             255 AGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT 314
                                                                                                                                                                                                                                                             374
                                                                                                                                                                                                                                                                                                                                                       CTTACACCAGTTTCTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTATTGCTGAC 420
                                                                                                                                                                                                                                                                                                                                                                                                         Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic; vulnerary; antiinflammatory; nootropic; neuroprotective; antianflammatory; human; cardiovascular disorder; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              secreted proteins, useful for detecting, preventing, prognosticating, treating and/or ameliorating cardiovascular
                                                                                                                                                                           301 ATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGG
                                                                                                                                                                                                                                                             315 ATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTCAGACAACAGCAGAAGAGTTAGGATTATTA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTCAGACAACAGCAGAAGAGTTAGGATTATTA 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACC50642 standard; cDNA; 1898 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders such as arrhythmia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-MAR-2002; 2002WO-US009785.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-NOV-2001; 2001US-0331287P
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CATGTGAAAATAAGTTGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAA 120
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                                                                                                                                                                                                                                                                                                             74
stimulate growth and differentiation of haematopoietic cells and bone marrow cells when used in combination with other cytokines, to maintain organs before transplantation or for supporting cell culture of primary tissues, to increase or decrease differentiation or proliferation of embryonic stem cells, or to modulate mammalian characteristics or metabolism. Note: The sequence data for this patent was published in electronic format and is available from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; digestive disorder; gastrointestinal disorder; mouth; oesophagus; stomach; small intestine; large intestine; liver; billary tract; pancreas; cancer; tumour; hyperproliferative disorder; immune disorder; inflammation; mound healing; drug screening; chromosome identification; chromosome mapping; cytostatic; antiinflammatory; immunosuppressive; vulnerary; gene therapy; gene; ss.
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                                                                                                                                                                                                      Length 1898;
                                                                                                                                                                Sequence 1898 BP; 595 A; 315 C; 332 G; 654 T; 0 U; 2 Other;
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                                                                                                                                                                                                 Score 453; DB 8; Le
Pred. No. 3.8e-132;
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                                                                                                                                                                                                                                    Matches 453; Conservative
                                                                                                                                                                                                                   Local Similarity
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AB271190-AB271478 represent cDNAs corresponding to 178 human secreted brotein genes, and ABP00011-ABP00299 represent the proteins they encode. CC protein genes, and ABP00011-ABP00299 represent the proteins they encode. AB271479-AB2714540 represent human secreted protein genomic fragments. The invention also encompasses antibodies specific for the secreted proteins, ct. the use of the secreted proteins and recombinant controls and lost cells comprising a nucleic acid of the invention. The secreted proteins, nucleic acids encoding them, antibodies or antibody fragments specific for the secreted proteins, and modulators of protein activity are useful for diagnosing, treating, ameliorating or preventing digestive disorders. Such conditions include disorders of the mouth, costophagus, stomach, small intestine, large intestine, liver, biliary tract and panoreas, and include cancers of these organs and tissues. The secreted proteins and their nucleic acids may also be used in the treatment of immune disorders, inflammation, inflection, chromosome of the invention may be used for chromosome identification, chromosome contents of the invention may be used for chromosome identification, chromosome biological samples, as hybridisation probes, and as molecular weight markers. The present sequence represents a human secreted protein-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240
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                                                                                                                                                                                                                             New human secreted proteins and nucleic acids, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating e.g. gastrointestinal diseases and disorders, or cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1898 BP; 595 A; 315 C; 332 G; 654 T; 0 U; 2 Other;
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                                                                                                                                                                                                                                                                                                            Claim 21; Page 853-854; 1216pp; English.
21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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                                                                                   (HUMA-) HUMAN GENOME
                                                                                                                            Ruben SM;
                                                                                                                                                                   WPI; 2003-029900/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                        P-PSDB; ABR00175.
                                                                                                                            Rosen CA,
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antianaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid; antidiabetic; immunosuppressive; dermatological; nephrotropic; antibacterial; virucide; fundicoide; antiparthisonian; neuroprotective; nootropic; antibacterial; virucide; fundicoide; antiparaetic; antiarteriosclerotic; vulnerary; cytostatic; haempooietic; haematologic; anaemia; autoimmune disorder; rheumatoid arthritis; inflammation; Grave's disease; diabetes; systemic lupus erythematosus; glomerulonephritis; neurodegenerative; Parkinson's, Alzheimer's; wound; hyperproliferative; atherosclerosis; cancer; haeterial; viral; fungal; parasitic infection; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human secreted polypeptide for diagnosing, preventing or treating hematopoietic or hematologic disorders (e.g. anemia), autoimmune disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or
                                                                                                       The invention relates to a novel human secreted polypeptide comprising defined sequence given in the specification. The polypeptide, nucleic acid molecule, antibody, agonist or antagonist of the invention may be useful for preparing a composition for diagnosing or treating a
                                                                                                                                                                                                                                                                                                                                                                   ATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGG
                                                                                                                                                                                 AGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein-related DNA - SEQ ID 356.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; SEQ ID NO 356; 2272pp; English.
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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P-PSDB; ADC74338.
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ADB91843. Also disclosed is a recombinant vector comprising a
DB91843. Also disclosed is a recombinant vector comprising of
the invention and a recombinant host cell comprising
colynucleotide of the invention, and a recombinant host cell comprising
the recombinant vector. The polypeptide of the invention is useful in
dentifying a binding partner by contacting the polypeptide with a
chinding partner, and determining whether the binding partner increases or
decreases activity of the polypeptide. The polypeptide, polynucleotide,
antibody or its fragment, agonist or antagonist are useful for preparing
a pharmaceutical composition for diagnosing or treating diabetes or
conditions related to diabetes. The present sequence is that of the human
immunoglobulin Fc portion used to generate fusion proteins, increasing
the stability of the fused protein as compared to the secreted protein
only. Note: The sequence data for this patent did not form part of the
printed specification, but was obtained in electronic format directly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid encoding a human secreted protein is useful in diagnosing or treating diabetes or conditions related to diabetes.
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435 TTTCAGACAACAGCAGAAGAGTTAGGATTATTA 467
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                                                                                                                                                                                                                  ADB91291 standard; cDNA; 1898
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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Matches 453;
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haemopoletic or haematologic disorder such as anaemia, autoimmune disorders such as rheumatoid arthritis, inflammation, Grave's disease, diabetes, systemic lupus erythematosus or glomerulonephritis, neurodegenerative disorders including Parkinson's disease and Alzheimer's disease, wounds and hyperproliferative disorders including and Alzheimer's atherosclerosis or cancer, as well as bacterial, viral, fungal or parasitic infections. The polypeptide may also be used during gene therapy procedures and for identifying a binding partner by contacting the polypeptide with a binding partner and determining whether the binding partner increases or decreases the activity of the polypeptide. The current sequence is that of the human secreted protein-related DNA of
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                                                                                                                                                                                                            Gaps
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0
                                                                                                                                                                                 98.7%; Score 453; DB 10; Length 1898; 100.0%; Pred. No. 3.8e-132; ive 0; Mismatches 0; Indels 0
                                                                                                                                                           Sequence 1898 BP; 595 A; 315 C; 332 G; 654 T; 0 U; 2 Other;
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/product= "Clone TEST120282420 protein"
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                                                                                                                                                                                              Best Local Similarity 100.
Matches 453; Conservative
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The Inventor.

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Con its partial peptide, an antibody binding to the polymentle or peptide or the polymentation of the encoded protein, and observing the binding to between the two, a transformant carrying the polymentation of the encoded protein, and observing the binding to between the two, a transformant carrying the polymentation as a propertion of substitution of the intense polymentation. The oligomentation as a primer for synthesising the polymelectide, or as a probe to substitute of proteins are useful as pharmaceutical agents and many disease-related proteins are useful as pharmaceutical agents and many disease-related proteins are useful as plantamaceutical agents and activity, or as targets of genes may be included in their expression and activity, or as targets of genes may be included in their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell cregeneration. Membrane proteins, signal transduction-related proteins, cregeneration. Membrane proteins, signal transduction-related proteins are encoding them can be used as indicators for diseases (e.g. osteoporosis, encoding them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours. The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The contrivity or expression of the invention. Note: Some of the sequence contrivity or expression of the invention. Note: Some of the sequence contribution such represented in the printed specification, but is based on sequence information supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                              Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATGTGAAAATAAGTTGCTCTCTGGATGGATGGTCGCTCAGTTATCCCAGTTGCAGAA 171
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Pred. No. 1.1e-131;
0; Mismatches 1; Indels 0;
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                                                                                                                                                                                                                                                    (HELI-) HELIX RES INST.
(REAS-) RES ASSOC BIOTECHNOLOGY.
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28-MAR-2002; 2002EP-00007401.
                                                                                                    05-NOV-2001; 2001JP-00379298.
25-JAN-2002; 2002US-00350978.
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Matches 452; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         ., Sugiyama T,
J, Isono Y, E
Yoshikawa T, C
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The present invention relates to novel GENSET polynucleotides (ABZ36404-ABZ36911) encoding polypeptides (ABP75963-ABP76368). The polynucleotides and polypeptides are useful in screening and diagnostic assays for abnormal GENSET expression and/or biological activity. They are also useful for screening of compounds for treating or preventing GENSET-related disorders, such as heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuronuscular, central nervous system (CNS), cardiovascular or gastrointestinal effects of the toxicity. The polynucleotides are useful for constructing or expanding chromosome maps
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                    ATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGGG
                                                                 CTTACACCAGTTTCTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTATTGCTGAC
                                                                                                 CTTACACCAGTTTCTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTATTGCTGAC
                                                                                                                                                                                                                                                                                                                                                                                Cytostatic; antiinflammatory; nootropic; neuroprotective; cardiant; gastrointestinal; gene therapy; GENSET; heavy metal toxicity; cancer; inflammatory disease; immune disorder; neuromuscular; toxicity; central nervous system; cardiovascular; gastrointestinal; gene; ss.
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Pred. No. 3.5e-130;
                                                                                                                                    TTTCAGACAACAGCAGAAGAGTTAGGATTATTA 453
                                                                                                                                                               TITCAGACAACAGCAGAAGAGTIAGGATTATTA 504
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                   BP
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                                                                                                                                                                                                                                                   ABZ36691 standard; cDNA; 497
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                                                                        AGCAGAAATCTGTATATATATTTGCGGATGAATTACATCTGGGAATGGGCTGCCCTGCAAAT
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                                                     AGCAGAAATCTGTATATTTTGCGGATGAATTACATCTGGGAATGGGCTGCCCTGCAAAT
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                                                                                                                                                                      <u>AGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT</u>
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                                                                                                                                                                                                                                       ATAGATCATGACCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGG
                                                                                                                                                                                                                                                                                                                                                 CTTACACCAGTITCTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTATTGCTGAC
                                                                                                          1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCTGAGAACCTC
                                                                                                                                                                  CATGTGAAAATAAGTTGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAA
                                                                                                                                                                                                                                                                     AGGGTAGTTTCTGAGGAAACTCTTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT
                                                                                                                                                                                                                                                                                       312 AGGGTAGTTTCTGAGGAAACTCTCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT
                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                     DB 8; Length 500;
                                                Sequence 500 BP; 129 A; 100 C; 113 G; 155 T; 0 U; 3 Other;
                                                                                        Indels
                                                                   Query Match 93.5%; Score 429; DB 8; Le Best Local Similarity 100.0%; Pred. No. 8.2e-125; Matches 429; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jobert S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein cDNA, SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH64748 standard; cDNA; 470 BP
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                                                                                                                                                                                                                                                                                                                                                                                                  TTTCAGACA 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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potentially secreted proteins. The nucleic acids and the polypeptides of they encode may be used in the prevention, treatment and disgnosis of diseases associated with inappropriate GENSET gene expression. For example, they be used to treat disorders associated with decreased GENSET gene expression by rectifying mutations or deletions in a patient's genome that affect the activity of GENSET or by supplementing the patients own production of GENSET polypeptides. Conversely, antisense nucleic acid molecules may be administered to down regulate GENSET expression by binding with the cells' own genes and preventing their expression. The sense and antisense nucleic acids may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence to determine which patients may be in need of restorative therapy. The GENSET polypeptides and be used as antigens in the production of antibodies and in assays to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   identify modulators (agonists and antagonists) of GENSET polypeptide expression and activity. The present sequence is a GENSET nucleic acid of the invention
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                                                                                                                                                                                                                                                                                    The invention relates to full length GENSET human nucleic acids encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Full length GENSET human nucleic acids encoding potentially secreted proteins, useful in gene therapy and vaccination against a variety of diseases, and for diagnosis of those diseases.
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Best Local Similarity 100.0%; Pred. No. 5.1e-67;
Matches 246; Conservative 0; Mismatches 0;
                                                                                                                                                                                                  Claim 7; Page 583; 921pp; English.
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This invention relates to novel polynucleotides encoding human secreted proteins. Specifically, it refers to the vectors, host cells, recombinant and synthetic methods for producing human polynucleotides, polypeptides and antibodies. Furthermore, it relates to screening methods to identify agonists and antagonists that can be used to inhibit or enhance the production of the secreted proteins. The present invention describes these compositions as useful for diagnosing, treating or production and function of the secreted proteins. The present invention describes these compositions as useful for diagnosing, treating or preventing disorders such as cancer, haematopoletic diseases including prostatitis and inguinal hermia, musculoskeletal diseases including systemic lupus erythematosus and goutt, cardiovascular disease including systemic lupus erythematosus and goutt, cardiovascular disease including arrhythmia and hypernatraemia, mixed fetal diseases including fetal arrhythmia and hypernatraemia, mixed fetal diseases including curinary incontinence and renal disorders, neural or sensory disease including and papersent and socupational lung disease, and docrine diseases including contal hypertension and irritable bowel syndrome and connective tissue or including diseases including scleroderma and epidermolysis bullosa. As such, there are various activites such as cytostatic, antianemic, antianemic, antiathmatic, antiathmatica
irritable bowel syndrome, epithelial disease, scleroderma; epidermolysts bullosa; cytostatic, antiament; antiartritic; antiathratic; antiathmatic; anti-HIV; immunosuppressive; antiathmatic; anti-HIV; immunosuppressive; antiinflammatory; antipsociatic; antibacterial; osteopathic; dermatological; antigout; immunomodulator; antiatrhythmic; cardiant; nocepopic; notabathic; neuroprotective; antiparkinsonian; tranquilizer; antidiabetic; anabolic; hypertensive; vulnerary; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acids and polypeptides, useful for diagnosing, treating, preventing or ameliorating diseases or disorders e.g. cancer, anemia, arthritis, asthma, inflammatory bowel disease or Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Greene JM;
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Yu G, Florence C,
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98WO-US021142.
99US-00288143.
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97US-0061527P.
97US-0061529P.
97US-0061532P.
97US-0061536P.
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Ferrie AM,
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DUAN R D.
RUBEN S M.
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FLORENCE C.
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OLSEN H.
                                                                                                                                                                                                              US2004010132-A1.
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                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-2000;
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08-APR-1999;
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(GREE/)
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(FLOR/)
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(OLSE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AGAAATCTGTATATATTTGCGGATGAATTACATCTGGGAATGGGCTGCCCTGCAAATCGG 120
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                                                                   hypertensive and
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dermatological, antigout, immunomodulator, antiarrhythmic, cardiant, nootropic, antilipemic, nephrotropic, uropathic, neuroprotective, antiparkinsonian, tranquilizer, antidiabetic, anabolic, hypertensive an vulnerary. This polynucleotide is a DNA fragment of a BAC clone that encodes a human secreted protein of the invention. NOTE: This sequence does not appear in the printed specification but has been obtained in electronic format from the US patent office at the following web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 AGAAATCTGTATATATTTGCGGATGAATTACATCTGGGAATGGGCTGCCCTGCAAATCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bour BA, Chicca J, Yen-Potin F;
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                                                                                                                                                                                                                                              www.segdata.uspto.gov/sequence.html; Document ID: 20040010132
                                                                                                                                                                                                                                                                                                                                                                                  Length 5013;
                                                                                                                                                                                                                                                                                                                  Sequence 5013 BP; 1442 A; 909 C; 826 G; 1836 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                  Score 183; DB 12;
Pred. No. 1.1e-46;
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                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Pred. ....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human GSSP3 genomic sequence.
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                                                                                                                                                                                                                                                                                                                                                                                             39.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 183; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTA 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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polypeptide, and polynuclectide sequences that encode it. The GSSP3
polypeptide reduces circulating blood glucose levels, increases insulin
sensitivity, and/or reduces body mass. The GSSP3 polypeptide and
polynucleotide sequences are useful in serum glucose regulation, fatty
acid metabolism, body weight loss, and prevention of body weight gain.
Compositions comprising GSSP3 polypeptides are useful for controlling
blood glucose levels, for treating metabolic-related diseases or
disorders (e.g. obesity, impaired glucose tolerance, insulin resistance,
blood glucose levels, for treating metabolic-related diseases or
disorders (e.g. obesity, impaired glucose tolerance, insulin resistance,
byperlipidaemias, atherosclerosis, heart disease, hypertension, stroke,
syndrome C, type I or II diabetes, diabetes related complications,
microangiopathy, neuropathy, neuropathy, nephropathy, polycystic ovarian
syndrome, ocular lesions, microangiopathic lesions, or syndromes such as
canthosts nigricans, leprechaunism and lipoatrophy). The polypeptides
are also useful to improve physical performance during work or exercise,
and to treat dyslexia, attention-deficit disorder, attention-
deficit/hyperactivity disorder, and psychiatric disorders such as
controlling and proceed thuman GSSP3 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5564 ATACATACATATGTATATGAGTTTATATATATCTTGTTCGTGATTGTGGCATCAGGACAAGG 5623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 GTGAAAATAAGTTGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10115 BP; 2860 A; 1941 C; 1815 G; 3475 T; 0 U; 24 Other;
                                                                           The present invention relates to the isolation of human GSSP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.9%; Score 183; DB 6; Length 10115; 100.0%; Pred. No. 1.5e-46; tive 0; Mismatches 0; Indels 0
                            Disclosure; Page 90-95; 97pp; English
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Matches 183; Conservative
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Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
su A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
                                                                                     Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
                                                                  Human cDNA 5'-end sequence, SEQ ID NO: 596.
AAK92136 standard; cDNA; 784 BP.
                                                                                                                                                                                                   08-JUL-1999; 99JP-00194486.
11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
                                                                                                                                                                              07-JUL-2000; 2000EP-00114089
                                          06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                (HELI-) HELIX RES INST.
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Wakamatsu A,
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9, 2006, 14:08:21

Search completed: May Job time: 592.3 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in invention leaders to primers for synthesising full length count of and and molecules encoding a human protein have been isolated been determined. Primers for synthesising the full length cDNA are useful for clarifying the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a cDNA provided in the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EDO
                                                                                                                                                           830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307 rággacrgargárccrccrccccrcrcccrrrrcagccggrrcaggagaagrccaarga 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367 crefecrerectatade crestrander carestadas de contra de carectadas de como d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to primers for synthesising full length cDNA
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19.7%; Score 90.2; DB 4; Length 784;
Best Local Similarity 57.7%; Pred. No. 1e-17;
Matches 161; Conservative 0; Mismatches 118; Indels C
                                                                                                                                                                                                                                                                                                                                               Claim 2; SEQ ID NO 596; 1380pp + Sequence Listing; English.
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                                                     WPI; 2001-524255/58.
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15, Appl 12739, A 13946, A 1, Appli 13185, A

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Sequence 13187, A
Sequence 13188, A
Sequence 58232, A
Sequence 74501, A
Sequence 135101,
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        Sequence
Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 43. Application US/09621976
Sequence 43. Application US/09621976
Patent No. 663963
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano. J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENERT.054RE.
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 43
US-09-949-016-11808
US-09-949-016-1338
US-09-949-016-73372
US-09-949-016-12661
US-09-949-016-12661
US-09-949-016-1388
US-09-949-016-1388
US-09-949-016-1388
US-09-949-016-1388
US-09-949-016-1338
US-09-949-016-13185
US-09-949-016-13185
US-09-949-016-13188
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100.0%; Score 459; DB 3; I
Best Local Similarity 100.0%; Pred. No. 1.5e-134;
Matches 459; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 53..511
NAME/KEY: sig_peptide
LOCATION: 53..103
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 10.6999998092651
OTHER INFORMATION: seq VLMLLAVLIWTGA/EN
                                                      44342
174029
174030
133559
263693
9870
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51043
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     636591
636591
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ORGANISM: Homo sapiens
     4444446661111111111111
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Sequence 1362, Ap
Sequence 1704, Ap
Sequence 2587, Ap
Sequence 1363, Ap
Sequence 5361, Ap
Sequence 55, Appl
Sequence 55, Appl
Sequence 17315, A
Sequence 17315, A
Sequence 17859, A
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Pred. No. 5.7e-132;
0; Mismatches 1;
                                                                                                                                                                                                         Sequence 1704, Application US/10104047
Patent No. 6943241
GENERAL INFORMATION:
TITLE OF INVENTION: No. 6943241e1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT PAPLICATION NUMBER: 2002-03-25
FRIOR FILING DATE: 2002-03-25
FRIOR FILING DATE:
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Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
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Best Local Similarity 99.8%;
Matches 452; Conservative (
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1704
LENGTH: 1492
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                                                                                                                                                      CTTACACCAGTTTCTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTATTGCTGAC 420
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                          293 AGGGTAGTTTCTGAGGAAACTCTCCTTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT
                                                                                              CTTACACCAGTTTCTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTATTGCTGAC
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98.7%; Score 453; DB 3; Length 642;
Best Local Similarity 100.0%; Pred. No. 1.3e-132;
Matches 453; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glocato, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 1852
LENGTH: 642
                                                                                                                                                                                                                                 TITCAGACAACAGCAGAAGAGTTAGGATTATTAATCTTC 459
                                                                                                                                                                                                                                                       473 TTTCAGACAACAGCAGAAAGAGTTAGGATTATTAATCTTC 511
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NAME/KEY: CDS

LOCATION: 53..156

LOCATION: 53..103

COTHER INFORMATION: VON Heijne matrix

OTHER INFORMATION: score 10.699998092651

CUTHER INFORMATION: seq VLMLLAVLIWTGA/EN

US-09-621-976-1362
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Sequence 1362, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
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                                                                                             Score 272; DB 3; Length 372; Pred. No. 1.1e-75;
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100.0%; Pred. No. 1.9e-67;
ive 0; Mismatches 0; Indels
                                                                                                                                  1; Indels
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APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
SUPPRING SEQ ID NOS: 19335
                                                                                                                                1; Mismatches
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OTHER INFORMATION: SCORE 10.6999998092651
OTHER INFORMATION: SEQ VLMLLAVLIWIGA/EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-621-976-1363

. Sequence 1363, Application US/09621976

. Patent No. 6639063

. GENERAL INFORMATION:
                                          COL
                                                                                             59.3%;
; NAME/KEY: misc_feature
; LOCATION: 351
; OTHER INFORMATION: n=a, g,
US-09-621-976-15700
                                                                                        Query Match
Best Local Similarity 98.7
Matches 294; Conservative
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Best Local Similarity 100.
Matches 246; Conservative
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ORGANISM: Homo sapiens
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LOCATION: 137..454
NAME/KEY: sig_peptide
LOCATION: 137..187
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                                                                                                                                                                                                                                                                                                              74.4%; Score 341.6; DB 3; Length 560; 93.1%; Pred. No. 1.5e-97;
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Fatent No. 6639063
GENERAL INFORMATION:
APPLICANT: Unas Milne Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OF INFORMATION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 15700
LENGTH: 372
         APPLICANT: Glordano, J.Y.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2587
                                                                                                                                                                                                                                                                                                                                ; Pred. No. 1.5e-97; 10; Mismatches 9
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 93.1%
Matches 434; Conservative
                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: 372..539
US-09-621-976-2587
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US-09-621-976-15700
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93989 ATGTGTGTGTACACTTTCATGAACTACACTTGGGCCTGGGTTGCCCCCCAAACCATGTTC 94048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCTGTATATATTTGCGGATGAATTACATCTGGGAATGGGCTGCCCTGCAAATCGGATAC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 ATACATATGTATATGAGTTTATATATATCTTGTTGTTGTGCCATCAGGACAAGGGTAG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 AAATAAGTTGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAAGCAGAA 127
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                                                                                                                                                                                                                                                                                       Score 90.2; DB 3; Length 9
Pred. No. 2.3e-17;
0; Mismatches 118; Indels
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OTHER INFORMATION: Incyte ID No. 6426186 200512.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jones, Karen A.
APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REPERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-100-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) NAME/KEY: unsure
; LOCATION: 927, 961, 987, 1048
; OTHER INNORWATION: a, t, c, g, or other
US-09-484-970B-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 55, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                          19.7%;
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 57.7<sup>3</sup>
Matches 161; Conservative
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SOFTWARE: PERL Program
SEQ ID NO 55
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                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17103
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US-09-484-970B-55
                                                                                                                                                                     LENGTH: 96690
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                                                                                                                                                                                                                                                                      Sequence 5361, Application US/09949016
; Sequence 5361, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REPERENCE: CLOO1307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SEQ ID NO 5361
; LEASE SEC OF Windows Version 4.0
; SEQ ID NO 5361
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Batent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: 05/04/14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
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                                                                       317 CGGATACATACATATGTATATGAGTTTATATATCTTGTTCGTGATTGTGGCATCAGGACA 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATACATATGTATATGAGTTTATATATCTTGTTCGTGATTGTGGCATCAGGACAAGGGTAG 247
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                                                                                                                         241 AGGGTA 246
                                                                                                                                                                   377 AGGGTA 382
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; ORGANISM: Human
US-09-949-016-5361
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POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28316 AATATGTATGTTTTTTAATTGTAAGGATATCTTTTATAAGTCTACCATGCAAACTCAATA 28375
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                                                                                                                                                                                                                                              Score 36.6; DB 3; Length 1125;
Pred. No. 0.26;
0; Mismatches 79; Indels 0
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61.3%; Pred. No. 3.3;
tive 0; Mismatches
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TITLE OF INVENTION: WITH HUMAN DISEASE, MET
FILE REPERENCE: CLOO1307
CURRENT PILIOS DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR PELICATION NUMBER: 60/231,758
PRIOR PELICATION NUMBER: 60/231,768
PRIOR PELICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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SOFTWARE: FastSEQ for Windows Version 4.0
                             60/096,409
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Patent No. 6812339
GENERAL INFORMATION:
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il Similarity 51.5%;
84; Conservative
  PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 7831
                                                                                                                                                  TYPE: DNA ORGANISM: Candida albicans
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Best Local Similarity 61.3
Matches 57; Conservative
                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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US-09-949-016-15859
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APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPBUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
PRIOR APPLICATION NUMBER: US 60/074,725
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 05/241,755
FRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 17315
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                                                                                                                                                                        234 CAGGACAAGGTAGTITCTGAGGAAACTCTCTTTTTCAAACCGAGCTGTACTTTACCCC 293
339 CTGTGCTGTCCATAGACTGGTTCATGGTCACAGTGCACCCTTCATGCTAAA-CAACG 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294 AAGGAATATAGATCATG--ACCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAA 351
                                               ATCTGTATATTTGCGGATGAATTACATCTGGGAATGGGCTGCCCTGCAAATCGGATAC
                                                                                           398 Argricroracacrrrcardacr---acarredecredecrececaaaccarerre
                                                                                                                                          188 ATACATATGTATATGAGTTTATATATCTTGTTGTGATTGTGGCATCAGGACAAGGGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58068 ricraritaraararararararararararararaaaaraaagracccrrrrarggcar
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                                                                                                                                                                                                                                      248 TTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACT 286
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Patent No. 6812339
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Best Local Similarity
Matches 102; Conserv
                                                                                                                                                                                                                                                                                                                                                                               US-09-949-016-17315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Human
US-09-949-016-17315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              343 TCTAGGAAATCAGTGTGGCTTACACCAGTTTCTACTGAGAATGAAATAAAATTGGATCCT
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| Sequence 2, Application US/08484565
| Sequence 2, Application US/08484565
| Patent No. 5763569
| GENERAL INFORMATION:
| APPLICANT: Edward M. Brown APPLICANT: James E. Garrett, Jr. |
| APPLICANT: James E. Garrett, Jr. |
| TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE |
| TITLE OF INVENTION: MOLECULES |
| NUMBER OF SEQUENCES: 20 |
| CORRESPONDENCE ADDRESSE: Lyon & Lyon & Lyon & Lyon & Lyon & STREET: First Interstate World Center |
| STREET: Glite 4700 |
| STREET: Glite 4700 |
| STREET: Glite 4700 |
| STREET: Glite Angeles |
| CITY: Los Angeles |
| STATE: California |
| CALLINGS |
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                                                        FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/09,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/834,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,64
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 13 August, 1991
ATTORNEY AGENT INFORMATION:
NAME: Heber, Sheldon O.
BEGISTRATION NUMBER: 0.3,13,005
                       PCT/US/94/12117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA to mRNA
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Best Local Similarity 52.0.
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 5006 base pair
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COTHER INFORMATION:
US-08-485-588-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 GAAAATAAGTIGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAAAGCAG 125
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: described below: 9
08/353,784
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Steven C. Hebert
APPLICANT: Forrest H. Fuller
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR PRIOR APPLICATION NUMBER: 60/241,755
FRIOR FILING DATE: 2000-10-20
FRIOR APPLICATION NUMBER: 60/237,768
FRIOR APPLICATION NUMBER: 60/237,768
FRIOR APPLICATION NUMBER: 60/231,498
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 15675
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First Interstate World Center
Suite 4700
633 West Fifth Street
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,588
FILING DATE: 7 June, 1995
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LOCATION: (1)...(49848)
OTHER INFORMATION: n = A,T,C or G
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-949-016-15675
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Pred. No. 1.8;
0; Mismatches 72; Indels 0; Gaps
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage COMPUTER: 1 EM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: FASTSEQ CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: TUNG DATE: 7 June, 1995

CLASSIFICATION DATA: 1995

RIGH APPLICATION DATA: 1995

RICH APPLICATION DATA: 1994

APPLICATION NUMBER: 08/353,784

FILING DATE: 9 December, 1994

APPLICATION NUMBER: 08/353,784

RILING DATE: 21 October, 1994

APPLICATION NUMBER: U.S. 08/292,827

FILING DATE: 22 August, 1994

APPLICATION NUMBER: U.S. 08/09,389

FILING DATE: 23 February, 1993

APPLICATION NUMBER: U.S. 08/09,389

FILING DATE: 21 PEDRUARY, 1993

APPLICATION NUMBER: U.S. 08/017,127

FILING DATE: 21 PEDRUARY, 1993

APPLICATION NUMBER: U.S. 07/834,161

FILING DATE: 12 February, 1993

APPLICATION NUMBER: U.S. 07/834,161

FILING DATE: 11 FEBRUARY, 1992

APPLICATION NUMBER: U.S. 07/834,161

FILING DATE: 11 FEBRUARY, 1993

APPLICATION NUMBER: U.S. 07/834,161

FILING DATE: 11 FEBRUARY, 1992

APPLICATION NUMBER: U.S. 07/834,161

FILING DATE: 11 FEBRUARY, 1993

APPLICATION NUMBER: U.S. 07/834,161

FILING DATE: 11 FEBRUARY, 1993

APPLICATION NUMBER: U.S. 07/834,161

FILING DATE: 23 August, 1991

ATTORNEY/AGENT INFORMATION: NAME: Hober Ghar Ober Charlen Charl
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REGISTRATION NUMBER: 38,179
REPERENCE/DOCKET VUMBER: 213/006
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
TELERAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGRYH: 5006 base pairs
TYPE: nucleic acid
STRANDENNES: single
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MOLECULE TYPE: CDNA to mRNA
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Search completed: May 9, 2006, 13:15:29 Job time : 150.7 secs

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| Cgn2_6/ptodata1/pubpna/USO9B_PUBCOMB.seq:*
| Cgn2_6/ptodata1/pubpna/USO9B_PUBCOMB.seq:*
| Cgn2_6/ptodata1/pubpna/USIO8_PUBCOMB.seq:*
| Cgn2_6/ptodata1/pubpna/USIOB_PUBCOMB.seq:*
             GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-10-98-512-27

US-10-104-047-1704

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US-09-876-997-19
US-10-643-836-19
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Listing first 45 summaries
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RESULT 1
US-09-731-872-19
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i Sequence 19, Application US/09731872

i Patent No. US20020102604A1

i GENERAL INFORMATION:
i APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Bougueleret, Lydie
i APPLICANT: Jobert, Severin
i TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
i FILE REFERENCE: 2 US/09/731,872

CURRENT APPLICATION NUMBER: US/09/731,872

CURRENT APPLICATION NUMBER: US 60/169,629

PRIOR APPLICATION NUMBER: US 60/187,470

PRIOR PILING DATE: 1999-12-08

PRIOR PILING DATE: 2000-03-06

NUMBER OF SEQ ID NOS: 482

SOFTWARE: Patent.pm

TENGRET PATENT ON US : 482

SEQ ID NO 19

TENGRET PATENT ON US : 482
  Sequence 3440, Ap Sequence 3442, Ap Sequence 3440, Ap Sequence 3421, Ap Sequence 12039, A Sequence 46080, A Sequence 46081, A Sequence 47775, A Sequence 61, Appl Sequence 61, Appl
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Sequence 3678, Ap
Sequence 276453,
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US-09-764-877-3440
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US-10-242-515-3440
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US-10-081-818-61
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LOCATION: 42..515
NAME/KEY: sig_peptide
LOCATION: 42..92
CTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 10.7019149919754
US-09-731-872-19
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ORGANISM: Homo sapiens
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APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Bougueleret, Lydie
APPLICANT: Jobert, Severin
TITLE OF INVANTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFRENCE: 78.US3.REC
CURRENT APPLICATION NUMBER: US/10/643,836
CURRENT APPLICATION NUMBER: US/09/731,872
PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR APPLICATION NUMBER: US 60/187,470
SPIOR APPLICATION NUMBER: US 60/187,470
PRIOR PILING DATE: 2000-03-06
SOFTWARE: PATENT PATENT
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                                                                                                                                                                                282 AGGGTAGTTTCTGAGGAAACTCTCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT 341
                                                                                                                                                                                                                                                                                                            342 ATAGATCATGACCTTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGG 401
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                                          CGGATACATACATATGTATATATGAGTTTATATATGTTCTTGTTCGTGATTGTGGCATCAGGACA
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CGGATACATACATATGTATGAGTTTTATATATCTTGTTCGTGATTGTGGCATCAGGACA
                                                                                                                     AGGGTAGTTTCTGAGGAAACTCTCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: SCORE 10.7019149919754
OTHER INFORMATION: SEG VLMLLAVLIWTGA/EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-643-836-19; Sequence 19, Application US/10643836; Publication No. US20050096458A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: sig_peptide
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LOCATION: 42..515
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Sequence 19, Application US/09876997
Sequence 19, Application US/09876997
Sequence 19, Application US/09876997
Sequence 19, Application No. US20030152921A1
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
APPLICANT: Bobert, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78 US4. CIP
CURRENT APPLICATION NUMBER: US/09/876,997
CURRENT PILING DATE: 2000-10-07
FRIOR FILING DATE: 2000-12-07
FRIOR PAPLICATION NUMBER: US 60/187,470
FRIOR APPLICATION NUMBER: US 60/187,470
FRIOR APPLICATION NUMBER: US 60/169,629
FRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 482
SOFTWARE: Patent.pm
SEQ ID NO 19
LENGTH: 691
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                                                                                              222 CGGATACATACATATGTATATGAGTTTATATATCTTGTTGGTGATTGTGGCATCAGGACA 281
                                                                                                                                                                                       241 AGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT 300
                                                                                                                                                                                                                           282 AGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT 341
                                                                                                                                                                                                                                                                                                                   ATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGG 360
                                                                                                                                                                                                                                                                                                                                                       342 ATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGG 401
                                                                                                                                                                                                                                                                                                                                                                                                                                               361 CTTACACCAGTTTCTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTATTGCTGAC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTACACCAGTTTCTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTATTGCTGAC 461
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162 AGCAGAAATCTGTATATATTTGCGGATGAATTACATCTGGGAATGGGCTGCCCTGCAAAT 221
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NAME/KEY: CDS
LOCATION: 42..515
NAME/KEY: sig_peptide
LOCATION: 42..92
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 10.7019149919754
OTHER INFORMATION: seq VLMLLAVLIWTGA/EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
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APPLICANT: YUE, Henry; YAO, Monique G.
APPLICANT: YUE, Henry; YAO, Monique G.
APPLICANT: BON, Craig H.; LU, Yan
APPLICANT: WARREN, Bridget A.; ELLIOTT, Vicki S.
APPLICANT: WARREN, Mariah R.; DING, Li
APPLICANT: TANG, Tom Y.; LAL, Preeti G.
APPLICANT: TANG, Tom Y.; LAL, Preeti G.
APPLICANT: LU, Dyung Aina M.; RICHARDSON, Thomas W.
APPLICANT: LU, Dyung Aina M.; RICHARDSON, Thomas W.
APPLICANT: TRAN, Uyen K.; KHARE, Reena
APPLICANT: CHAWLA, Narinder K.
TITLE OF INVENTION: ROCIEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
                                                                                           412
                                                                                                                                             420
       293 AGGGTAGTTTCTGAGGAAACTCTCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT 352
                                                                                                                                                                                     CTTACACCAGTTTCTACTGAGAATGAAATAGGATCCTAGTCCTTTTATTGCTGAC 472
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                                                                                           353 ATAGATCATGACCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGG
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                                                                                                                                                                                                                                    TITCAGACAACAGCAGAAGAGITAGGAITATTA 453
                                                                                                                                                                                                                                                           100.0%; Pred. No. ...
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CURRENT APPLICATION NUMBER: US/10/467,535
CURRENT PILING DATE: 2003-08-08
PRIOR APPLICATION NUMBER: US/20/203715
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: US 60/264,111
PRIOR APPLICATION NUMBER: US 60/271,175
PRIOR APPLICATION NUMBER: US 60/271,175
PRIOR APPLICATION NUMBER: US 60/271,175
PRIOR FILING DATE: 2001-02-3
PRIOR FILING DATE: 2001-03-08
PRIOR PILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US 60/274,503
PRIOR PILING DATE: 2001-03-08
PRIOR PILING DATE: 2001-03-08
PRIOR PILING DATE: 2001-03-09
NUMBER: OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 5284076CB1
US-10-467-535-16
                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 16, Application US/10467535; Publication No. US20040146970A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.(
Matches 453; Conservative
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LENGTH: 1480
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APPLICANT: Ebbets-Reed, Dana
APPLICANT: Ebbets-Reed, Dana
APPLICANT: Chicca, John
APPLICANT: Chicca, John
APPLICANT: Chicca, John
APPLICANT: Chicca, John
APPLICANT: History Frances
APPLICANT: Bihain, Bernaces
APPLICANT: Bihain, Bernaces
TITLE OF INVENTION GSSP3 Polynucleotides and Polypeptides and Uses Thereof
FILE REFERENCE: 4-102USO3REG
CURRENT PILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US 60/266,156
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-02
RUNBER OF SEQ 1D NOS: 3
SOFTWARE: Patentin version 3.0
241 AGGGTAGTTTCTGAGGAAACTCTCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT 300
                                                                                                                   341
                                                                                                                                                           301 ATAGATCATGACCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGG 360
                                                                                                                                                                                       CTTACACCAGTITCTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTATTGCTGAC 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AGCAGAAATCTGTATATTTGCGGATGAATTACATCTGGGAATGGGCTGCCCTGCAAAT 180
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                                                                                                                                                                                                                                                                                                                                           TITCAGACAACAGCAGAAGAGTIAGGAITAITA 453
                                                                                                                                                                                                                                                                                                                                                                            TTTCAGACACAGCAGAAGAGTTAGGATTATTA 494
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Publication No. US20040235709A1
GENERAL INFORMATION:
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LOCATION: (104)..(526)
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LOCATION: (53)..(103)
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ATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGGG
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                                                                                      ATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGG
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100.0%; Pred. No. 4.7e-133;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATLE OF INVENTION: 62 Human Secreted Proteins
TITLE OF INVENTION: 62 Human Secreted Proteins
FILE REPERENCE: PSO39P1
CURRENT APPLICATION NUMBER: US/10/798,512
CURRENT FILING DATE: 2004-03-12
FRIOR APPLICATION NUMBER: US/99/684,524
FRIOR APPLICATION NUMBER: PCT/US00/08979
FRIOR FILING DATE: 2000-10-10
FRIOR FILING DATE: 2000-44-06
FRIOR FILING DATE: 1999-04-09
FRIOR FILING DATE: 1999-04-09
FRIOR FILING DATE: 1999-04-09
FRIOR FILING DATE: 1999-04-06
FRIOR RELING DATE: 1999-04-06
FRIOR FILING DATE: 1999-04-26
                                                                                                                                                                                                                                                                                                                                                            TTTCAGACAACAGCAGAAGAGTTAGGATTATTA 467
                                                                                                                                                                                                                                                                                                                               TITCAGACAACAGCAGAAGAGITAGGAITATTA 453
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Publication No. US20040152164A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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OTHER INFORMATION:
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NAME/KEY: SITE
LOCATION: (1398)
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NAME/KEY: SITE
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        209 CGGATACATACATATGTATATGAGTTTATATATCTTGTTCGTGATTGTGGCATCAGGACA 268
                                                                                            269 AGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT 328
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4.7e-133;
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Publication No. US20030050442A1

GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 62 Human Secreted Proteins
FILE REFERENCE: P2039P1
CURRENT FILING DATE: 2002-01-18

PRIOR APPLICATION NUMBER: 09/684,524

PRIOR PILING DATE: 2000-10-10

PRIOR APPLICATION NUMBER: 60/1000/08979

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

PRIOR PILING DATE: 1999-04-06

PRIOR PELING DATE: 1999-04-06
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NAME/KEY: SITE
LOCATION: (1398)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1428)
COTHER INFORMATION: n equals a,t,g, or c
US-10-050-704-27
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 CGGATACATACATATGTATATGAGTTTATATATCTTGGTTCGTGATTGTGGCATCAGGACA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292 AGGGTAGTTTCTGAGGAAGTCTCTCTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTACACCAGTTTCTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTATTGCTGAC 471
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                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: HELLE RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20030236392Alel full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 98.3%; Score 451.4; DB 6; Best Local Similarity 99.8%; Pred. No. 1.3e-132; Matches 452; Conservative 0; Mismatches 1;
                                                                                                                                   453
                                                                                                                                                         TTTCAGACAACAGCAGAAGAGTTAGGATTATTA 453
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Parent No. US20020102604A1
GENERAL INFORMATION
PAPLICANT: Dumas Milne Edwards, Jean Baptiste
                                                                                                                                TTTCAGACAACAGCAGAAGAGTTAGGATTATTA
                                                                                                                                                                                                                                                                                                        US-10-104-047-1704
Sequence 1704, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1704
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                                     CTTACACCAGTTTCTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTATTGCTGAC 434
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301 ATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTG
                                                                                                                   CTTACACCAGTTTCTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTATTGCTGAC
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98.7%; Score 453; DB 9; Length 1898;
Best Local Similarity 100.0%; Pred. No. 4.7e-133;
Matches 453; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                          TTTCAGACAACAGCAGAAGAGTTAGGATTATTA 453
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TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS966CT
CURRENT APPLICATION NUMBER: US/10/472,533
CURRENT FILING DATE: 2003-09-20
FRIOR PELLONG NUMBER: US 60/331,287
PRIOR FILING DATE: 2001-11-3
PRIOR PILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/306,171
PRIOR APPLICATION NUMBER: US 60/277,340
PRIOR APPLICATION NUMBER: US 60/277,340
PRIOR APPLICATION NUMBER: US 60/277,340
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
SROFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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NAME/KEY: misc feature
COCATION: (1428)...(1428)
GOTHER INFORMATION: n equals a,t,g, or c
US-10-472-533-175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1398)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 175, Application US/10472533
Publication No. US20050197285A1
GENERAL INFORMATION:
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US-10-472-533-175
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Sequence 24, Application US/10643836

Bublication No. US20050096458A1

GENERAL INPORMATION:

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Dougueleret, Lydie

APPLICANT: Dobert, Severin

APPLICANT: Bougueleret, Lydie

CURRENT FILING DATE: 2000-12-07

PRIOR FILING DATE: 1999-12-08

PRIOR FILING DATE: 1999-12-08

PRIOR APPLICATION NUMBER: US 60/187,470

PRIOR FILING DATE: 2000-03-06

NUMBER OF SEQ ID NOS: 482

SOFFWARE: Patent. Pm
                                                                                                                                                                                                                                                                                                                                                                                                                                    137 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCTGAGAACCTC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATGTGAAAATAAGTTGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197 CATGTGAAAATAAGTTGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAA 256
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                                                                                                                                                                                                                                                                                     Length 470;
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                                                                                                                                                                                                                                                                                          Score 246; DB 3;
Pred. No. 2.1e-67;
                                                                                                                                                                                                                                                                         53.6%; Sco...
100.0%; Pred. No. 2...
0; Mismatches
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LOCATION: 137..187
COTHER INFORMATION: Won Heijne matrix
OTHER INFORMATION: Score 10.7019149919754
OTHER INFORMATION: seg VLMLLAVLWTGA/EN
US-10-643-836-24
                                                                 NAME/KEY: CDS
| IOCATION: 137..454
| IOCATION: 137..187
| CTHER INFORMATION: Von Heijne matrix OTHER INFORMATION: score 10.7019149919754
| IOCHER INFORMATION: seq VLMLLAVLIWTGA/EN US-09-876-997-24
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 246; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
                      ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGGTA 382
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LOCATION: 137..454
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Sequence 24, Application US/09876997

Bublication No. US2003015221A1

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Bougueleret, Lydie

APPLICANT: Jobert, Severin

TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS

FILE REFERENCE: 78.US4.CIP

CURRENT APPLICATION NUMBER: US/09/876,997

CURRENT PILING DATE: 2000-12-07

PRIOR APPLICATION NUMBER: US 60/187,470

PRIOR PILING DATE: 2000-03-06

PRIOR APPLICATION NUMBER: US 60/187,470

PRIOR APPLICATION NUMBER: US 60/169,629

PRIOR PILING DATE: 1999-12-08

NUMBER OF SEQ ID NOS: 482

SEQ ID NO 24

LENGTH: 470
                    APPLICANT: JOSET, SEVETIN
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78 US3.RES
CURRENT APPLICATION NUMBER: US 60/169,629
PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR FILING DATE: 2000-03-06
NUMBER OF SEQ ID NOS: 482
SOFTWARE: Patent.pm
SEQ ID NO 24
LENGTH: 470
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Best Local Similarity 100.0%; Pred. No. 2.1e-67;
Matches 246; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: CDS
LOCATION: 137.454
NAME/KEY: sig_peptide
LOCATION: 137.187
OTHER INFORMATION: SCORE 10.7019149919754
OTHER INFORMATION: SCORE 10.7019149919754
Bougueleret, Lydie
                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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  APPLICANT:
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APPLICANT: Salter-Cad, Luisa
APPLICANT: Sabter-Red, Dana
APPLICANT: Babets-Red, Dana
APPLICANT: Babets-Red, Dana
APPLICANT: Chicca, Barbara A.
APPLICANT: Chicca, John
APPLICANT: Stances
APPLICANT: Binain, Bernard
CURRENT APPLICATION NUMBER: US/10/467,046
CURRENT FILING DATE: 2003-08-01
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.0
SSFTWARE: Patentin version 3.0
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; Publication No. US20040235709A1
; GENERAL INFORMATION:
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NAME/KEY: misc_feature
LOCATION: (2986).
OTHER INFORMATION: n is a,
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NAME/KEY: misc_feature
LOCATION: (4105)..(4105)
OTHER INFORMATION: n is a,
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LOCATION: (8197)..(8197)
OTHER INFORMATION: n is a,
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LOCATION: (3847)..(3848)
OTHER INFORMATION: n is a,
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LOCATION: (3879)..(3879)
OTHER INFORMATION: n is a,
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OTHER INFORMATION: n is a,
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OTHER INFORMATION: n is a,
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LOCATION: (7347)..(734
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LOCATION: 5443...5646
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6649...6747
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LOCATION: 8907...9774
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LOCATION: 2387...2501
                                                                244 GTA 246
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LOCATION:
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                                                            1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCTGAGAACCTC
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                         0; Gaps
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                       0; Indels
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Best Local Similarity 100.0%; Pred. No. 2.1e-67; Matches 246; Conservative 0; Mismatches 0;
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39.9%; Score 183; DB 3; I
Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 183; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: 53 Human Secreted Proteins TITLE OF INVENTION: 53 Human Secreted Proteins FILE REPRENCE: PZ018P2
CURRENT APPLICATION NUMBER: US/09/984,429
CURRENT PILING DATE: 2001-10-30
PRIOR PILING DATE: 2000-11-01
PRIOR PELING DATE: 1999-04-08
PRIOR FILING DATE: 1999-04-08
PRIOR PELING DATE: 1999-04-08
PRIOR PRIDICATION NUMBER: 60/061,463
PRIOR PRILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
PRIOR PELING DATE: 1997-10-09
PRIOR PELING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
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Publication No. US20040010132A1
GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.0
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CRGANISM: Homo sapiens
US-09-984-429-532
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Search completed: May 9, 2006, 15:02:51
Job time : 1222.4 secs
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Sequence 39, Application US/10287971

Publication No. US20040067882A1

GENERAL INFORMATION:

FILE REPERENCE: 2102-2480A

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

FILE REPERENCE: 2102-2480A

CURRENT FILING DATE: 2002-11-05

PRIOR PELLORION NUMBER: 09/997, 425

PRIOR PELLORION NUMBER: 10/035,568

PRIOR APPLICATION NUMBER: 10/035,568

PRIOR APPLICATION NUMBER: 60/338,626

PRIOR APPLICATION NUMBER: 60/401,479

PRIOR APPLICATION NUMBER: 60/333,072

PRIOR APPLICATION NUMBER: 60/348,283

PRIOR APPLICATION NUMBER: 60/349,283

PRIOR APPLICATION NUMBER: 60/333,072

PRIOR APPLICATION NUMBER: 60/349,262

PRIOR APPLICATION NUMBER: 60/349,262

PRIOR APPLICATION NUMBER: 60/349,262

PRIOR PILING DATE: 2002-01-10-6

PRIOR PILING DATE: 2002-01-10-6

PRIOR APPLICATION NUMBER: 60/406,181

PRIOR FILING DATE: 2002-00-02

PRIOR PILING DATE: 2002-00-02

PRIOR PILING DATE: 2002-00-06

PRIOR PILING DATE: 2002-00-07

PRIOR PILING DATE: 2002-00-06

PRIO
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0
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Best Local Similarity 100.0%; Pred. No. 1.3e-46;
Matches 183; Conservative 0; Mismatches 0; Indels
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                                              PEATURE:
NAME/KEY: misc_feature
LOCATION: (8334). (8336)
OTHER INFORMATION: n is a, c,
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NAME/KEY: misc_feature
LOCATION: (8342). (8342)
OTHER INFORMATION: n is a, c
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NAME/KEY: misc feature
LOCATION: (9942)...(9942)
COTHER INFORMATION: n is a,
US-10-467-046-1
LOCATION: (8293)..(8293)
OTHER INFORMATION: n is a,
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; NAME/KEY: CDS
; LOCATION: (100)..(735)
US-10-287-971-39
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5624 GTA 5626
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                                                                                                                                                                                                                                                                                                                                                         239 ATGTGTGTGTACACTTTCATGAACTACACTTGGGCCTGGGTTGCCCCCCAAACCATGTTC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                 188 ATACATATGTATATATGTTTATATATCTTGTTGTGTGGCATCAGGACAAGGGTAG 247
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                                                                                                        8 TAGAAGTCTTGATGCTCCTCGCTGTCTTGGATTTTGGACCGGTGCTGAGAACCTCCATGTGA
                                                         Gaps
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0
Length 838;
Score 90.2; DB 7; Length 8 Pred. No. 1.3e-17; 0; Mismatches 118; Indels
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  Query Match
Best Local Similarity 57.7%;
Matches 161; Conservative
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; Sequence 1704, Application US/11072512; Publication No. US20060029945A1; GENERAL INFORMATION:
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ISONO, YUUKO
HIO, YURI
OTSUKA, KAORU
NAGAI, KEIICHI
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SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRIE, RYOTARO
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                     May 9, 2006, 13:13:06; Search time 945 Seconds (without alignments) 1978.089 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                    1 atggcgttagaagtcttgat.......agttaggattattaatcttc 459
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| SIDSS/ptodata/1/pubpna/USO6_NEW_PUB.seq1:*
| SIDSS/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
| SIDSS/ptodata/1/pubpna/USO8 NEW PUB.seq:*
| SIDSS/ptodata/1/pubpna/USO8 NEW PUB.seq:*
| SIDSS/ptodata/1/pubpna/USO9 NEW PUB.seq:*
| SIDSS/ptodata/1/pubpna/USO9 NEW PUB.seq:*
| SIDSS/ptodata/1/pubpna/USO9 NEW PUB.seq:*
| SIDSS/ptodata/1/pubpna/USO0 NEW PUB.seq:*
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                             GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9306428 seqs, 2036268586 residues
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459
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                 - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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	Description	704 Sequence 1704, Ap	Sequence			Sequence 76829		-	8				S	-	
SUMMARIES	. al	US-11-072-512-1704	US-10-475-075-564	US-10-475-075-563	US-10-821-234-181	US-09-925-065A-768295	US-09-925-065A-46080	US-09-925-065A-46081	US-10-301-480-147318	US-10-301-480-147319	US-10-301-480-760727	US-10-301-480-760728	US-09-925-065A-29822	US-09-925-065A-29823	US-09-925-065A-47775
	Query Match Length DB	1492 18	497 11	500 11	1141 10	564 7	580 7	580 7	580 11	580 11	580 12	580 12	1524 7	1524 7	1524 7
de	Query Match I	98.3	97.2	93.5	19.7	9.8	8.6	9.8	8.6	9.8	8.6	9.8	9.8	9.8	9.8
	Score	451.4	446	429	90.2	39.4	39.4	39.4	39.4	39.4	39.4	39.4	39.4	39.4	39.4
	Result No.	7	7	m	4	υ S	y U	0 7	υ 8	ნ	c 10	c 11	c 12	c 13	c 14

APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR PAPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN VOY: 2.1

TYPE: DNA ORGANISM: Homo sapiens

LENGTH: 1492 SEQ ID NO 1704

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Sequence	Sequence	Sequence 131061,	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 13233	Sequence 276453	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence 546990	Sequence	Sequence	Sequence	Sequence 552224	Sequence 530174,	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 506156,	Sednence
US-09-925-065A-47776	US-10-301-480-131060	US-10-301-480-131061	US-10-301-480-149013	US-10-301-480-149014	US-10-301-480-744469 .	US-10-301-480-744470	US-10-301-480-762422	US-10-301-480-762423	US-10-995-561-13233	US-09-925-065A-276453	US-10-995-561-13259	US-10-301-480-548415	2 US-10-301-480-1161824	US-10-750-185-54368	US-10-750-623-54368	US-09-925-065A-546990	US-10-301-480-524940	US-10-301-480-1138349	US-09-925-065A-940832	US-09-925-065A-552224	2 US-10-301-480-530174	US-10-301-480-1143583	US-11-112-908-61	US-11-112-908-60	US-10-301-480-37618	US-10-301-480-37619	US-10-301-480-651027	US-10-301-480-651028	US-09-925-065A-506156	US-10-301-480-612896
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1524	1524	1524	1524	1524	1524	1524	1524	1524	199130	579	387780	835	835	1111	1111	1221	1221	1221	726	1088	1088	1088	159497	171427	1241	1241	1241	1241	608	717
9.	8.6	8.6	8.6	8.6	8.6	8.6	8.6	9.6	8.1	7.7	7.7	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.3	7.3
39.4	39.4	39.4	39.4	39.4	39.4	39.4	39.4	39.4	37.4	35.4	35.2	34.6	34.6	34.4	34.4	34.2	34.2	34.2	34	34	34	34	34	34	33.8	33.8	33.8	33.8	33.6	33.6
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VS-10-475-075-563

VS-10-475-075-563

Sequence 563, Application US/10475075

; Deblication No. US20060053498A1

; GENERAL INFORMATION:
    APPLICANT: Bejanin, Stephane
    APPLICANT: Dumas Milne Edwards, Jean-Baptiste
    APPLICANT: Jobert, Severin
    APPLICANT: Jobert, Severin
    APPLICANT: Jobert, Severin
    APPLICANT: Glordano, Jean-Yves
    TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins
    FILE REFERENCE: G-081US03PcT
    CURRENT APPLICATION NUMBER: US/10/475,075
    FILE REPEATION NUMBER: CT/IB01/00914
    PRIOR FILING DATE: 2003-10-17
    PRIOR FILING DATE: 2001-04-18
    NUMBER OF SEQ ID NOS: 918
    SEQ ID NO 563
    LENGTH: 500
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                                                                                                                   ATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGG
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                                                                                       1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCTGAGAACCTC
                            Gaps
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100.0%; Pred. No. 2.7e-109; tive 0; Mismatches 0;
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OTHER INFORMATION: score 10.6999998092651
OTHER INFORMATION: seq VLMLLAVLIWTGA/EN
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; LOCATION: 1..3

; OTHER INFORMATION: n = a, g,

US-10-475-075-563
Best Local Similarity 100. Matches 446; Conservative
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ORGANISM: Homo sapiens
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NAME/KEY: sig_peptide
LOCATION: 72..122
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NAME/KEY: CDS
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| Sequence 564, Application US/10475075
| Sequence 564, Application No. US20060053498A1
| Publication No. US20060053498A1
| Publication No. US20060053498A1
| APPLICANT: Bejanin Stephane
| APPLICANT: Dumas Milne Edwards, Jean-Baptiste
| APPLICANT: Jobert, Severin
| APPLICANT: Johert, Severin
| APPLICANT: Johert, Severin
| APPLICANT: Johert, Severin
| APPLICANT: Johert, Johert,
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                                                                                                                                                                                                                                                                                                                                                                                                                            121 AGCAGAAATCTGTATATATTTGCGGATGAATTACATCTGGGAATGGGCTGCCCTGCAAAT 180
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                                                           Length 1492;
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                                                                                                                         Indels
                                                              DB 18;
                                                              Score 451.4; DB 18
Pred. No. 1.3e-110;
0; Mismatches 1;
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LOCATION: 52..102
UNTER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 10.699998092651
OTHER INFORMATION: seq VLMLLAVLIWTGA/EN
                                                              98.3%;
99.8%;
                                                              Query Match
Best Local Similarity 99.8
Matches 452; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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NAME/KEY: CDS
LOCATION: 52..495
   US-11-072-512-1704
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LENGTH: 497
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ATACATATGTATATGAGTTTATATATCTTGTTCGTGATTGTGCCATCAGGACAAGGGTAG 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              491 AGCCACACGCCTACCAGTTCACCTGTTACTGAATGTGGCATCAGGGCCAAAGCTG
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GRNERAL INFURKATION:

TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome ITITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2000-10-24

PRIOR PELING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR PELING DATE: 2000-11-30

PRIOR PELING DATE: 2001-11-16

PRIOR PELING DATE: 2001-01-16

PRIOR PELING DATE: 2001-01-16

PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086

SOFTWARE: FRASEQ for Windows Version 4.0

LENGTH: 564
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 10827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71; Indels
                                                                                                                                                                                                                                                           248 TITCIGAGGAAACTCTCTTTTTCAAACCGAGCTGTACT 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-925-065A-768295/c
; Sequence 768295, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 53.6
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-09-925-065A-768295
                                                                                                                             188
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Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Adarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: ALBALIANION: Methods for Diagnosis and Treatment of Preeclampsia
ITILE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT FILING DATE: 2004-04-07
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: PL SEQ Genes Version 1.0
SEQ ID NO 181
                                                                                                                                                                                    61 CATGTGAAAATAAGTTGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAA 120
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                                                                                                                                              1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCTGAGAACCTC
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                    DB 11; Length 500;
                                                                                    Indels
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             93.5%; Score 429; DB 11; L
100.0%; Pred. No. 9.7e-105;
iive 0; Mismatches 0;
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Query Match
Best Local Similarity 100.0
Matches 429; Conservative
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TTTCAGACA 500
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ORGANISM: Homo sapiens
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Sequence 147319, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
TITLE OF INVENTION: in the Human Genome
TITLE OF INVENTION UNMER: US/10/301,480
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301, 480
CURRENT FILING DATE: 2002-11-21
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSEQ for Windows Version 4.0
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143 TCTATTGGAAGAAATTGTTACATAAGGATGTGG 111
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                                                                                                                                                               ; Sequence 147318, Application US/10301480; Publication No. US20060057564A1
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Best Local Similarity 53.64
Matches 82; Conservative
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CORGANISM: Homo sapien
US-10-301-480-147318
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US-10-301-480-147319
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US-10-301-480-147319/c
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LENGTH: 580
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Sequence 46081, Application US/09925065A

PUDLication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

TITLE OF INVENTION: NUMBER: US/09/925,065A

CURRENT FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR FILING DATE: 2001-01-16

SEQ ID NO 46081

LENGTH: 580

LENGTH: 580
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Best Local Similarity 53.6%; Pred. No. 1.5;
Matches 82; Conservative 0; Mismatches 71;
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PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-6
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-6
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FRESER FOR WINDOWS Version 4.0
SEQ ID NO 46080
                                                                                                                                                                                                                                                                          TYPE: DNA; ORGANISM: Homo sapiens
US-09-925-065A-46080
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US-09-925-065A-46081/c
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
PLIE REFERENCE: 108827.135
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                                      Length 580;
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                                    Score 39.4; DB 12;
Pred. No. 1.5;
0; Mismatches 71;
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
FRIOR PELING DATE: 2000-10-24
FRIOR FILING DATE: 2000-11-20
FRIOR FILING DATE: 2000-11-20
FRIOR FILING DATE: 2000-11-30
FRIOR FILING DATE: 2000-11-30
FRIOR FILING DATE: 2000-11-6
FRIOR FILING DATE: 2001-01-16
FRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
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53.6%; Pred. No. 2;
tive 0; Mismatches
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                                  Query Match
Best Local Similarity 53.6%;
Matches 82; Conservative
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Best Local Similarity 53.64
Matches 82; Conservative
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US-09-925-065A-29823/c
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Publication No. US20060057564A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms:

TITLE OF INVENTION: In the Human Genome

FILE REFERENCE: 108827.137

CURRENT APPLICATION NUMBER: US/10/301,480

CURRENT APPLICATION NUMBER: US 10/215,598

FRIOR FILING DATE: 2002-08-09

FRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: FastESQ for Windows Version 4.0

SEQ ID NO 760728
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IIILE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR PILING DATE: 2002-08-09
PRIOR PILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 760727
LENGTH: 580
                                             263 TTGATGAAATGAGCATGCAGATATGTATATAGCATATATCTACATTTTATTAAAAATACA 204
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Pred. No. 1.5;
0; Mismatches 71;
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Publication No. US20060057564A1
GENERAL INFORMATION:
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Best Local Similarity 53.6%;
Matches 82; Conservative
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US-10-301-480-760727
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; ORGANISM: Homo sapien
US-10-301-480-760728
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleocide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/225,065A
CURRENT FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/250,147
PRIOR FILING DATE: 2000-11-20
PRIOR PELING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-01-16
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Pred. No. 2;
0; Mismatches 71;
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
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PRIOR FILING DATE: 2001-01-6
PRIOR FILING DATE: 2001-01-6
PRIOR FILING DATE: 2001-01-6
PRIOR FILING DATE: 2001-03-6
PRIOR FILING DATE: 2001-03-6
PRIOR FILING DATE: 2001-03-6
PRIOR FILING DATE: 2001-03-6
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
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SEQ ID NO 29823
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US-09-925-065A-47775/c
'Sequence 47775, Application US/09925065A
'Publication No. US20040181048A1
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Best Local Similarity 53.6%;
Matches 82; Conservative
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CONGANISM: Homo sapiens
US-09-925-065A-29823
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-20
PRIOR PELING DATE: 2000-11-16
PRIOR PELING DATE: 2001-01-16
PRIOR PELING DATE: 2001-01-16
PRIOR PELING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PSELSEQ for Windows Version 4.0
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RESULT 15
US-09-925-065A-47776/c
Sequence 47776, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
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Job time : 946 secs
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CORGANISM: Homo sapiens
US-09-925-065A-47776
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us-10-664-025-43_copy_53_511.rst

108.2 23.6 389 1 AU044924 AU044924 HO044924 101 22.0 559 9 AQ723272 HS 2085_B 90.2 19.7 583 2 BG184286 BB14286 BB211198 90.2 19.7 627 2 BG620477 BG520477 6026.77619 90.2 19.7 66 2 BG520607 CC26.77619 90.2 19.7 66 2 BG620477 CC26.7729 90.2 19.7 820 6 CF693309 CC2617729 90.2 19.7 820 6 CF693309 CC662309 GC2617729 90.2 19.7 820 6 CF693309 CC662309 GC2617729 90.2 19.7 820 6 CF693309 CC663109 GC2617729 90.2 19.7 882 BC623009 BC32309 GC2647871 90.2 19.7 882 CC4489318 GC2647871 90.2 19.7 4 CK618096 CK604318 GCK604394 GCK604394 90.2 19.7	B1463012 B1463012 B1463012 ON 603204535F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5270384 5', mRNA sequence. B1463012.1 GI:1523368 B1463012.1 GI:1523018	
0.0 0 0.000000000000000000000000000000	RESULT 1 B1463012 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES SOUTCE
GenCore version 5.1.8 Copyright (c) 1993 - 2006 Biocceleration Ltd. OM nucleic - nucleic search, using sw model Run on: May 9, 2006, 12:54:43; Search time 5670 Seconds (without alignments) 3787.526 Million cell updates/sec Title: US-10-664-025-43_COPY_53_511 Perfect score: 459 Sequence: 1 atggcgttagaagtcttgatagttaggattattaatctc 459 Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0 Searched: 41078325 seqs, 23393541228 residues Total number of hits satisfying chosen parameters: 82156650 Minimum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database: EST:*	1 453 98.7 626 3 BI463012 BI463012 60204535 2 453 98.7 76 2 BG772527 602020619 3 453 98.7 78 BI520154 BI520154 BI520154 4 440 95.9 577 5 BX18111 BX18111 5 410.4 89.4 619 1 AM664990 AM664990 BI498038 7 378.6 82.5 516 2 BR97277 BR96490 BI99806.x 7 378.6 82.5 516 1 AM608935 AM664990 BI99806.x 8 318 69.3 508 1 AM608935 AM608935 AM608935 AM608935 AM608935 AM608935 AM608936 AM60893 AM608930 AM60893 AM60893

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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gp Ph.D.
Email: cgapbs-r@mail.nih.gp Ph.D.
Email: cgapbs-r@mail.nih.gp Ph.D.
Email: cgapbs-r@mail.nih.gp Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
TobN ibrary Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMIO770 row: e column: 05
High quality sequence stop: 773.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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(NIMH/NHGRI, National Institutes of Health). Note: this a NIH_MGC Library."
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1 (bases 1 to 776)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGGTAGTTTCTGAGGAAACTCTCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGGTAGTTTCTGAGGAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hominidae, Homo.

1 (Dases 1 to 878)

NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                          Length 776;
                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                          98.7%; Score 453; DB 2; Le
100.0%; Pred. No. 1.4e-119;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTCAGACAACAGCAGAAGAGTTAGGATTATTA 453
                    /clone="IMAGE:4837612"
/lab_host="DH10B"
db xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B1520154 878
603071295F1 NIH_MGC_119 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:15344946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                    Matches 453; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
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Tourindary now.

Ebert L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, P. and Korn, B.
Radelof, U., Schneider, P. and Korn, B.
Human Unigeneset - RZPD3
Unpublished (2003)
Contact: Ina Rolfs
RAPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD: IMAGPSB0122574.
RZPD IMAGPSB0122574.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/Ggi-
bin/showLib.pl.cgi/response7lib/be-972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg G. D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 101
Fax: +49 30 32639 101
This clone is available royalty-free from RZPD;
Contact RZPD (clone@rzpd.de) for further information. Seq primer:
NJ3r. Primer sequence: TTTCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab host="DH10B"
/clone lib="Soares testis NHT"
/clone="Vector: pt773D-Pac"(Pharmacia) with a modified
/note="Vector: pt773D-Pac"(Pharmacia) with a modified
/note="Vector: pt773D-Pac"(Pharmacia) with a modified
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cots, and was constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCTGAGAACCTCCATGTGAAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAAAGCAGAAATCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAATATAGATCATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 TCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCTGAGAACCTCCATGTGAAAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 577;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGp998D122574 ; IMAGE:1030619"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.9%; Score 440; DB 5; Le
llarity 100.0%; Pred. No. 7.5e-116;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                               Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .577
                                                                                                                                                                        Hominidae; Homo.
                                                                         Homo sapiens
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Best Local S
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                                            SOURCE
ORGANISM
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Matches
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JOURNAL
COMMENT
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            KEYWORDS
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BX118111 GI:27881212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 ATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTACACCAGTTTCTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTATTGCTGAC 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                     DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can }
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.m column: 24
High quality sequence stop: 851.
Location/Qualifiers
Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.7%; Score 453; DB 3; Le
100.0%; Pred. No. 1.5e-119;
:ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTCAGACAACAGCAGAAGAGTTAGGATTATTA 453
                                                                                                                                                                                                                                                                                                        1. .878 | /organism="Homo sapiens" | /organism="Homo sapiens" | /mol_type="mRNA" | /db xrefs"taxon:9606" | /clone="IMAGE:5163455" | /tissue_type="medulla" | /tissue_type="medulla" | /lab host="DHIOB" | /clone_lib="NIH_MGC_119"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 453; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390
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VERSION
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BX118111
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/d_one="IMAGE:298039"
//lab_host=="IMAGE:29808"
//lab_host=="DH108"
//lab_host="DH108"
//clobe_lib="Soares NFL T_GBC_S1"
//ab_host="DH108"
//abce="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_l: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCT_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731339. Subtraction by Bento Soares and M. Patima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi; Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi; Mammalia; Homo.

Hominidae; Homo.

I (bases 1 to 619)

S NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

I Unpublished (1997)

Conteat: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov

This clone is available royalty-free through LLNL; contact the IMAGE Conscrtium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco.

High quality sequence stop; 460.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h198h06.x1 Soares NFL T GBC S1 Homo sapiens CDNA clone IMAGE:2980379 3', mRNA sequence.
                                                         AGCAGAAATCTGTATATATTTGCGGATGAATTACATCTGGGAATGGGCTGCCCTGCAAAT 180
                                                                                                                                      241 AGGGTAGTTTCTGAGGAAACTCTCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT 300
                                                                                                                                                                                                                                                    431 AGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT 490
                                                                                                                                                                                                                                                                                                  ATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGG 360
                                                                                                                                                                                                                                                                                                                  491 ATAGATCATGACCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGG 550
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                                                                                                                                                                                                                                                                                                                                                                                          CTTACACCAGTTTCTACTGAGAATGAAA--TAAAAATTGGATCCTAGTCCTTTTATTGCTG
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTITICAGACAACAGC 626
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Homo sapiens
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/mol_type="mRNA"

/db_tref="taxcon: 9606"

/clone="th4fass: 5266642"

/lab_host="nH10B"

/clone="INH1 MGC_97"

/clone="forgan: testis, Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamH1; Site_2: Sall-XhoI (gcgan: testis, Vector: pBluescript RS+); Site_1: BamH1; Site_2: Sall-XhoI (gcgan: testis, Vector) asize-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is
                                                                                                                                                                                                                                                                                                                          b1459538 11H_MGC_97 Homo sapiens cDNA clone IMAGE:5266642 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 CTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTATTGCTGACTTTCAGACAACAG 420
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CTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGGCTTACACCAGTTT 373
                                                                                        374 CTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTATTGCTGACTTTCAGACAACAG 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RTKEN)

TOSHIYUki and Piero Carninci (RTKEN)

TOSHIYUki and Piero Carninci (RTKEN)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be the incound through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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91.2%; Score 418.8; DB 3;
Best Local Similarity 99.1%; Pred. No. 1.1e-109;
Matches 432; Conservative 0; Mismatches 2;
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                                                                                                                                                                                                              421 CAGAAGAGTTAGGATTATTA 440
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Homo sapiens
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1 (bases 1 to 778)
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314
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Sfil (ggccgcctcggcc); Site 2: Sfil (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATANGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCCGACATG-dT(30) BN-3' (Where B = A, C, or G and N = A, C, G, or T). Average insert size 1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 13-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 TATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTG 359
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 508)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Unpublished (1997)
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbe-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco
High quality sequence stop: 451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 AGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCCAAGGAAC
                                                                                                                                                                                                                                                                                                 1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCTGAGAACCTC
                                                                                                                                                                                                                                                                                                                                                                              CATGTGAAAATAAGTTGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAA
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                                                                                                                                                                                                                  82.5%; Score 378.6; DB 2; Length 516; 98.7%; Pred. No. 4e-98; ive 0; Mismatches 4; Indels 1
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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AW572898/c
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/db_xref="taxon:9606"
/db_xref="taxon:95288"
/lab_host="DH108 (T1 phage-resistant)"
/clone lib="NIH MGC 82"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE972717 516 bp mRNA linear EST 04-OCT-2000 601652136F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935288 5',
                                                                            ICTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAAAGCAGAAATCTGTATATT 140
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1 (bases 1 to 516)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Ontact: Robert Strausberg, Ph.D.

Email: cgapbs-romail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                321 AATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGGCTTACACCAGTTTCTACTGA
                                                        GCTCCTCGCTGTCTTGATTTGGACCGGTGCTGAGAACCTCCATGTGAAAAAAAGTTGCTC
                                                                                                                                                                                                                                                                                                               315 AATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGGCTTACACCAGTTTCTACTGA
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Clone distribution: MGC clone distribution information can J
Gound through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
Plate: Lickny77 row: h column: 09
High quality sequence stop: 505.
Location/Qualifiers
                          1;
                      7; Indels
Best Local Similarity 98.2%; Pred. No. 2.7e-107; Matches 425; Conservative 0; Mismatches 7;
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/organism="Homo sapiens"
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Homo sapiens
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A1554902
te53g03.x1 Soares NFL T GBC_S1 Homo sapiens cDNA clone
IMAGE2090452 3', mRNA Sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAACCGAGCTGTACTTTACCCCAAGGAATATAGATCATGACCCTCAGGAAATCCATTTG 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGTGTTCCACCTCTAGGAAATCAGTGTGGCTTACACCAGTTTCTACTGAGAATGAAATA 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 GAGTGTTCCACCTCTAGGAAATCAGTGTGGCCTTACACCAGTTTCTACTGAGAATGAAATA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       391 AAATIGGAICCTAGICCTITIATIGCIGACTITCAGACAACAGCAGAAGAGTIAGGAITA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Patima Bonaldo. "
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 2.0)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP ttp://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     370 TAICTIGITICGIGATIGIGGCAICAGGACAAGGGIAGTITCTGAGGAAACTCTCCTTITI
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100.0%; Pred. No. 2.7e-76;
iive 0; Mismatches 0;
                    Insert Length: 629 Std Error: 0.00
Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 424.
                                                                                                       1. .430
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                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1030619"
                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI554902
AI554902.1 GI:4487265
                                                                                                                                                                                                                      /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
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Best Local Similarity 100.
Matches 303; Conservative
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Unpublished (1997)
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             /lab_host="DH108"
/clone lib="Soares NFL T GBC S1"
/clone lib="Soares NFL T GBC S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Ecc RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NHT, and B-cell NCI CGAP GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M. A.G. E. Clones 297486-730997, 682632-687239, 726408-728711, and 729096-73199. Subtraction by Bento Soares and M. Patima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     430 bp mRNA linear EST 02-MAR-1998
af53h06.81 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1030619
34' mRNA sequence.
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Bukaryotta.

Mammalia, Butheria; Buarchontoglires; Primates; Catarrhini;

Mammalia, Bunneria; Buarchontoglires; Primates; Catarrhini;

1 (Dases 1 to 430)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,

Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,

Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,

Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 TCAAACCGAGCTGTACTTTACCCCCAAGGAATATAGATCATGACCCTCAGGAAATCCATTT
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                  Query Match 69.3%; Score 318; DB 1; Length 508; Best Local Similarity 100.0%; Pred. No. 1.3e-80; Matches 318; Conservative 0; Mismatches 0; Indels
/clone="IMAGE:2932128"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAGTGTTCCACCTCTAG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 GGAGTGTTCCACCTCTAG 191
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Contact: Wilson RK
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
from through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/brp/image/image.html
Insert Length: 395 Std Brror: 0.00
Seq primer: -40ml3 fwd. ET from Amersham.
                     CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:1737606"
                                                                                                                                                                                                                 Location/Qualifiers
    cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                            /sex="male"
                                                Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 AGGGTA 246
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                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_txef="txexon:9606"
/clone="InAGE:209042"
/lab_host="DH10B"
/clone_lib="Soares NFL T GBC S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (feral Tung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.B. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731339. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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qd99c04.xl Soares_testis_NHT Homo sapiens CDNA clone IMAGE:1737606
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae; Homo.
1 (bases 1 to 331)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                 Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 656 Brror: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 458.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  420 GAAAGCAGAAATCTGTATATATTTGCGGATGAATTACATCTGGGAATGGGCTGCCCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 ACAAGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.2%; Score 290; DB 1; Length 480; 100.0%; Pred. No. 1.6e-72; ive 0; Mismatches 0; Indels
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3', mRNA sequence.
AI138881
AI138881.1 GI:3644853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 290; Conservative
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DEPINITION
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VERSION
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TITLE
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COMMENT
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/lab_host="DH10B"
/clone_lib="Soares testis NHT"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            598 bp mRNA linear EST 17-DEC-2003
H3059H12-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
H3059H12 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          331 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCTGAGAACCTC 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CATGTGAAAATAAGTTGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                271 CATGTGAAAATAAGTTGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 CGGATACATACATATGTATATGAGTTTATATATCTTGTTCGTGATTGTGGCCATCAGGACA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Musinae; Mus.
1 (Dases 1 to 598)
Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X.,
Grahovac,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCTGAGAACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 53.6%; Score 246; DB 1; Length 331; Best Local Similarity 100.0%; Pred. No. 7.4e-60; Matches 246; Conservative 0; Mismatches 0; Indels
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Mus musculus
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BG081002.2 GI:40015217
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Sclurograth, murologea; muritae; mur.
Sclurograth, murologea; muritae; mur.
Sclurograth, murologea, muritae; mur.
Nikaido, T., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yaqi, N., Tomaru, Y., Haseqawa, Y., Nogami, A.,
Schombach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Hume, D.A., Quackenbush, J., Schrind, L.M., Kanapin, A.,
Batalov, S., Beisel, K., Bake, J.A., Bradt, D., Brusic, V.,
Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J. Grimmond, S.,
Kawaji, H., Kawasawa, Y., Kedierski, R.M., King, B. L., Konagaya, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., L., Miki, H., Nagashima, T.,
Maltais, L., Marchionni, L., Pertes, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Oi, D., Ramachandran, S.,
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shinada, K.,
Sultana, R., Yangner, L., Wahlestedt, C., Wang, Y., Waranabe, Y.,
Wells, C., Wilming, L.G., Wynshaw, Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Yonno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.,
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY731676 RIKEN full-length enriched, 2 days pregnant adult female ovary Mus musculus cDNA clone E330031A07 5', mRNA sequence.
341 AATTATTGTTTGGAACTTCAGATAGTCCCTTTGCAGTGTTCTGCCTCTCGGAAGTCTGTG 400
                                                                                                                                                                                                                                                                                   Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                      AATATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTG 357
                                                                                                                                                                                                                                         358 IGGCTIACACCAGTITCTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTATIGCI 417
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Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,F.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Imoteani,K., Ishii,Y., Itchi,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                         GACTTTGAAGCTACACCAGAAGAGTTGGGGTTATTAA 497
                                                                                                                                                                                                                                                                                                                                                                                  GACTITCAGACACAGCAGAAGAGTTAGGATTATTAA 454
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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BY731676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab host="DH10B"
/clone_lib="NIA Mouse 15K cDNA Clone Set"
/clone_lib="NIA Mouse 15K cDNA Clone Set"
/clone is among a rearrayed set of 15.247 clones from 11 clone is among a rearrayed set of 15.247 clones from 11 clone is among a rearrayed set of 15.247 clones from 11 clone is among a rearrayed set of 15.247 clones from 11 clones from unfertilized egg to blastocyst, embryonic part of E7.5 cmbryos, extraembryonic part of E7.5 cmbryos, extraembryonic part of E7.5 cmbryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and cmbryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals
                                                                                                                                                                                                                                                                                                            National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please plate: http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details.
Plate: H3059 row: H column: 12
Seq primer: -21M13 Reverse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 AACAAAAGAAATCCATATATTTTTGCTGATGAATTATATCTGGGACAGAACTGCCGTGTA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 ATGGCTTTAGAGGTCTTGGTTTATCTTGCTGTCTTGGTTTTGGACTTGTGCTTGGGACATT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CATGTGAAAATAAGTTGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 AATCGGATACATATGTATATGAGTTTATATATCTTGTTCGTGATTGTGGCATCAGG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 ACAAGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCTGAGAACCTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             // sex="Clones arrayed from a variety of cDNA libraries"
dev_stage="Clones arrayed from a variety of cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enrichment in the t-complex and under-representation
the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
                                             and
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                                          Genome-wide expression profiling of mid-gestation placenta embryo using a 15,000 mouse developmental cDNA microarray Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
                                                                                                                                                                         On Jan 26, 2001 this sequence version replaced gi:12563570. Other ESTs: H3059H12-3
Contact: George J. Kargul
Laboratory of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
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          Wood, W.H. III, Becker, K.G. and Ko, M.S.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="niaEST:H3059H12-5"
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/clone lib="NIH MGC 257"
/clone lib="NIH MGC 257"
/clone lib="NIH MGC 257"
/clone lib="Organ: Occyte; Vector: pExpress-1; Site_1: ECORV; Site_2: NOLI: CDNA was primed using oligo-dT primer:
5'-pGACTAGTTCTAGATGCGGAGGCGCCC(T) 25-3' and cloned into the ECORV/NOLI sites of pExpress-1. Size-selection >0.5 kb resulted in an average insert size of 1.0kb. This is a normalized library (primary library is NIH_MGC 256) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MGC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CO810251 862 bp mRNA linear EST 06-AUG-2004
AGENCOURT 30258260 NIH MGC_257 Mus musculus cDNA clone
IMAGE:30931566 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CATGTGAAAATAAGTTGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAA 120
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Coffice of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Enabl: gapbs-remail.nih,gov
Tissue Procurement: Dr. Kathleen Horner, Stanford University
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Rlate: NDAM1179 row: h column: 07
High quality sequence stop: 654.
             286 ACAAAGGTTATCTCAAATGAAATCGTCTGTTTTGAAACCGAGATGTACTTTCGTCCAAGG
                                                                                                AATATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTG
                                                                                                                                                 TGGCTTACACCAGTTTCTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTATTGCT
                                                                                                                                                                                                                                                                                                                                                  406 TGGCTTATGCCACTATCTACTGAGGAGGATCCAAAACCTGTTAAGAGTCCCTTTATGACT
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:10090"
/clone="IMAGE:30931566"
/lab_host="DH10B_TONA"
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                                                                                                                                                 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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/note="Site 1: Sall; Site 2: BamH; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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/dev_stage="2 days pregnant adult"
/lab_host="DH108"
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/db_xref="taxon:10090"
/clone="E330031A07"
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Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.

Enther details.

EDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RIKEN full-length enriched, 2 days pregnant adult female ovary"

/note="Site_1: Sall, Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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/dev_stage="2 days pregnant adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 2 days pregnant
                                                                                                                                                                                                                        Computational Analysis of Full-Length Mouse cDNAs Compared with uman Genome Sequences Mamm. Genome. 12, 673-677 (2001)
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/db_xref="taxon:10090"
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Bultaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

Sciurognathi; Muroidea; Muridae; Mus.

1 (bases 1 to 642)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BB557840 RIKEN full-length enriched, 2 days pregnant adult female ovary Mus musculus cDNA clone E330031A07 3', mRNA sequence.
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Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Earninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
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Matsuuras,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
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GENSET.
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Command line parameters:
-WODEL=frame+ n2p.model -DEV=xlh
-Q=/abss/ABSSWEB_gool/US10664025/runat_08052006_173448_28291/app_query.fasta_1
-Q=/abss/ABSSWEB_gool/US10664025/runat_08052006_173448_28291/app_query.fasta_1
-Q=/abss/ABSSWEB_gool/US10664025/runat_DEVEX=0.1 -LOOPELT=0.1 -LOOPEXT=0
-UNITS_bits -START=1 -END=-1 -WATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -TRR SCORE=pct -TRR MAX=100 -TRR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXEN=200000000 -HOST=abss07
-OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXEN=200000000 -HOST=abss07
-OUTFWT=pto -NORM=CORE=0 - NATI - DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPDP=10 -XGAPEXT=0.5 -FGAPEVT=7
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3327.968 Million cell updates/sec
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Abg91353 Human C
Abg1324 Human G
Abr47931 Human g
Abr00175 Human g
Adcy1338 Human s
Adcy1338 Human s
Adcy1333 Human s
Ab538337 Human s
Ab65550 Human p
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                                                                                                                                                                           atggcgttagaagtcttgat.....agttaggattattaatcttc
                                                                                       9, 2006, 10:01:14 ; Search time 18.18 Seconds
                         Ltd.
           GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration
                                                        - protein search, using frame plue n2p model
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ADB65520
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geneseqp2001s:*
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score greater than or equal to
and is derived by analysis of
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seq length: 200000000
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Xgapop 10.0 , Xc
Ygapop 10.0 , Yc
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16-DEC-2002 (first entry)

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potentially secreted proteins. The nucleic acids and the polypeptides they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GENEST gene expression. For example, they be used to treat disorders associated with decreased GENSET gene expression by rectifying mutations or deletions in a patient's gene expression by rectifying mutations or deletions in a patient's gene expression by rectifying mutations or deletions in a patient's patients own production of GENSET polypeptides. Conversely, antisense nucleic acid molecules may be administered to down regulate GENSET expression by binding with the cells' own genes and preventing their expression by binding with the cells' own genes and preventing their expression by binding with the cells' own genes and preventing their expression by binding with the cells' own genes and preventing their probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence to determine which patients may be in need of restorative therapy. The GENSET polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of GENSET polypeptide of expression and activity. The present sequence is a GENSET polypeptide of
                                                                                                                                     The invention relates to full length GENSET human nucleic acids encoding
diseases, and for diagnosis of those diseases
                                                                Claim 21; Page 804; 921pp; English
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Sequence 158 AA;

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121 AGCAGAAATCTGTATATATTGCGGATGAATTACATCTGGGAATGGGCTGCCCTGCAAAT 180
                                                                                                                                                                                                                                                                                                                                   CGGATACATACATATGTATATGAGTTTATATATCTTGTTCGTGATTGTGGCATCAGGACA 240
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                                                                                                                                                                                                                                                                                                                                                                                                              81 ArgValValSerGluGluThrLeuLeuPheGlnThrGluLeuTyrPheThrProArgAsn 100
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                                                                                                                                                                     1 MetAlaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAlaGluAsnLeu
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                                                                                                                                                                                                                              21 HisValLysIleSerCysSerLeuAspTrpLeuMetValSerValIleProValAlaGlu
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Matches:
Conservative:
Mismatches:
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100.0%
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Alignment Scores:
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ABG97353 standard; protein; 158 AA

RESULT 2

ABG97353

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The invention relates to an isolated polypeptide comprising CGDD1-12 (cell growth, differentiation and death), a naturally occurring amino caid sequence at least 90% identical to CGDD, a biologically active caid sequence at least 90% identical to CGDD, a biologically active fragment or an immunogenic fragment. Also included are the polymucleotides encoding CGDD1-12, a recombinant polymucleotide comprising a promoter sequence operably linked to the CGDD polymucleotides, a cell transformed with the recombinant polymucleotide, an anti-copy screening for compounds which bind to/modulate or are antibody, screening for compounds which bind to/modulate or are antibody, screening for compounds which bind to/modulate or are compliants of CGDD polymucleotide, polymucleotide and a cGDD polymucleotide microarray. The polypeptides, polymucleotides, agonists and antagonists are useful for diagnosing, treating or creventing disorders associated with aberrant expression of CGDD, particularly cell proliferative (e.g. arteriosclerosis, atherosclerosis, particularly cell proliferative (e.g. arteriosclerosis, atherosclerosis, cirrhosis, pepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia cyvera, psoriasis, primary thromobocytopaenia or cancer), developmental cycles (e.g. renal tubular acidosis, anaemia or mental retardation), creproductive disorders (e.g. infertility or a disruption in the menstrual cycle), or autoimmune/inflammatory disorders (e.g. AIDS, cycleroperosis, pancreatitis, rheumatoid arthritis, contact dermatitis, crohn's disease, diabetes mellitus, contact dermatitis, crohn's disease, diabetes mellitus, cycleoporosis, pancreatitis, rheumatoid arthritis, cycleoporosis, pancented arthritis, cycleoporosis, pancented arthritis, cycleoporosis, pancented arthriti
                                                                                                                rannamic of 19 years, disorder; arteriosclerosis; atherosclerosis; cell proliferative disorder; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; paroxysmal nocturnal haemoglobinuria; psoriasis; polycythaemia vera; primary thromobocytopaenia; developmental disorder; renal tubular acidosis; anaemia; mental retardation; epilepsy; AIDS; neurological disorder; Alzheimer disease; Parkinson's disease; asthma; reproductive disorder; infertility; autoimmune disorder; gout; allergy; inflammatory disorder; acquired immunodeficiency syndrome; uveitis; autoimmune thyroiditis; contact dermatitis; Crohn's disease; infection; diabetes mellitus; glomerulonephritis; Irritable bowel syndrome; multiple sclerosis; osteoarthritis; osteoporosis; pancreatitis;
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Burford N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human proteins associated with cell growth, differentiation and death, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), cancer, atherosclerosis or hepetitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Warren BA, Elliott VS,
TY, Lal PG, Duggan BM,
Khare R, Walia NK;
                                                                                                   Human; cell growth; differentiation; death; CGDD; cancer;
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J, Tang 1
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Richardson TW, Tran UK,
                                                 Human CGDD4, INCYTE 5284076CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-FEB-2001; 2001US-0268111P.
23-FEB-2001; 2001US-0271175P.
08-MAR-2001; 2001US-0274503P.
09-MAR-2001; 2001US-0274552P.
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Lu DAM,
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121 AGCAGAAATCTGTATATATTTGCGGATGAATTACATCTGGGAATGGGCTGCCCTGCAAAT 180
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sequences of proteins associated with CGDD. The present sequence represents a CGDD protein
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                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                             Sequence 158 AA;
                                                  Alignment Scores:
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The present invention relates to the isolation of human GSSP3
polypeptide, and polynucleotide sequences that encode it. The GSSP3
polypeptide reduces circulating blood glucose lavels, increases insulin sensitivity, and/or reduces body mass. The GSSP3 polypeptide and sensitivity, and/or reduces are useful in serum glucose regulation, fatty polynucleotide sequences are useful in serum glucose regulation, fatty compositions comprising GSSP3 polypeptides are useful for controlling blood glucose levels, for treating metabolic-related diseases or compositions comprising GSSP3 polypeptides are useful for controlling blood glucose levels, for treating metabolic-related diseases or hyperlipidaemias, atheroscierosis, heart disease, hypertension, stroke, syndrome C, type I or II diabetes, diabetes related complications, microangiopathy, retinopathy, neuropathy, nephropathy, polycystic ovarian syndrome, ocular lesions, microangiopathic lesions, or syndromes such as acanthosis nighticans, leprechaunism and lipoatrophy). The polypeptides are also useful to improve physical performance during work or exercise, and to treat dyslexia, attention-deficit disorder, attention-deficit/hyperactivity disorder, and psychiatric disorders such as chizophrenia. The present sequence represents human GSSP3 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reducing circulating glucose levels or increasing insulin sensitivity, useful for reducing body mass or preventing body weight gain, comprises administering composition comprising GSSP3 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Chicca J, Yen-Potin F;
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Mismatches:
Indels:
/label= Mature_GSSP3_polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                           Bour BA,
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                                                                                                                                                                                                                                                                                                                                                                                                                           Salter-Cid L, Ebbets-Reed D,
                                                                                                                                                                                                          01-FEB-2002; 2002WO-IB001333.
                                                                                                                                                                                                                                                                                    02-FEB-2001; 2001US-0266156P.
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241 AGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT 300

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1. .17 /label= Signal_peptide 18. .158

Peptide Protein

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to novel human secreted proteins (ABR49633-ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins and their coding sequences (ACC50344-ACC50856). The proteins can detair coding sequences are useful for the preparation of a diagnostic or pharmaceutical composition for diagnosing or treating a cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary disorders (e.g., arrhythmia, tachycardia, cardiac arrest, coronary carteriosclerosis and mycoardial ischaemia), neural disorders, immune system disorders and/or cancerous diseases and conditions, for treating thrombosis and arteriosclerosis, for treating proliferation, to treat inflammation or infection, for treating thrombosis and arteriosclerosis, for treating or neurodegenerative conditions such as Alzheimer's disease and Parkinson's disease, to enhance bone and periodontal regeneration and aid in tissue caransplants or bone grafte, to prevent skin aging or hair loss, to stimulate growth and differentiation of haematopoietic cells and bone marrow cells when used in combination with other cytokines, to maintain or symmary tissues to increase or decrease differentiation or proliferation of corpus to metabolism. Note: The sequence data for this patent was published in
                           81 ArgValValSerGluGluThrLeuLeuPheGlnThrGluLeuTyrPheThrProArgAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human secreted proteins, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating cardiovascular disorders such as arrhythmia.
                                                                                                                                                                                                                                                                                                                              Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic; vulnerary; antiinflammatory; nootropic; neuroprotective; antiparkinsonian; gene therapy; human; cardiovascular disorder.
                                                                                 CTTACACCAGTTTCTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTATTGCTGAC
                                                                                                                                     TTTCAGACAACAGCAGAAGAGTTAGGATTATTA 453
                                                                                                                                                  Claim 13; SEQ ID NO 822; 1881pp; English
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                                                                                                                                                                                                                                                                                                      Human secreted protein, SEQ ID 822
                                                                                                                                                                                                                     ABR47931 standard; protein; 158
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; secreted protein; digestive disorder; gastrointestinal disorder; mouth; oesophagus; stomach; small intestine; large intestine; liver; biliary tract; pancreas; cancer; tumour; hyperproliferative disorder; immune disorder; inflammation; infection; wound healing; drug screening; chromosome identification; chromosome mapping; cytostatic; antiinflammatory; immunosuppressive; vulnerary; gene therapy.
                                                                                                                                                                                                                                                                                                    CATGTGAAAATAAGTTGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ArglleHisThrTyrValTyrGluPheIleTyrLeuValArgAspCysGlylleArgThr
                                                                                                                                                                                                                                                                                   1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCTGAGAACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human gene 165 encoded secreted protein HTELS08, SEQ ID NO:464.
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Mismatches:
Indels:
electronic format and is available from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Matches:
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Best Local Similarity:
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Pred. No.:
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DB:
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The invention relates to isolated nucleic acid molecules ADB91065-
ADB91844 and ADB91835-ADB91911 encoding human secreted proteins ADB91449-
ADB91844. Also disclosed is a recombinant vector comprising a
polymucleotide of the invention, and a recombinant host cell comprising
the recombinant vector. The polypeptide of the invention is useful in
clentifying a binding partner by contacting the polypeptide with a
binding partner, and determining whether the binding partner increases or
decreases activity of the polypeptide. The polypeptide, polynucleotide,
antibody or its fragment, agonist or antagonist are useful for preparing
antibody or its fragment for diagnosing or treating diabetes or
conditions related to diabetes. The present sequence is that of the human
immunoglobulin Fc portion used to generate fusion proteins, increasing
the stability of the fused protein as compared to the secreted protein
only. Note: The sequence data for this patent did not form part of the
printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences.
   1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCTGAGAACCTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid encoding a human secreted protein is useful in diagnosing treating diabetes or conditions related to diabetes.
                                                                                                                                                                                                                                                                                                                                                    Secreted protein; gene therapy; antidiabetic; diabetes; human.
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Matches:
Conservative:
Mismatches:
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                                                                                                   TTTCAGACAACAGCAGAAGAGTTAGGATTATTA
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                                                                                                                                                                                                                                                                                                              Human secreted protein #SEQ ID 621.
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                AB271190-AB271478 represent cDNAs corresponding to 178 human secreted protein genes, and ABP0011-ABP00299 represent the proteins they encode. AB271479 AB271479 represent human secreted protein genomic fragments. The invention also encompasses antibodies specific for the secreted proteins, the use of the secreted proteins in drug screening, and recombinant convectors and host cells comprising a nucleic acid of the invention. The secreted proteins, nucleic acids encoding them, antibodies or antibody fragments specific for the secreted proteins, and modulators of protein activity are useful for diagnosing, treating, ameliorating or preventing digestive disorders. Such conditions include disorders of the mouth, coesophagus, stomach, small intestine, large intestine, liver, biliary tract and pancreas, and include cancers of these organs and tissues. The secreted proteins and their nucleic acids may also be used in the treatment of immune disorders, and to promote wound healing. Nucleic acids of the invention may be used for chromosome identification, chromosome mapping, in gene therapy, for identifying individuals from minute biological samples, as hybridiantion probes, and smolecular weight in arkers. The present sequence represents a human secreted protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
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Matches:
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
                                                     (HUMA-) HUMAN GENOME SCI INC
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N-PSDB; ABZ71354.
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                                                                                                                                                                                                                                             AGCAGAAATCTGTATATTTTGCGGATGAATTACATCTGGGAATGGGCTGCCCTGCAAAT 180
                                                                                                                                                             81 ArgValValSerGluGluThrLeuLeuPheGlnThrGluLeuTyrPheThrProArgAsn 100
                                                                                                                                                                                                       antianaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid; antidiabetic; immunosuppressive; dermatological; nephrotropic; antiparkinsonian; neuroprotective; nootropic; antibacterial; virucide; fungicide; antiparastic; antiarteriosclerotic; vulnerary; cytostatic; haemopoletic; haematologic; anaemia; autoimmune disorder; rheumatoid arthritis; inflammation; Grave's disease; diabetes; systemic lupus erythematosus; glomerulonephritis; neurodegenerative; Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis; cancer; bacterial; viral; fungal; parastic infection; gene therapy;
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21 HisValLysIleSerCysSerLeuAspTrpLeuMetValSerValIleProValAlaGlu
                                                                                 SerArgAsnLeuTyrIlePheAlaAspGluLeuHisLeuGlyMetGlyCysProAlaAsn
                                                                                                             CGGATACATACATATGTATATGAGTTTATATATCTTGTTCGTGATTGTGGCATCAGGACA
                                                                                                                         ArgileHisThrTyrValTyrGluPheIleTyrLeuValArgAspCysGlylleArgThr
                                                                                                                                                    241 AGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT
                                                                                                                                                                                           ATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human secreted polypeptide for diagnosing, preventing or treating hematopoietic or hematologic disorders (e.g. anemia), autoimmune
                               CATGTGAAAATAAGTTGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAA
                                                                                                                                                                                                                                                                                    TTTCAGACAACAGCAGAAGAGTTAGGATTATTA 453
                                                                                                                                                                                                                                                                                                                                                                                              Human secreted protein - SEQ ID 971
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                                                                                                                                                                                                                                                                                                                                    ADC74338 standard; protein; 158
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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The invention relates to a novel human secreted polypeptide comprising a defined sequence given in the specification. The polypeptide, nucleic acid molecule, antibody, agoinst or antiagonist of the invention may be useful for preparing a composition for diagnosing or treating a haemopoietic or haematologic disorder such as anaemia, autoimmune disorders such as rheumatold arthritis, inflammation, Grave's disease, claseres systemic lupus erythematosus or glomerulomephritis, neurodegenerative disorders including Parkinson's disease and Alzheimer's atherosclerosis or cancer, as well as bacterial, viral, fungal or parasitic infections. The polypeptide may also be used during gene the rolypeptide with a binding partner and determining whether the binding partner increases or decreases the activity of the polypeptide. The current sequence is that of the human secreted protein of the
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or
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disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer
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                                                                  Claim 16; SEQ ID NO 971; 2272pp; English.
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Best Local Similarity:
Query Match:
DB:
                   atherosclerosis).
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Sequences AAB38121-B38396 represent the amino acid sequences of 62 human secreted proteins encoded by the genes AAC69512-C69587. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic diagnosis, treatment and prevention of: (a) autoimmune diseases e.g. rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms of the breast or liver; (c) cardiovascular disorders e.g. cardiac arrest; (d) cerebrachascular disorders e.g. cardiac arrest; (f) nervous system disorders e.g. Alzheimer's disease; (g) infections caused by bacteria, viruses and fungi; and (h) ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing collaral ocal proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid molecules encoding 62 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
                                                     Immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective; nootropic; antibacterial; virucide; fungicide; opthalmalogical; human; vulnerary; gene therapy; infection; secreted protein.
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                                                                                                                                                                                                                                                                                                                                                                                                      Shi Y;
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Florence KA, Moore PA,
                   Human secreted protein encoded by gene 17 clone HTELS08.
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, Olsen HS, Ebner R,
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26-APR-1999;
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Lafleur DW
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AGCAGAAATCTGTATATATTGCGGATGAATTACATCTGGGAATGGGCTGCCCTGCAAAT 180
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cell regeneration, membrane protein; signal transduction-related protein;
transcription-related protein; osteoporosis; neurological disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
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                                                                         CTTACACCAGTTTCTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTATTGCTGAC
CGGATACATACATATGTATATGAGTTTATATATCTTGTTCGTGATTGTGGCATCAGGACA
                ArglleHisThrTyrValTyrGluPhelleTyrLeuValArgAspCysGlylleArgThr
                                                         AGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT
                                                                                                                ATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGG
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                                                                                                                                                                                                                                                   Human protein encoded by clone TESTI20282420.
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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25-JAN-2002; 2002US-00350978.
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Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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Homo sapiens.

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for detecting the polynuclectide. The polynuclectides and encoded proteins are useful as pharmaceutical agents and many disease-related genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell respentation. Membrane proteins, signal transduction-related proteins, transcription-related proteins, disease-related proteins and genes encoding them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours. The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence presented is a protein of the invention. Note: Some of the sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the
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Best Local Similarity:
                                                                                                                                                                                                                                                                              Sequence 158 AA;
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The present invention relates to novel GENSET polynucleotides (ABZ36404-ABZ3691) encoding polypeptides (ABP75953-ABP75958). The polynucleotides and polypeptides are useful in screening and diagnostic assays for abnormal GENSET expression and/or biological activity. They are also useful for screening of compounds for treating or preventing GENSET-related disorders, such as heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, central nervous system (CNS), cardiovascular or gastrointestinal effects of the toxicity
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                                                                                                                                                                                                                                New GENSET polynuclectides and polypeptides, useful for treating heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, CNS, cardiovascular or gastrointestinal effects of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 HisValLys11eSerCysSerLeuAspTrpLeuMetValSerValI1eProValAlaGlu
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Matches:
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                                                                                             18-APR-2001; 2001WO-IB000914.
                                                                                                                        18-APR-2001; 2001WO-IB000914
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Best Local Similarity:
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                                       WO200283898-A1
                                                                                                                                                   (GEST ) GENSET
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The invention relates to full length GENSET human nucleic acids encoding potentially secreted proteins. The nucleic acids and the polypeptides they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GENSET gene expression. For example, they be used to treat disorders associated with decreased GENSET gene expression by rectifying mutations or deletions in a patient's gene expression by rectifying mutations or deletions in a patient's can patients own production of GENSET polypeptides. Conversely, antisense nucleic acid molecules may be administered to down regulate GENSET expression. The sense and antisense nucleic acids may also be used as DNA probability and quantitate the presence of symbolic acid sequences in samples, and hence to determine which similar nucleic acid sequences in samples, and hence to determine which patients may be in need of restorative therapy. The GENSET polypeptides
                                                                                                                                                                                                                                                                                         CTTACACCCAGTTTCTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTATTGCTGAC
       SerArgAsnLeuTyrIlePheAlaAspGluLeuHisLeuGlyMetGlyCysProAlaAsn
                                             CGGATACATACATATGTATATGAGTTTATATATCTTGTTCGTGATTGTGGCATCAGGACA
                                                                   ArgileHisThrTyrValTyrGluPheIleTyrLeuValArgAspCysGlyIleArgThr
                                                                                                                      AGGGTAGTTTCTGAGGAAACTCTCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT
                                                                                                                                                                                               ATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGG
                                                                                                                                                                                                                      Full length GENSET human nucleic acids encoding potentially secreted proteins, useful in gene therapy and vaccination against a variety of diseases, and for diagnosis of those diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;
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|PheGlnThr 143
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N-PSDB; AAH64748.
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                                                                                                                                                                                                                                                              Cytostatic; antiinflammatory; nootropic; neuroprotective; cardiant; gastrointestinal; gene therapy; GENSET; heavy metal toxicity; cancer; inflammatory disease; immune disorder; neuromuscular; toxicity; central nervous system; cardiovascular; gastrointestinal.
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TTTCAGACAACAGCAGAAGAGTTA
                                                                                                              ABP76237 standard; protein; 143
                                                                                                                                                                                                                              Human GENSET protein SEQ ID 787.
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Best Local Similarity:
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may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of GENSET polypeptide expression and activity. The present sequence is a GENSET polypeptide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 HisValLys1leSerCysSerLeuAspTrpLeuMetValSerVallleProValAlaGlu 40
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2001US-0336600P.
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                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                               Sequence 106 AA;
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07-DEC-2001; 2
12-DEC-2001; 2
17-DEC-2001; 2
                                                                     the invention
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                                                                                                                                                                                                                                                               Query Match:
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The invention relates to a novel isolated NOVX polypeptide. The cardiant, hypotensive, antiatreriosclerotic, virucide, antibacterial, cardiant, hypotensive, antiatreriosclerotic, virucide, antibacterial, fungicide, protozoacide, nootropic, neuroprotective, antiparkinsonian, anticonvulsant, osteopathic, antiatrhritic, antinilammatory.

Consideration incleic acid molecules and antibaces may be useful for colypeptides, nucleic acid molecules and antibaces may be useful for treating or diagnosing diseases including metabolic disorders such as diabetes and obesity, infectious disease, anorexia cancer, cardiovascular diseases including hypertension and atherosclerosis, cardiovascular disorders such as Alzheimer's disease, Parkinson's disease and epilepsy, immune disorders, asthma and dyslipidaemia.

Confiscorers, inflammatory skin disorders, asthma and dyslipidaemia.

Furthermore, the nucleic acids and polypeptides may also be used to defferentiation and proliferation, haemopoiesis, wound healing and andiogenesis, as well as in gene therapy. Finally, the nucleic acids may be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The current sequence is that of the human NOV protein of the invention.
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9 LeuMetIlleLeuLeuThrSerAlaLeuSerAlaGlySerGlyGlnSerProMetThrVal 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alsobrook JP, Alvarez E, Anderson DW, Baron M, Boldog FL;
Burgess CE, Casman SJ, Chapoval A, Dhanabal M, Edinger SR, Eisen A;
Blerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;
Grosse WM, Guo X, Hackett C, Ji W, Kekuda R, Khramtsov NV;
Lepley DM, Li L, Macdougall JR, Malyankar UM, Mazur A, Mcqueeney K;
Mezes PS, Miller CE, Millet I, Mishra VS, Padigaru M, Patturajan M;
Pena CEA, Peyman JA, Rastelli L, Rieger DK, Shenoy SG, Shimkets RA;
Smithson G, Starling G, Spytek KA, Stone DJ, Tchernev VT, Twomlow N;
Vernet CAM, Zerhusen BD, Zhong M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated NOVX polypeptides and polynuclectides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections.
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Conservative:
Mismatches:
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17-APR-2002; 2002US-037328BP.
15-MAY-2002; 2002US-037328BP.
17-MAY-2002; 2002US-0381495P.
28-MAY-2002; 2002US-0383534P.
29-MAY-2002; 2002US-0383829P.
29-MAY-2002; 2002US-0383829P.
29-MAY-2002; 2002US-03884024P.
07-AUG-2002; 2002US-040178BP.
26-AUG-2002; 2002US-040178BP.
                                                                                                                                                                                                                                                                                                                                                                     31-OCT-2002; 2002US-00287971
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225.50
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N-PSDB; ADE28662.
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Best Local Similarity:
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GAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAATATAGATCATGAC 312
                                                                                                            366
AGTIGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAAAGCAGAAATCTG 132
                                                                                                                 9
              48
                                                                   88
                                                                                                                                                                                                       Human; NOVX; congenital heart defect; cardiomyopathy; atherosclerosis; hypertension; pulmonary stenosis; scleroderma; adenocarcinoma; haemophilis; graft-versus-host disease; cancer; neurodegenerative disorder. Alzheimer's disease; Parkinson's disease; multiple sclerosis; diabetes; obesity; bronchial asthma; acquired immunodeficiency syndrome; AlDS; Crohn's disease; infectious disease; anorexis immune disorder.
       49 CysValHisPheHisGluLeuHisLeuGlyLeuGlyCysProProAsnHisValGlnPro
                                                             CCTCAGGAA-----ATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGGCTTACA
                                                    193 TAIGTATATGAGTTTATATATCTTGTTGTGGCATCAGGACAAGGGTAGTTTCT
                                                                                                                                                  ADM93408 standard; protein; 212 AA
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2001US-0335162P.
2001US-0333912P.
2001US-0334300P.
2001US-0334300P.
2001US-0334300P.
2002US-0386968P.
2002US-0380968P.
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2001US-0333072P.
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2002US-0401626P
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2002US-0401695P
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                                                                                                                                                                                          Human NOVX polypeptide #20.
                                                                                                                                                                              (first entry)
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ANDERSON D W.
BARON M.
BOLDOG F L.
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29-NOV-2001;
29-NOV-2001;
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21-NOV-2001;
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16-MAY-2002;
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26-AUG-2002;
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(BOLD/)
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Alsobrook JP, Alvarez E, Anderson DW, Baron M, Boldog FL;
Burgess CE, Casman SJ, Chapoval A, Dhanabal M, Edinger SR, Eisen A;
Ellerman K, Ettenberg S, Gangolli EA, Gerlach V, Gorman L;
Grosse WM, Guo X, Hackett C, Ji W, Kekuda R, Khramtsov NV;
Lepley DM, Li L, Macdougall JR, Malyankar UM, Mazur A, Mcqueeney K;
Mezes PS, Miller CE, Millet I, Mishra V, Padigaru M, Patturajan M;
Pena CEA, Peyman JA, Rastelli L, Rieger DK, Rothenberg ME;
Shenoy SG, Shimkets RA, Smithson G, Spaderna SK, Starling G;
Spytek KA, Stone DJ, Trcherme VT, Twomlow N, Vernet CAM;
Zerhusen BD, Voss EZ, Zhong M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human NOVX polypeptides and the polynucleotides encoding them. The NOVX polypeptides and polynucleotides are useful for determining the presence of or predisposition to a disease associated with altered levels of the sequences in a mammalian subject, and for treating or preventing a pathology associated with NOVX. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated NOVX polypeptide useful treating or preventing disorders or syndromes such as Alzheimer's disease, Parkinson's disease, multiple sclerosis, diabetes, obesity, cancer, bronchial asthma, Crohn's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ROTHENBERG M E. SHENOY S G. SHINKERTS R A. SMITHSON G. SPADERNA S K. STARLING G. SPYTEK K A.
                                                                                                                                                                                                                                                                                                                                                                              MACDOUGALL J R.
                                                                                                                                                                                                                                                                                                                                                                                               MALYANKAR U M.
MAZUR A.
                                                                    ELLERMAN K.
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KHRAMTSOV N V.
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TCHERNEV V T.
TWOMLOW N.
                                                                                                                      ETTENBERG S.
GANGOLLI E A.
GERLACH V.
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PATTURAJAN M.
PENA C E A.
PEYMAN J A.
RASTELLI L.
RIEGER D K.
  CASMAN S J.
CHAPOVAL A.
DHANABAL M.
EDINGER S R.
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MILLER C E.
MILLET I.
MISHRA V.
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ZERHUSEN B I
VOSS E Z.
                                                                                                                                                                                                                                                                                                                                         LEPLEY D M.
                                                                                                                                                                                       GORMAN L.
GROSSE W M.
                                                                                                                                                                                                                                                   HACKETT C.
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(CASM)
(CHAP/)
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(EDIN/)
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(VOSS/)
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and antibodies that bind immunospecifically
                                             atheroscierosis, hypertension, pulmonary stenosis, scleroderma, adheroscierosis, hypertension, pulmonary stenosis, scleroderma, adenocarcinoma, haemophilia, graft-versus-host disease, cancer, neurodegenerative disorders, Alzhensier, disease, Parkinson's disease, multiple sclerosis, diabetes, obssity, bronchial asthma, acquired immunodeficiency syndrome (AIDS), Crohn's disease, infectious disease, anorexia and immune disorders. This sequence represents a human NOVX polypeptide of the invention. Note: The sequence data for this patent is also available from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 AGTIGCICTCTCGGACTGGTIGAIGGTCTCAGTTATCCCAGTIGCAGAAAGCAGAAATCTG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 GAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAATATAGATCATGAC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          313 CCTCAGGAA-----ATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGGCTTACA 366
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9 LeuMetIleLeuLeuThrSerAlaLeuSerAlaGlySerGlyGlnSerProMetThrVal 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune suppressor; haematopoiesis regulator; tissue growth; chemotaxis; activin/inhibin; chemokinesis; haemostasis; thrombolysis; receptor/ligand activity; anti-inflammatory; tumour inhibitor; cadherin/tumour invasion suppressor.
polypeptides, polynucleotides and antibodies that bind immunospecifica to the polypeptides are useful for treating or preventing disorders or syndromes such as congenital heart defects, cardiomyopathy,
                                                                                                                                                                                                                                                                                                                                                                                           GTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCTGAGAAACCTCCATGTGAAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 TATGTATATGAGTTTATATATATCTTGTTGTGGCATCAGGACAAGGGTATTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secreted protein; human; nutritional supplements; immune stimulant;
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40
33
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                               Sequence 212 AA;
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Best Local Similari
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Pred. No.:
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DB:
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This sequence represents a human secreted protein of the invention. The DNA encoding this sequence was isolated from a human adult placenta CDNA library, and was designated clone ej265.4. The DNAs and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Although no supporting data is given. Suggested activities include nutritional sources or supplements, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemocatic/chemokinneic activity, haemostatic and thrombolytic activity, receptor/ligand activity, and inflammatory activity. The DNAs are also stated to be useful for gene therapy. A host cell transfected with the DNA, or its subfragments and variants is useful for recombinant production of the human secreted
                                                                                                                                                                                                                                                                                   New polynucleotides encoding secreted human proteins - derived from human foetal brain, adult brain, foetal kidney, adult ovary, adult retina, adult placenta or adult uterus cDNA libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 AGTIGCICICIGGACIGGITGAIGGICICAGTIAICCCAGTIGCAGAAAGCAGAAAICIG 132
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Search completed: May 9, 2006, 10:04:48 Job time: 92.9 secs

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Sequence 3903, Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:

APPLICANT: Dunas Milne Edwards, J.B.

APPLICANT: Glordano, J.Y.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2.

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT PILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SEQ ID NO 3903

LENGTH: 153
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ORGANISM: Homo sapiens
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-G=/abss/ABSSWEB spool/U310664025/runat 08052006 173459 28431/app_query.fasta_1
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-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-NCDN=6 -ICPD=3 -NO MMAP -NGG_SCORE=0 -MAIT -DSPBLCCK=100 -LONGLOG
-NCDN=6 -ICPD=3 -NO MMAP -NGG_SCORE=0 -MAIT -DSPBLCCK=100 -LONGLOG
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Sequence 5222, Ap
Sequence 3674, Ap
Sequence 11232, A
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3: /cgn2_6/ptodata/1/iaa/HCOMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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US-09-621-976-5222
US-10-104-047-3674
US-09-621-976-5223
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US-09-513-975-6447
US-09-723-806A-8
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Patent No. 6943241

GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
1TILE OF INVENTION: No. 6943241e1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE:
PRIOR APPLICATION NUMBER:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3674
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CRGANISM: Homo sapiens
US-10-104-047-3674
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                                                                                                                                                                                                                                                                                                             Sequence 5222, Application US/09621976
Patent No. 639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054FR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5222
LENGTH: 158
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ORGANISM: Homo sapiens
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Query Match:
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; NAME/KEY: SIGNAL
; LOCATION: -17..-1
US-09-621-976-5222
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US-09-621-976-5222
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Pred. No.:
                                          121
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2000-04-14
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   CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                         ORGANISM: Human
                                                                                                                                                                                                                          US-09-949-016-11232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
US-09-621-976-6447
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                                                                                                                                                                                                                                                            Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 56
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Patent No. 681239
Patent No. 6812339
Fatent No. E812339
Fatent No. E812339
Fatent INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
                                                 101 IleAspHisAspProGlnGluIleHisLeuGluCysSerThrSerArgLysSerValTrp 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGATACATACATATGTATATGAGTTTATATATCTTGTTCGTGATTGTGGCATCAGGACA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CATGTGAAAATAAGTTGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 AGCAGAAATCTGTATATATTTGCGGATGAATTACATCTGGGAATGGGCTGCCCTGCAAAT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCTGAGAACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-664-025-43_COPY_S3_511 (1-459) x US-09-621-976-5223 (1-106)
                                                                                                                                                                                                                                                 APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054 PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT APPLICATION NUMBER: US/09/621,976
SOFTWARE: Patent.pm
SEQ ID NO 5223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
                                                                                           421 TITCAGACAACAGCAGAAGAGITAGGATTATTA 453
                                                                                                                  Indels:
Gaps:
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Patent No. 6639063
GENERAL INFORMATION:
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100.0%
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 AGGGTA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 Argval 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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US-09-621-976-5223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-09-949-016-11232
                                                                                                                                                                                    -09-621-976-5223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
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73 AGTIGCICITGGACIGGITGAIGGICTCAGITAICCCAGITGCAGAAAGCAGAAAICIG 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 GAGGAAACTCTCTTTTCAAACCGAGCTGTACTTTACCCCAAGGAATATAGATCATGAC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313 CCTCAGGAA-----ATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGGCTTACA 366
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13 LeuMetIleLeuLeuThrSerAlaPheSerAlaGlySerGlyGlnSerProMetThrVal 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 LeuCysSerIleAspTrpPheMetValThrValHisProPheMetLeuAsnAsnAspVal 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 GTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCTGAGAACCTCCATGTGAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-664-025-43_COPY_53_511 (1-459) x US-09-949-016-11232 (1-216)
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Patent No. 663963

GENERAL INFORMATION:
APPLICANT: Unas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 6447
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FLING DATE: 2000-10-20
PRIOR FLING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-03
PRIOR PELING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11232
LENGTH: 216
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TGCCCTGCAAATCGGATACATACATATGTATATGAG----TTTATATATCTTGTTGGTGAT 225
                                        112 LeuGİyİİEThrAlaGlyAlaHisArgLeuTrpSerHisArgThrTyrLysAlaArgLeu 131
                                                                                                                                                                                 289 ACCCCAAGGAAT----ATAGATCATGACCTCAGGAAATCCATTTGGAGTGTTCCACC 342
                                                                                                                                                                                                                                                                       152 TrpAlaArgAspHisArgAlaHisHisLysPheSerGluThrHisAlaAspProHisAsn 171
                                                                                                                                                                                                                                                                                                                                                                                     373 TCTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTATTGCTGAC------- 420
                                                                                                                                                                                                                                                                                                                                                                                                                         192 ValLysGluLysGlyGlyLysLeuAspMetSerAspLeuLysAlaGluLysLeuValMet 211
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                                                                                                                                                                                                                                                                                                                                                172 serargargGlyPhePhePheSerHisValGlyTrpLeuLeuValArgLysHisProAla 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||||||::: ::: |||
73 ArgAsnIleIleLeuMetAla---LeuLeuHisValGlyAlaLeuTyrGlyIleThrLeu 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 IGCCCIGCAAAICGGAIACAIACAIAIGIAIAIGAG---IIIIAIAIAICIIGIICGIGAI
                                                                                                                                                                ----AGGACAAGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/09723806A
; Sequence 8, Application US/09723806A
; Patent No. 6686185
; GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: USES THEREFOR
TILLE OF INVENTION: USES THEREFOR
FILE REFERENCE: 10448-024001
; CURRENT PRILING DATE: 2000-11-28
; PRIOR RAPPLICATION NUMBER: US/09/723,806A
; PRIOR PRILING DATE: 2000-11-28
; PRIOR PELING DATE: 2000-13-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 AGAAATCTGTATATATTTGCGGATGAATTACATCTGGGA-------
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Matches:
Conservative:
Mismatches:
Indels:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
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Best Local Similarity:
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CRGANISM: Rattus
US-09-723-806A-8
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                                                                                                                                  21 ProValSerThrGluAsnGluIleLy8LeuAspProSerProPheIleAlaAspPheGln 40
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73 ArgAsnIleIleLeuMetAla---LeuLeuHisValGlyAlaLeuTyrGlyIleThrLeu 91
                                                                                                           308 ATGACCCTCAGGAAATCCATTTGGAG-TGTTCCACCTCTAGGAAATCAGTGTGGCTTACA
                                                                      US-10-664-025-43_COPY_53_511 (1-459) x US-09-621-976-6447 (1-56)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/558,823
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGRIT INFORMATION:
NAME: ROGALSKY E8G., Peter
REGISTRATION NUMBER: 38,601
REFERENCE/DOCKET NUMBER: 19603/400
TELEROMNICATION INFORMATION:
TELEROMNICATION INFORMATION:
TELEROMNICATION INFORMATION:
TELERATION E9603-1600
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 anino acids
TYPE: amino acid
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CITY: Rochester STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
Mismatches:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Knipple, Douglas C.
APPLICANT: Roelofs, Wendell L.
APPLICANT: Roller, Stuart J.
TITLE OF INVENTION: PHEROMONE DESATURASES
CORRESPONDENCE: 19
                     Indels:
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                                    Gaps:
                                                                                                                                                                                                                                                                             41 ThrThrAlaGluGluLeuGlyLeuLeu 49
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COMPUTER REARBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                  US-08-558-823-19; Sequence 19, Application US/08558823; Patent No. 5876994; GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
Best Local Similarity:
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                 Query Match:
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                      304 GATCATGACCCTCAGGAAATC-----CATTTGGAGTGTTCCACCTCTAGGAAATCAGTG 357
                                                                                                                                                                                                                                                                        Sequence 3954, Application US/09107433
Patent No. 6800744
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                                                                                                                                                                         406 CCTTTTATTGCTGACTTTCAGACAACAGCAGAAGAGTTAGGATTATTAATCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
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Matches:
Conservative:
Mismatches:
Indels:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/05153
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (B) LÖCATION 1...165
SEQUENCE DESCRIPTION: SEQ ID NO: 3954:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 3954:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 amino acida
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
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Query Match:
DB:
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Pred. No.:
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No
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Sequence 3248, Application US/09583110

Sequence 3248, Application US/09583110

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

FILE REFERENCE: PATHOU-07A

CURRENT APPLICATION NUMBER: US 09/107,433

PRIOR FILING DATE: 1998-06-30

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1998-05-12

NUMBER OF SEQ ID NOS: 5322

LENGTH: 158
                                                                   289 ACCCCAAGGAAT----ATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACC 342
                                                                                           -----AGGACAAGGGTAGTTTCTGAGGAAACTCTCTTTTTCAAACCGAGCTGTACTTT 288
                      |||| ::::::|||
|32 ProLeuArgIlePheLeuIleIleAlaAsnThrMetAlaPheGlnAsnAspValTyrGlu 151
                                                                                                                                                                        373 TCTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTATTGCTGAC------ 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 SerGlnAsnLysGlnLysTrpHisIleTyrAlaGlyGln---TyrLeuGlyThrGlyLeu 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuValGlyAlaSerLeuValAlaAlaTyrValValAsnPheValProGluGluTrpMet 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 ValGlyLeuLeuGlyLeuIleProlleTyrLeu-------GlylleArgPheAla 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1
                                                                                                                                            343 ICTAGGAAATCAGTG-----CCAGTT
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                                                                                                                                                                                                                                                                                                             11|||||||::: |||||||||::: 212 PheGlnArgArgTyrTyrLysProGlyLeuLeuLeu
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Matches:
Conservative:
Mismatches:
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86 IleValGlyGluAspAla---
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Sequence 7887, Application US/09328352
Batent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7887
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                                                                                                                                                  ------GlubeutyrbeutrpProlleAshAla 235
                                                                                                                                                                                        GATCATGAC-----CCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTG 357
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236 AspGlnGlnGlyThrProGlnGlnValArgLysValIleAspThrMetLysLysGlu--- 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 GlnAlaGluThrArgGlnLysGluTyrGluSerSerArgGlnProAspAlaIleAspPhe 129
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                                                ATACATACATATGTATATGAGTTTATATATATCTTGTTCGTGATTGTGCCATCAGGACAAGG
                                                                    190 ACATATGTATATGAGTTTATATATCTTGTTGTGATTGTGGCATCAGGACAAGGGTAGTT
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US-09-328-352-7887
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Best Local Similarity:
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US-09-328-352-7887
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Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al

TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: WUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 2709.20104001
CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR PILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342
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|149 TrpMetSerAlaAspAsnAlaLeuIleTyrValAspAsnIleArgAspAlaLeuValLys 168
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                                                                                                    -----AGCAGAAATCTGTATATTTGCGGATGAATTACATCTGGGAATGGGC--- 168
                                                                                                                                                                                                                                            -----ATATATCTTGTGGGATTGTGGCATCAGGACAAGG 243
                                                                                                                                                                                                                                                                                                              244 GTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAATATA 303
                                                                                                                                                                                                                                                                                                                                                                                304 GATCATGACCTTCAGGAAATC----CATTTGGAGTGTTCCACCTCTAGGAAATCAGTG 357
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                                                  18 ValTyrileSerThrSerileAspTyrLeuileileLeuileileLeuPheAlaGlnLeu 37
                                                                                                                      38 SerGlnAsnLysGlnLysTrpHisIleTyrAlaGlyGln---TyrLeuGlyThrGlyLeu 56
                                                                                                                                                                                           86
                                                                                                                                                                                                                                                                            77 ValGlyLeuLeuGlyLeuIleProileTyrLeu------GlyIleArgPheAla 92
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                                                                                                                                                                        ---TGCCCTGCAAATCGGATACATACATATGTATATGAGTTT---------
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US-10-664-025-43_COPY_53_511 (1-459) x US-09-107-433-3954 (1-165)
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Conservative:
Mismatches:
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76.00
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Best Local Similarity:
Query Match:
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US-09-489-039A-10162
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LENGTH: 323
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253 GAGGAAACTCTCTTTTTCAAACCGAGCTGTACTTTACCCCCAAGGAATATAGATCAT--- 309
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                                                                                                          73 ProGluAsnCysGluProLeuIleSerGlyAspSerAspAspThrValArgPheGluVal 92
    RESULT 14
US-08-484-158B-18
is Sequence 18, Application US/08484158B
is Patent No. 5976545
is GENERAL INFORMATION:
APPLICANT: Harris Ph.D., Jeffrey D.
APPLICANT: Harris Ph.D., Jeffrey D.
TITLE OF INVENTION: Pharmaceutical Compositions for TITLE OF INVENTION: Immunocontraception
invention of Sequences:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Applicant Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OFENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/484,158B
FILING DATE: 07-JUNE-95
CLASSIFICATION: 514
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COUNTRY: United States of America
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APPLICATION NUMBER: 08/149,223
FILING DATE: 09-NOV-93
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/012,990
FILING DATE: 29-JAN-93
PRIOR APPLICATION NUMBER: 07/973,341
FILING DATE: 09-NOV-92
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
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INFORMATION FOR SEQ ID NO:
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REGISTRATION NUMBER: 3
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                                                                                                                                           APPLICANT: Harris Ph.D., Jeffrey D.
APPLICANT: Hau, Kuang T.
APPLICANT: Hou, Kuang T.
APPLICANT: Podolski, Joseph S.
TITLE OF INVENTION: Materials and Methods for Immunocontraception
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
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COUNTRY: United States of America

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
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COMPUTER: PATENTIN NOV-1993
FILING DATE: 09-NOV-1993
PRIOR APPLICATION NUMBER: 08/012,990
FILING DATE: 29-JAN-1993
PRIOR APPLICATION NUMBER: 09-NOV-1993
PRIOR APPLICATION NUMBER: 09-NOV-1993
PRIOR APPLICATION NUMBER: 09-NOV-1993
ATPORNEY/AGENT INPORMATION:
NAMM: AMMER: 09-NOV-1992
ATPORNEY/AGENT INPORMATION:
NAMM: AMMER: 09-NOV-1992
NAMM: AMMER: 09-NOV-1992
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                                                                             Sequence 18, Application US/08484993B
Patent No. 5837497
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6653
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INFORMATION FOR SEQ ID NO: 18:
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amino acid
190 SerAlaThrGlu 193
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STREET: 6300 Sear
CITY: Chicago
STATE: Illinois
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105 GluAspAlaLeuValTyrSerThrPheLeuLeuHisAsnProArgProMetGlyAsnLeu 124
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56 AsnLeuPheGlyThrGlyArgLeuValArgProAlaAspLeuThrLeuGly------
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Patent No. 5981228
GENERAL INFORMATION:
APPLICANT: Harris Ph.D., Jeffrey D.
APPLICANT: Podolbki, Joseph S.
TITLE OF INVENTION: Materials and Methods for Immunocontraception NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                     1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCT--
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Conservative:
Mismatches:
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CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
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156 ValProPheArgThrThr 161
              LENGTH: 424 amino acids TYPE: amino acid
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75.50
37.18
22.68
9.18
SEQUENCE CHARACTERISTICS
                             TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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Best Local Similarity:
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                                                                           US-08-484-158B-18
                                                                                                           Alignment Scores:
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56 AsnLeuPheGlyThrGlyArgLeuValArgProAlaAspLeuThrLeuGly----- 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              310 ------GACCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424
427
27
50
67
                   MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
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Matches:
Conservative:
Mismatches:
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                                                                                   SOFTWARE: Patentin Release #1.0, v
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,596A
                                                                                                                                                                   PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER:
11-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
07/973,341
FILING DATE: 09-NOV-1992
ATTONREY/AGRET INFORMATION:
NAME: CLOUGH, DAVIG W.
REGISTRATION NUMBER: 36,107
                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6653
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amino acid
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Sequence 260, Application US/09731872
| Sequence 260, Application US/09731872
| Patent No. US20020102604A1
| GENERAL INFORMATION:
| APPLICANT: Dumas Milne Edwards, Jean Baptiste
| APPLICANT: Dumas Milne Edwards, Jean Baptiste
| APPLICANT: Dobert, Severin
| TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
| FILE REFERENCE: 78 US/09/731,872
| CURRENT APPLICATION NUMBER: US/09/731,872
| CURRENT PILING DATE: 1999-12-08
| PRIOR FILING DATE: 1999-12-08
| PRIOR PILING DATE: 2000-03-06
| NUMBER OF SEQ ID NOS: 482
| SEQ ID NO 260
| LENGTH: 158
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US-10-111-224-91

US-10-111-224-91

US-10-270-49-91

US-10-287-971-42

US-10-287-971-42

US-10-450-763-42407

US-10-450-763-42006

US-10-450-763-7701

US-10-10-864-761

US-10-10-864-151

US-10-10-864-151

US-10-10-11-30-14

US-10-17-12-14

US-10-17-12-14

US-10-17-12-14

US-10-756-149-5461

US-10-76-149-5461

US-10-78-111-16

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   ORGANISM: Homo sapiens
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Sequence 113, App
Sequence 3, Appli
Sequence 260, App
Sequence 3674, App
Sequence 2674, App
Sequence 265, App
Sequence 265, App
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Sequence 260, App
                                                                                               May 9, 2006, 10:09:27 ; Search time 16.29 Seconds (without alignments) 3531.927 Million cell updates/sec
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                                                                                                                                                                                         atggcgttagaagtcttgat.....agttaggattattaatcttc
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
               GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                   protein search, using frame_plus_n2p model
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US-10-876-997-260
US-10-467-535-4
US-10-798-512-113
US-10-798-512-113
US-10-463-86260
US-10-472-533-464
US-10-10-472-533-464
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Maximum Match 100%
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238, App 5461, Ap 42, Appl 40643, A 2111, Ap 253855,

6, Appli 8, Appli 147028,

9, Appli 35932, A 42, Appl

14, Appl 14, Appl 309950,

741, App 151, App

3954, Ap 3336, Ap 8692, Ap 11647, A

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61 CATGTGAAAATAAGTTGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAA 120
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                                                                   21 HisvallysileSerCysSerLeuAspTrpLeuMetValSerVallleProValAlaGlu 40
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Mismatches:
Indels:
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Matches:
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Publication No. US20030050442A1

GENERAL INFORMATION:

TITLE OF INVENTION: 62 Human Secreted Protein

FILE REFERENCE: P2039P1

CURRENT APPLICATION NUMBER: US/10/050,704

CURRENT FILING DATE: 2002-01-18

PRIOR APPLICATION NUMBER: OF/050,08979

PRIOR PILING DATE: 2000-10-10

PRIOR PILING DATE: 2000-10-10

PRIOR PILING DATE: 1999-04-05

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

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PRIOR FILING DATE: 1999-04-09

SEQ ID NOS: 344

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 150
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Best Local Similarity:
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Pred. No.:
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US-09-876-260

US-09-876-260

Sequence 260, Application US/09876997

Publication No. US20030152921A1

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Jobert, Lydie

APPLICANT: Jobert, Lydie

APPLICANT: Jobert, Lydie

TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS

FILE REFERENCE: 78.US4.CIP

CURRENT APPLICATION NUMBER: US 09/731,872

PRIOR APPLICATION NUMBER: US 60/187,470

PRIOR PLIING DATE: 2000-03-06

PRIOR FILING DATE: 1999-12-08

NUMBER OF SEQ ID NOS: 482

SEQ ID NO 260

SEQ ID NO 260

LENGTH: 158
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                          61 ArgileHisThrTyrValTyrGluPheIleTyrLeuValArgAspCysGly1leArgThr 80
                                                                                                 21 HisValLys1leSerCysSerLeuAspTrpLeuMetValSerVallleProValAlaGlu 40
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US-10-664-025-43_COPY_53_511 (1-459) x US-09-731-872-260 (1-158)
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ORGANISM: Homo sapiens
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                                                                                                                                                 61 CATGTGAAAATAAGTTGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAA
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                                       US-10-664-025-43_COPY_53_511 (1-459) x US-10-467-535-4 (1-158)
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GENERAL INCREMILLOW.

TITLE OF INVENTION: 62 Human Secreted Proteins
TITLE REFERENCE: PZ039P1
CURRENT APPLICATION NUMBER: US/10/798,512
CURRENT FILING DATE: 2004-03-12
FRIOR PILLING DATE: 2000-10-10
FRIOR APPLICATION NUMBER: PCT/US00/08979
FRIOR APPLICATION NUMBER: PCT/US00/08979
FRIOR FILING DATE: 2000-04-06
FRIOR APPLICATION NUMBER: 60/128,693
FRIOR FILING DATE: 1999-04-09
FRIOR PILING DATE: 1999-04-09
FRIOR APPLICATION NUMBER: 60/130,991
FRIOR PILING DATE: 1999-04-05
NUMBER: OF SEQ ID NOS: 344
SOPTWARE: PAGENTIN VET: 2.0
SEQ ID NO 113
LENGTH: 158
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ORGANISM: Homo sapiens
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Best Local Similarity:
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APPLICANT: YUE, Henry; YAO, Monique G.
APPLICANT: SUGN, CTaig H.; LU, Yan
APPLICANT: BAUGSH, Bridget A.; ELLOTT, Vicki S.
APPLICANT: BAUGSH, Mariah R.; DING, Li
APPLICANT: WARREN, Bridget A.; ELLOTT, Vicki S.
APPLICANT: TAN, Yuming; GIETZEN, Kimberly J.
APPLICANT: TAN, Yugen K.; KHARE, Reena
APPLICANT: TAN, Uyen K.; KHARE, Reena
APPLICANT: TIAN, Uyen K.; KHARE, Reena
APPLICANT: CINVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
FILE REFERENCE: PF-0903 USN
CURRENT FILING DATE: 2003-08-08
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-03
PRIOR APPLICATION NUMBER: US 60/221,175
PRIOR PRILING DATE: 2001-02-03
PRIOR PILING DATE: 2001-02-03
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
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Mismatches:
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No:
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LENGTH: 158
TYPE: PRT
ORGANISM: Homo sapiens
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Query Match:
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US-10-49-486-260, Application US/10643836

j Sequence 260, Application US/10643836

j Bublication No. US20050096458A1

GENERAL INFORMATION:

APPLICANT: Unmas Millne Edwards, Jean Baptiste

APPLICANT: Bougueleret, Lydie

APPLICANT: Bougueleret, Lydie

APPLICANT: Bougueleret, Lydie

TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS

TITLE REFERENCE: 78 USJ.REG

CURRENT APPLICATION NUMBER: US/10/643,836

CURRENT FILING DATE: 2000-12-07

PRIOR APPLICATION NUMBER: US 60/169,629

PRIOR APPLICATION NUMBER: US 60/169,629

PRIOR PILING DATE: 2000-03-06

NUMBER OF SEQ ID NOS: 482

SOFTWARE: Patent.pm

SEQ ID NO 260

LENGTH: 158
                                                                                                      121 AGCAGAAATCTGTATATATTTGCGGATGAATTACATCTGGGAATGGGCTGCCCTGCAAAT 180
                                                                                                                                                                          ATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGG 360
  CATGTGAAAATAAGTTGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAA 120
                                                                                                                                                            241 AGGCTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT 300
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Matches:
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ORGANISM: Homo sapiens
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Best Local Similarity:
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LOCATION: -17...-1
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Publication No. US20040235709A1

GENERAL INFORMATION:

APPLICANT: Salter-Idd, Luisa

APPLICANT: Chicca, Barbara A.

APPLICANT: Chicca, John

APPLICANT: Chicca, John

APPLICANT: Chicca, John

APPLICANT: Chicca, John

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APPLICANT: Chicca, John

APPLICANT: Chicca, John

APPLICANT: Chicca, John

APPLICANT: Chicca, John

APPLICANT: Bhain, Bernard

FILE REFRENCE: G-102US03RG

CURRENT APPLICATION NUMBER: US/10/467,046

CURRENT APPLICATION NUMBER: US/0266,156

PRIOR FILING DATE: 2001-02-02

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PatentIn version 3.0

SEQ ID NO 3

LENGTH 158
                                                                                                                                              301 ATAGATCATGACCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGG 360
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                                                      21 HisValLys1leSerCysSerLeuAspTrpLeuMetValSerVallleProValAlaGlu 40
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ORGANISM: Homo sapiens
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; LOCATION: (1)..(17)
US-10-467-046-3
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US-10-467-046-3
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   ATAGATCACCCTCAGGAAATCCATTTGGAGTGTTCCACTCTAGGAAATCAGTGGG
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                                                                                                                                                                                                                                                                                                           ASOLIA 1970-104-047-3674

Sequence 3674, Application US/10104047

Sequence 3674, Application US/10104047

Sequence 3674, Application US/10104047

SEQUENCE OF INTERCATION:

APPLICANT: HELIX RESEARCH INSTITUTE

TITLE OF INVENTION: NO. US20030236392A1e1 full length cDNA

FILE REFERENCE: H1-A0105

CURRENT FILING DATE: 2002-03-25

PRIOR PILING DATE: 2002-03-25

NUMBER: OF SEQ 1D NOS: 4096

SOFTWARE: PATENTIN VEY: 2.1

SEQ 1D NO 3674

LENGTH: 158

TYPE: RT

TYPE: RT

CRANISM: HOMO Sapiens

US-10-104-047-3674
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HisValLysIleSerCysSerLeuAspTrpLeuMetValSerValIleProValAlaGlu 40
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                            121 AGCAGAAATCTGTATATATTTGCGGATGAATTACATCTGGGAATGGGCTGCCCTGCAAAT
                                                                                           CGGATACATACATATGTATATGAGTTTATATATCTTGTTCGTGATTGTGGCATCAGGACA
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Matches:
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Publication No. US20050197285A1
GENERAL INPORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Human Secreted Proteins
FILE REPRENCE: PS906CT
CURRENT APPLICATION NUMBER: US/10/472,533
CURRENT FILING DATE: 2003-09-20
PRIOR PEPLING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/331,287
PRIOR APPLICATION NUMBER: US 60/336,171
PRIOR APPLICATION NUMBER: US 60/306,171
PRIOR APPLICATION NUMBER: US 60/306,171
PRIOR APPLICATION NUMBER: US 60/306,171
PRIOR APPLICATION NUMBER: US 60/377,340
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/277,340
PRIOR APPLICATION NUMBER: US 60/277,340
PRIOR APPLICATION NUMBER: US 60/277,340
PRIOR APPLICATION NUMBER: US 60/277,340
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Score: 789.00
Percent Similarity: 100.0$
Best Local Similarity: 100.0$
Query Match: 95.5$
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US-10-472-533-464
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Sequence 265, Application US/10643836

Sequence 265, Application WS/10643836

Sequence 265, Application No. US20050096458A1

GENERAL INFORMATION:

APPLICANT: Dumas Miller Edwards, Jean Baptiste

APPLICANT: Dumas Miller Edwards, Jean Baptiste

APPLICANT: Dumas Miller Edwards, Jean Baptiste

APPLICANT: Dumas Miller Edwards, Jean Baptiste

APPLICANT: Dumas Miller Edwards, Jean

TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING FOTENTIALLY SECRETED PROTEINS

FILE REFERENCE: 78.US3.REG

CURRENT FILING DATE: 2003-08-19

FRIOR PELING DATE: 1200-12-07

PRIOR PELING DATE: 1209-12-08

PRIOR PILING DATE: 2000-30-6

NUMBER OF SEQ ID NOS: 482

SEQ ID NO 265

LENGTH: 106
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS FILE REFERENCE: 78. US4. CIP
CURRENT APPLICATION NUMBER: US 09/731,872
PRIOR PILING DATE: 2001-06-08
PRIOR PLILING DATE: 2000-12-00
PRIOR FILING DATE: 2000-12-00
PRIOR FILING DATE: 1999-12-08
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 482
SOFTWARE: PARENT. DATE: 1999-12-08
SOFTWARE: PARENT. DATE: 1999-12-08
SOFTWARE: PARENT. DATE: 1999-12-08
SOFTWARE: PARENT. DATE: 1999-12-08
SOFTWARE: PARENT. DATE: 1999-12-08
LENGTH: 106
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Matches:
Conservative:
Mismatches:
Indels:
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429.00
100.0%
100.0%
51.9%
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ORGANISM: Homo sapiens
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81 Argval 82
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Best Local Similarity:
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; NAME/KEY: SIGNAL
; LOCATION: -17..-1
US-09-876-997-265
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DB:
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Sequence 265, Application US/09731872

Patent No. US20020102604A1

GENERAL INPORMATION:

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Bougueleret, Lydie

APPLICANT: Jobert, Severin

TILLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS

FILE REFERENCE: 78.033.REG

CURRENT APPLICATION NUMBER: US 60/169,629

PRIOR APPLICATION NUMBER: US 60/169,629

PRIOR APPLICATION NUMBER: US 60/187,470

PRIOR APPLICATION NUMBER: US 60/187,470

PRIOR APPLICATION NUMBER: US 60/187,470

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PRIOR APPLICATION NUMBER: US 60/187,470

PRIOR APPLICATION NUMBER: US 60/187,470

PRIOR APPLICATION NUMBER: US 60/187,470

PRIOR APPLICATION NUMBER: US 60/187,470
                                361 CTTACACCAGTTTCTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTATTGCTGAC 420
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Matches:
Conservative:
Mismatches:
Indels:
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US-09-876-997-265
Sequence 265, Application US/09876997
Publication No. US20030152921A1
GENERAL INFORWATION:
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Dougueleret, Lydie
APPLICANT: Jobert, Severin
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ORGANISM: Homo sapiens
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81 ArgVal 82
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Best Local Similarity:
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; NAME/KEY: SIGNAL
; LOCATION: -17..-1
US-09-731-872-265
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US-09-731-872-265
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73 AGTIGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAAAGCAGAAATCTG 132
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9 LeuMet11eLeuLeuThrSerAlaLeuSerAlaGlySerGlyGlnSerProMetThrVal 28
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                                                                                                                                               US-10-664-025-43_COPY_53_511 (1-459) x US-10-287-971-40 (1-212)
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/745,763
FILING DATE: 18-Jun-2000
CLASSIFICATION: <un
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42
                            Conservative:
                                                   Mismatches:
Indels:
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ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Merberg, David
Treacy, Maurice
Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROFIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McCoy, John M.
LaVallie, Edward R.
Collins-Racie, Lisa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: SPUTUNGEY, SUZZAIDE A.
REGISTRATION NUMBER: 41, 323
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 203, Application US/09745763
Patent No. US20020065394A1
GENERAL INFORMATION:
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TELEFAX: (617) 976-5851
INFORMATION FOR SEQ ID NO: 203:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
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225.50
60.8%
33.3%
27.3%
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                         Percent Similarity:
Best Local Similarity:
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Sequence 40, Application US/10287971
Publication No. US20040067882A1
GENERAL INFORMATION:
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-48094
CURRENT APPLICATION NUMBER: US/10/287,971
CURRENT FILING DATE: 2001-11-05
PRIOR PELICATION NUMBER: 10/035,568
PRIOR FILING DATE: 2001-11-29
PRIOR PELICATION NUMBER: 60/336,626
PRIOR PELICATION NUMBER: 60/336,626
PRIOR PELING DATE: 2001-11-05
PRIOR PELING DATE: 2001-11-05
PRIOR PELING DATE: 2001-11-06
PRIOR PELING DATE: 2001-11-06
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PRIOR PELING DATE: 2001-11-09
PRIOR PELING DATE: 2001-11-09
PRIOR PELING DATE: 2001-11-09
PRIOR PELING DATE: 2001-11-09
PRIOR PELING DATE: 2001-01-09
PRIOR PELING DATE: 2002-07-07
PRIOR PELING DATE: 2002-07-07
PRIOR PELING DATE: 2002-07-07
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Conservative:
Mismatches:
Indels:
Gaps:
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                    ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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ArgVal 82
                                                                  ; NAME/KEY: SIGNAL
; LOCATION: -17..-1
US-10-643-836-265
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LENGTH: 212
TYPE: PRT
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9 LeuMetIleLeuLeuThrSerAlaPheSerAlaGlySerGlyGlnSerProMetThrVal 28
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Matches:
Conservative:
Mismatches:
Indels:
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Publication No. US20040002591A1
GENERAL INFORMATION:
APPLICANTION:
TITLE OF INVENTION: 50 Human Secreted Proteins
FILE REFERENCE: PZ016P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/047,021
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: US 60/262,066
PRIOR PILING DATE: 2001-01-18
PRIOR PILING DATE: 2001-11-28
PRIOR PLILING DATE: 2000-11-28
PRIOR PLILING DATE: 1999-03-04
PRIOR PLILING DATE: 1999-03-04
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PRIOR PLILING DATE: 1997-09-12
                                   TOPOLOGY: linear
ULE TYPE: protein
ENCE DESCRIPTION: SEQ ID NO: 203:
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                 STRANDEDNESS: <Unknown>
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223.50
60.0%
33.3%
TYPE: amino acid
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Best Local Similarity:
                                                   MOLECULE
SEQUENCE
US-09-745-763-203
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                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
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; OTHER INFORMATION: Xaa equals any amino acid
US-10-047-021-91
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PRIOR APPLICATION NUMBER: US 60/090,112
PRIOR FILING DATE: 1998-06-22
WUMBER OF SEQ ID NOS: 206
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 91
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Job time : 82.45 secs
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223.50
60.0%
33.3%
                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity:
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Perfect score:

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Sequence:

Scoring table:

Searched:

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Sequence 2662, Ap
Sequence 3014, Ap
Sequence 8, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 11, Appl
Sequence 12, Appli
Sequence 12, Appli
Sequence 5, Appli
Sequence 6908, Ap
Sequence 6908, Ap
Sequence 6908, Ap
                     Sequence 777,
Sequence 774,
Sequence 779,
Sequence 775,
                                                                                                                                                                                                  US-10-453-372-1154
US-10-453-372-1154
US-10-453-372-1154
US-10-453-372-1154
US-10-453-372-1154
US-10-453-372-1152
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US-10-127-340-1
US-10-11-937-2962
                                                                                           US-11-096-568A-8621
US-11-096-568A-8620
US-11-096-568A-8619
US-11-188-298-7840
US-11-045-004-81
US-11-072-512-3492
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US-11-183-205-8

US-11-227-340-8

US-11-227-340-11

US-11-255-794-12

US-11-255-794-5

US-11-255-794-5

US-11-079-463-6908

US-11-079-463-8891
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APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHIKO
APPLICANT: YOSHIKWA, TSUTOMU
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: MAGAHARI, KENJI
APPLICANT: MAGAHARI, XENJI
APPLICANT: MASHONO, YASUHIKO
ITIE OP INVENTION: NOVEL full length cDNA
FILE REFERENCE: 084335-0191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
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Sequence 3674, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
APPLICANT: ISOGAN, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
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SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YUKI
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OTSUKA, KAORU
APPLICANT:
APPLICANT:
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Sequence 788, App
Sequence 787, App
Sequence 1033, Ap
Sequence 773, App
                                                                                                                  May 9, 2006, 10:10:23 ; Search time 4.77 Seconds (without alignments) 1336.144 Million cell updates/sec
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             GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                   OM nucleic - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-11-072-512-3674
US-10-475-075-788
US-10-475-075-787
US-10-821-234-1033
US-10-995-561-773
                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                        235405 segs, 46284737 residues
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Match Length DB
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Database

95.0 93.8 91.0 27.1

785 775 752 223.5 85.5

Score

Result Š.

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RESULT 3

URANGE 10-475-075-787

Sequence 787, Application US/10475075

Publication No. US20060053498A1

GENERAL INFORMATION:
APPLICANT: Bejanin, Stephane
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Johert, Severinn
APPLICANT: Giordano, Jean-Yves
TITIE REFERENCE: G-081US03PCT:
CURRENT APPLICATION NUMBER: US/10/475,075

CURRENT APPLICATION NUMBER: US/10/475,075

CURRENT APPLICATION NUMBER: PCT/IB01/00914

PRIOR FILING DATE: 2003-10-17

NUMBER OF SEQ ID NOS: 918

SEQ ID NO 787

LENGTH: 143
                                                                                                                                                                                                                                                                                  241 AGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT 300
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Matches:
Conservative:
Mismatches:
Indels:
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -17..-1
    ORGANISM: Homo sapiens
                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                 ; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -17..-1
US-10-475-075-788
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Pred. No.:
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WESTEAL INFORMATION:

Publication No. US20060053498A1

Sequence 788, Application US/10475075

Publication No. US20060053498A1

Sequence 788, Application No. US20060053498A1

APPLICANT: Bejanin, Stephane

APPLICANT: Tanaka, Hiroaki

APPLICANT: Jobert, Severin

APPLICANT: Glordano, Jean-Yves

TITLE OF INVENTION: Pull.1-ength human cDNAs encoding potentially secreted proteins

FILE REFERENCE: G-081US03PCT

CURRENT APPLICATION NUMBER: US/10/475,075

CURRENT FILING DATE: 2001-04-18

FILE REFERENCE: G-081US03PCT

CURRENT PILING DATE: 2001-04-18

NUMBER OF SEQ ID NOS: 918

SEQ ID NO 788

LENGTH 148

LENGTH 148
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Matches:
Conservative:
Mismatches:
Indels:
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| PRIOR FILING DATE: 2001-11-05
| NUMBER OF SEQ ID NOS: 4096
| SOFTWARE: PatentIn Ver. 2.1
| SEQ ID NO 3674
| LENGTH: 158
| TYPE: PRT
| ORGANISM: Homo sapiens
| US-11-072-512-3674
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785.00
99.3%
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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Sequence 773, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERRENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 773
LENGTH: 3803
                                                                                                                                                                                                                                                                                                                       GAGGAAACTCTCTTTTTCAAACGGAGCTGTACTTTACCCCAAGGAATATAGATCATGAC 312
                                                                                                                                                                                                                                                                                                                                         73 AGTIGCICICIGGACIGGITGAIGGICICAGITAICCCAGITGCAGAAAGCAGAAAICIG 132
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13 LeuMetIleLeuLeuThrSerAlaPheSerAlaGlySerGlyGlnSerProMetThrVal 32
                                                                                                                                                 33 LeuCysSerIleAspTrpPheMetValThrValHisProPheMetLeuAsnAsnAspVal 52
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                                                                 13 GTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCTGAGAACCTCCATGTGAAATA
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Best Local Similarity:
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US-10-995-561-773
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GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Pree
FILE OF INVENTION: Methods for Diagnosis and Treatment of Pree
CURRENT APPLICATION WUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR PILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: PLE SEQ Genes Version 1.0
SEQ ID NO 1033
LENGTH: 216
                                                                                                                                                       US-10-664-025-43_COPY_53_511 (1-459) x US-10-475-075-787 (1-143)
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141 PheGlnThr 143
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; ORGANISM: Homo sapiens
US-10-821-234-1033
                                                                           Percent Similarity:
Best Local Similarity:
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US-10-821-234-1033
JS-10-475-075-787
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Pred. No.:
                               Alignment Scores:
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531 HisPheThrSerLeuGluLeuValProProSerThrLeuThrThrHisLeuLysAla 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----TCAGTGTGGCTTACACCAGTTTCT-----ACTGAGAATGAAATAAATTG 396
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FUDIcation No. US20050272054A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CENDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: CENDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARER: FastSEQ for Windows Version 4.0
SEQ ID NO 777
LENGTH: 5335
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354 LygLeuThrLeuAlaLysAsnThrLeuGln----------
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US-10-995-561-774
Sequence 774, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
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85.50
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25.4%
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459 GluPro 460
                                397 GATCCT 402
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Best Local Similarity:
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551 GluPro
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US-10-995-561-777
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US-10-995-561-777
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                                                                                                                                                                                                                                                                                                         Sequence 71, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS (TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastsEQ for Windows Version 4.0
LENGTH: 3960
                238 ACAAGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGG
                                                                                                  298 AATATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACC---TCTAGGAAA---
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Best Local Similarity:
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US-10-995-561-771
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; ORGANISM: Homo sapiens
US-10-995-561-779
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US-10-955-561-779

US-10-955-561-779

Sequence 779, Application US/10995561

Publication No. US20050272054A1

GENERAL INFORMATION:

TITLE OF INVENTION: CARDINOVASCULAR DISORDERS AND DRUG RESPONSE,

TITLE OF INVENTION: DETECTION AND USES THEREOF

TITLE OF INVENTION: DETECTION AND USES THEREOF

TITLE OF INVENTION: UNMARER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE FRAEERE FREESE FOR Windows Version 4.0

SEQ ID NO 779

LENGTH: 5415
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APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1559
CURRENT PELLING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 774
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Best Local Similarity:
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Sequence 775, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOCTHARRE: FactSEQ for Windows Version 4.0
SEQ ID NO 775
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--------AlaAspAlaAlaHisLeuGluSerGlyGlnProValGlnCysGlu 470
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511 ArgLeuGlnAspGluLeuValThrLeuArgLeuGluCysThrAsnLeuTyrArgLysGly 530
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531 HisPheThrSerLeuGluLeuValProProSerThrLeuThrThrHisLeuLysAla 550
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ORGANISM: Homo sapiens
US-10-995-561-775
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Best Local Similarity:
Query Match:
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US-11-096-568A-8620

Sequence 8620, Application US/11096568A

Sequence 8620, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1552PUS2

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT PILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 8620

LENGTH: 394
                                -GCGGATGAATTACATCTGGGAATG 165
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                                                                                                                                                                -----AGGGTAGTTTCTGAG 255
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175 ValLeuLeuAsnAspAsnAspPheAlaSerLysValPheCysAsnMetProSerGluGlu 194
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SerbeuleuSerGlnHisLeubeuHisGluAsnValAlaAspSerTyrLeuProLeuPro 60
                                                               61 AlaSerSerAsnMetTyrTrpPheSerLysAspGlnAlaSerAsnTyrGlnPheGlyPhe
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, OTHER INFORMATION: Ceres Seq. ID no. 15169116
US-11-096-568A-8620
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                                  118 GAAAGCAGAAATCTGTATATTT
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195 LysGlyCysIleCysPhe 200
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Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REPERENCE: 2750-1592PUS2
CURRENT APPLICANT: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
                                                                AAAATAAGTTGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAAAGCAGA 126
                                                                                                                                                                                                                456 -------AlaAspAlaAlaHisLeuGluSerGlyGlnProValGlnCysGlu 470
                                                                                                                                                                                                                                                178 AATCGGATACATACATATGTATATGAGTTTATATATTTTGTTTCGTGATTGTGGCATCAGG 237
                                                                                                                                                                                                                                                                   238 ACAAGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGG 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                -----TCAGTGTGGCTTACACCAGTTTCT-----ACTGAGAATGAAATAAAATTG 396
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21 LeuThrLeuAlaLeuTrpPheSerArgAspGlySerHisAspGluAspMetLysLeuIle 40
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                                               7 TTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCTGAGAACCTCCATGTG
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               US-10-664-025-43_COPY_53_511 (1-459) x US-10-995-561-775 (1-5464)
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| OTHER INFORMATION: Ceres Seq. ID
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ORGANISM: Glycine max
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551 GluPro 552
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US-11-096-568A-8621
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Pred. No.:
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LENGTH: 242
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Qy 118 GAAAGCAGAAATCTGTATATTTTGCGGATGAATTACATCTGGGAATG 165 Db 217 AlaSerSerAsnMetTYTTpPheSerLysAspGlnAlaSerAsnTyrGlnPheGlyPhe 236 Qy 166 GGCTGCCCTGCAAATCGGATACATACATATGATATATATTTTGTTCGTGAT 225 Db 237 AsnilaSerTxpAlaArgLeuHisValLeuGlyTyrAspIleTyrIleSerGlnAsp 255 Qy 226 TGTGGCATCAGGACA	RESULT 14 US-11-188-298-7840 Sequence 7840, Application US/11188298 Publication No. US20060075522A1 SERREAL INFORMATION: APPLICANT: Abad, Mark S. et al. TITLE OF INVENTION: GENES AND USES FOR FLANT IMPROVEMENT FILE REFERENCE: 38-21(53452)B CURRENT FILING DATE: 2005-0-22 PRIOR APPLICATION NUMBER: 60/592,978 RIOR APPLICATION NUMBER: 60/592,978 SEQ ID NO 7840 LENGTH: 460 TYPE: PRT ORGANISM: GIBBERELLA ZEAE PH-1 US-11-188-298-7840	Alignment Scores: Pred. No.: Scores:
0y 118 GAAAGCAGAAATCTGTATATTTTGGGGATGAATTACATCTGGGAATG 165 Db 213 AlaSerSerAsmMetTyTTTPheSerLysAspGlnAlaSerAsmTytGlnPheGlyPhe 232 0y 166 GGCTGCCTGCAAATCGGATACATACATATGTATATATATA	RESULT 13 US-11-096-568A-8619 Sequence 8619, Application US/11096568A Fublication No. US2060048240A1 Publication No. US2060048240A1 GENERAL INFORMATION: Sequence-Determined DNA Fragments and Corresponding Polypeptides TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides TITLE OF INVENTION: Therby FILE REFERENCE: 2750-1592PUS2 CURRENT APPLICATION NUMBER: US/11/096,568A CURRENT APPLICATION NUMBER: US/11/096,568A CURRENT SEQ ID NOS: 34471 SEQ ID NO 8619 LENGTH: 398 TYPE: PRT ORGANISM: Glycine max FEATURE: REACTION REACTION NAME/KFY: misc feature	JOCATION: (1)(1981) JOCATION: (1)(1981) JOCATION: (1)(1981) JOCATION: Ceres Seq. ID no. 15169115 JOTHER INFORMATION: Ceres Seq. ID no. 15169115 July

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NUMBER OF SEQ ID NOS: 2854
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| 171 CysGluIleAlaAspLeuProAspLeuAsnThrGlySerGluThrValLysLysValLeu 190
                                                                                                                    358 ----TGGCTTACACCAGTTTCTACTGAG-----AATGAAATAAAATTGGAT--- 399
                                                                                                                                    191 AsnAspTrp1leSerTrpLeuValThrGluTyrSerPheAspGlyIleArg1leAspThr 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
                                                          334 TGT------TCCACCTCTAGGAAATCAGG------
                                                                                                                                                                              400 -------CCTAGTCCTTTTATTGCTGACTTTCAGACAACAGCA 435
                                                                                                                                                                                                  211 ValLysHisValGluLysSerPheTrpProAspPheGlnLysAlaAla 226
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PRIOR FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: 10/257,023
PRIOR FILING DATE: 2002-10-08
PRIOR APPLICATION NUMBER: PCT/FR01/01118
PRIOR APPLICATION NUMBER: FC 00/04,629
PRIOR FILING DATE: 2000-04-11
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GOMEZ-LOPEZ, NURIA
MADUENIO, ENCARNA
PABLOS, BETRIZ DE
WEHLAND, JURGEN
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CURRENT APPLICATION NUMBER: US/11/045,004
CURRENT FILING DATE: 2005-01-28
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DOMINGUEZ-BERNAL, GUSTAVO
GARRIDO-GARCIA, PATRICIA
TIERREZ-MARTINEZ, ALBERTO
AMEND, ALEXANDRA
CHAKRABORTY, TRINAD
DOMANN, EUGEN
HAIN, THORSTEN
BERCHE, PATRICK
CHARBIT, ALAIN
DURANT, LIONEL
PEREZ-DIAZ, JOSE-CLAUDIO
BAQUERO, FERNANDO
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Publication No. US20060078901A1
GENERAL INFORMATION:
APPLICANT: BUCHRIESER, CARMEN
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COUVE, ELISABETH
RUSNIOK, CHRISTOPHE
FSIHI, HAFIDA
DEHOUX, PIERRE
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CHETOUANI, FARID
NEDJARI, HAFED
GLASER, PHILIPPE
KUNST, FRANCK
COSSART, PASCALE
DANIELS, JUSTIN
GOEBEI, WERNER
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ENTIAN, KARL-DIETER
HAUF, JORG
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KUHN, MICHAEL
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325 eAsnSerIleTyrAsnAsnLysGlyThrValMetValValSerThrArgAsnAsnGlyAl 345
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199 GlyIleAsnHisLeuHisTxpHisArgValPheAspLysAsp------
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                                                                                                    ORGANISM: Listeria monocytogenes US-11-045-004-81
SOFTWARE: Patentin version 3.3 SEQ ID NO 81 LENGTH: 440
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Maximum Match 100%
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
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seq length: 2000000000
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ALIGNMENTS

Accession: A60503
A; Residues: 1-22 ckIDA
A; Residues: 1-42.4 klassarian polymenter of come pellucida glycoprotein zp3
C; Species Mesocricetus auratus (golden hamster)
C; Species Mesocricetus auratus (golden hamster)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: A60503
R; Kinloch, R.A.; Ruiz-Seiler, B.; Wassarman, P.M.
Dev. Biol. 142, 414-421, 1990
A; Title: Genomic organization and polypeptide primary structure of zona pellucida glyco; A; Reference number: A60503; MUID:91078540; PMID:2257975
A; Reference or authors in A60503
A; Molecule type: DNA
A; Residues: 1-422 ckIDA
A; Residues: 1-422 ckIDA
A; Residues: 1-422 ckIDA
A; Cross-references: UNIPARC:UP100001744E3; GB:M63629
A; Note: the authors translated the codon CAA for residue 251 as Glu, and AGG for residue C; Comment: This sulfated glycoprotein in the zona pellucida of the cocyte is a receptor C; Superfamily: sperm-binding glycoprotein zP3; ZP domain homology
C; Keywords: glycoprotein; cocyte
F; 45-300/Domain: ZP domain homology cZPH>

422 51 30 66 71 12 Conservative: Mismatches: Indels: Length: Matches: Gaps: 0.0778 92.50 37.2% 23.4% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB: No.: Score:

x A60503 (1-422) US-10-664-025-43_COPY_53_511 (1-459)

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1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCTGAGAACCTC 60	=======================================	1 MetGlyLeuSerTyrGlnLeuLeuLeuCysLeuLeuLeuCysGlyGlyAla 17
CGCTGTCTTGATTTGGA		<i>ICYBLeuLeuLeuCygG</i>
AAGTCTTGATGCTCCT	=======================================	erTyrGlnLeuLeuLe
1 ATGGCGTTAG	=	1 MetGlyLeuS
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Command line parameters:

Command line parameters:

OMODELEframe+ n.2D; model - DEV-x1h

-0=/abs/ABSSWEB spool/US10664025/runat_08052006_173455_28373/app_query.fasta_1

-0=/abs/ABSSWEB spool/US10664025/runat_08052006_173455_28373/app_query.fasta_1

-DB=PIR -QFWT=fastan - SUPFIX=n.2p.rp - MINNATCH=0.1 - LOOPCL=0 - LOOPEXT=0

-UNITS-bite - START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi - LIST=45

-DOCALIGN=200 - THR_SCORE=pct - THR_MX=100 - THR_MN=0 - ALIGN=15 - MODELED

-OUTFWHT-ptc - NORM=SXt - HEAPSIZE=500 - MINLEN=0 - AMXLEN=200000000 - HOST=abss07

-USER=US10664025_@CGN 1 1 35_@runat 08052006_173455_28373 - NCPU=6 - ICPU=3

-NO WAAP - NEG_SCORES=0 - WAIT - DSPBLOCK=100 - LONGLOG - DEV_TIMEOUT=120

-NARN TIMEOUT=30 - THREADS=1 - XGAPPEXT=0 - XGAPPEXT=0.5 - FGAPPOP=6 - FGAPEXT=7

Command line parameters:

Total number of

Minimum DB E Maximum DB E

score:

Run on:

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Sequence:

Scoring table:

PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	sperm-binding qlyc	retinoblastoma bin	actin binding prot	actin binding prot	actin binding prot	MGC1 protein precu	hypothetical prote	stearoyl-CoA 9-des	thiamin biosynthes	probable bacteriop	cadmium resistance	hypothetical prote	hypothetical prote	hypothetical prote
DI	A60503	F48727	F42725	30847	T30849	T18346	70519	124699	482094	AE0152	195188	198055	T45895	33152
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Query Match	11.2	10.5	10.2	10.2	10.2	9.6	9.5	9.3	9.3	9.3	9.5	9.2	9.5	9.5
Score	92.5	86.5	84.5	84.5	84.5	79.5	78.5	77	76.5	76.5	92	16	9/	9/
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ATTTGCGGATGAATTACATCTGGGAAAATTGCGGAAAATTGCGGAAAATTGCGGAAATTACATCTGGGAAATTACTATTATTGTATTTGGAAACTCTCTTTTTCAAAAATGAGAAACTCCTTTTTCAAAAATGAGAAACTCTTTTTCAAAAAGAGAAATCCATTTTGGAGTATGAAATCCATTTGGAGTTATACATTTGGAGTATGAAATTCATTTGGAGTATTTTTTTT	CysGlu 413 LYCAGG 237 :::: :::: ::::: ::::::::::::::::::::	Oy Oy Oy Oy Oy Oy Oy Oy C,Species C	Db 494 LeuGlnIleLeuArgAspGluLy9TyTYrGlnLeuGluGluLeuAlaPheArgValMet 513 Qy 298 AATATAGATCATCACCACAGGAATCATTGGAGTGTTCCACCTCTAGGAAA 351 ii: iii iii
A.Title: Cloning and characterization of mouse ACF7, a novel member of the dystoning A.Reference number: 220900; MUID:97124842; PMID:8954775 A.Accession: T30847 A.Status: preliminary; translated from GB/EMBL/DDBJ A.Molecule type: mRNA A.Residues: 1-1885 <ber> A.Cross-references: UNIPARC:UPI000016D119; EMBL:UG7204; NID:g1675223; PID:g1675224 C.Genetics: A.Gene: mACF7</ber>	el member of the dystonin subf	Alignment Pred. No. Score: Percent S: Best Local Query Matc DB:	Alignment Scores: Pred. No.: Pred. No.: 84.50 Matches: 84.50 Matches: 84.50 Matches: Percent Similarity: 10.24 Mismatches: 25 Query Match: 2
tion: 4 ily: plectin; alpha-actinin actin-binding Scores:	domain homology; ribosomal protein S	<i>ර්</i> සි	CTGTCTTGAT
Pred. No.: 0.734 Length: 1885 Score: 84.56 Matches: 36 Percent Similarity: 41.5\$ Conservative: 23 Best Local Similarity: 25.4\$ Mismatches: 58 Query Match: 10.2\$ Indels: 25		Oy GD	AAAATAAGTTGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAAAGCAGA
. Gaps: 10-664-025-43_COPY_53_511 (1-459) x T30847 (1-1885)		රු සි	127 AATCTGTATATATTTGCGGATGAATTACATCTGGGAATGGGCTGCCCTGCA 177
OY 7 TTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGGGCTGAGAACCTCCATGTG	IGAGAACCTCCAIGIG 66 BLeuAsnCysGluGlu 448	ò a	178 AATCGGATACATATGTATATGGTTTATATATCTTGTTGTGATTGTGGCATCAGG 237
Oy 67 AAAATAAGTTGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAAAGCAGA	AGTTGCAGAAAGCAGA 126	S d	238 ACAAGGGTAGTTTCTGAGGAAACTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGG 297 :::::::::::: 642 LeuGlnIleLeuArgAspGluLysTyrTyrGlnLeuGluGluLeuAlaPheArgValMet 661
OY 127 AATCTGTATATATGGGATGAATTACATCTGGGAATGGGCTGCCTGC	CCCTGCA 177 nProvalGlnCysGlu 473	& 2 6	298 AATATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAA 351 :::
Qy 178 AATCGGATACATAGTATATGAGTTTATATATATGTGGGATGGGCATCGGG ::: ::	IGATTGTGGCATCAGG 237 ::: 3GlnLeuGlnValAsp 493	λο qa	352TCAGIGIGGCTTACACCAGTTTCTACTGAGAATGAAATTG 396 ::: 682 HisPheSerSerLeuGluLeuValProProSerThrLeuThrThrThrHisLeuLysAla 701
Oy 238 ACAAGGGTAGTITCTGAGGAACTCTCTTTTCAAACGGAGCTGTACTTTACCCCAAGG	STACTTTACCCCAAGG 297	ò	397 GATCCT 402 :::

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A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: G70519
A;Accession: G70519
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-135 <COL>A;COSS-references: UNIPROT:007719; UNIPARC:UPI000001020; GB:Z97193; GB:AL123456; NID:ç
C;Genetics:
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-4,'I',6-10,'G',12-13,'SA',16-20,'A',22-25,'GQ',28-30,'G',32-33,'FE',36,'N'
A;Cross-references: UNIPARC:UF10000088198; GB:S75730; NID:g861452; PIDN:AAB32826.1; PID:
C;Superfamily: acyl-CoA desaturase; stearoyl-CoA desaturase homology
C;Keywords: oxidoreductase; unsaturated fatty acid biosynthesis
F;113-307/Domain: stearoyl-COA desaturase homology <SDH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-358 <THI>
A;Cross-references: UNIPROT:P07308; UNIPARC:UPI00004210A; GB:J02585; NID:g206859; PIDN:
R;Mihara, K.
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A;Title: Structure and regulation of rat liver microsomal stearoyl-CoA desaturase gene.
A;Reference number: JX0150; MUID:91210202; PMID:1982442
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NyAlternate names: acyl-CoA desaturase; Delta9 fatty acid desaturase
C;Species: Rattus norvegicus (Norway rat)
C;Daccession: A24699; UXO150; ISB133
R;Thiede, M.A.; Ozols, J.; Strittmatter, P.
J. Biol. Chem. 261, 13230-13335, 1986
A;Title: Construction and sequence of cDNA for rat liver stearyl coenzyme a A;Reference number: A24699; MUID:87008535; PMID:2428815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 ATTTGGACCGGTGCTGAGAACCTCCATGTGAAAATAAGTTGCTCTCTGGACTGGTTGATG
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C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv1914c
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A;Residues: 1-290,'A', 292-358 <MIH>
A;Cross-references: UNIPARC:UP100000E69BF
R;Baba, H.; Fuss, B.; Matson, J.B.; Zane, L.T.; Macklin, W.B.
Neurochem. Res. 19, 1091-1099, 1994
A;Title: Identification of novel mRNAs expressed in oligodendrocytes.
A;Reference number: IS8133; MUID:95098214; PMID:7800118
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                                                                                                   MCI protein precursor - Mycoplasma gallisepticum
C;Species: Mycoplasma gallisepticum
C;Species: Mycoplasma gallisepticum
C;Species: Mycoplasma gallisepticum
C;Date: 15-0ct-1999 #text_change 09-Jul-2004
C;Accession: T18346
R;Keeler Jr., C.L.; Hnatow, L.L.; Whetzel, P.L.; Dohms, J.E.
Infect. Immun. 64, 1541-1547, 1996
A;Title: Cloning and characterization of a putative cytadhesin gene (mgcl) from Mycopl, A;Reference number: 218881; MJID:96201559; PMID:8613358
A;Accession: T18346
A;Accession: T18346
A;Accession: T18346
A;Residues: 1-1122 <KEE>
A;Residues: 1-1122 <KEE>
A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetic code: SGC3
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, P.; Connor, R.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
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|SerSerProArgGlyAlaAsnGlyAsnIlePheLeuGlySerAlaIleThrTrpGlyThr 511
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C;Species: Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Un1-1998 #sequence_revision 17-Un1-1998 #text_change 09-Jul-2004
C;Accession: G70519
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCCACACTGATTTCCTAGAGGTGGAA----CACTCCAAATGGATTTCCTGAGGGTCATGA
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|SerTyrAspTyrAsnSerValArgPheAlaAla-----
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44.6%
25.0%
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Qy 55 AACCTCCATGTGAAAATAAGTTGCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTT 114 bb	Qy 190ACATATGTATATATATATTTTGTTCGTGATTGTGGCATCAGGACA 240 bb 64 MetGlyThrThrTyrAsnileLysTyrIleGinGinPro 76 Qy 241 AGGGTAGTTTCTGAGGAAACTCTCTTTTTCAAACGAGGTGTACTTTACCCCAAGGAAT 300 Db 77 GlyileAlaAspSerLysThrLeuGinThrGlu	Qy 301 ATAGATCATGACCCTCAGGAAATCCATTTGGAGTCTTCCACCTCTAGGAAATCAGTGTGG 360	RESULT 10 AE0152 probable bacteriophage protein YPO1246 [imported] - Yersinia pestis (strain C092) C; Species: Yersinia pestis C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004 C; Accession: AE0152 R; Parkhill, J; Wren, B.W.: Thomson, N.R.: Tithall, R.W.: Holden, M.T.G.: Prentice M.R.	deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001 A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Recession: AE0152 A;Recession: AF0152 A;Returus: pre-liminary A;Residues: 1-468 «KUR» A;Residues: 1-468 «KUR» A;Residues: U-468 «KUR» A;Genetics: A;Genetics: A;Genetics: A;Genetics:	ignment Scor ed. No.: ore: roent Simila st Local Sim ery Match: :	40 TGGACCGGTGCTCAAAATAAGTTGCTCTCTGGACTGGTTGATGGTCTCTCTGGACTGGTTGATGGTCTCTCTGGACTGGTTGATGGTCTCTCTGGACTGGTTGATGGTCTCTCTGTGACTGAC	Oy 160 GGAATGGGCTGCCTGCAATCGGATACATACATATGTATATATAT 213
Score: Percent Similarity: 39.5% Conservative: 22 Best Local Similarity: 25.0% Mismatches: 22 Best Local Similarity: 25.0% Mismatches: 20 Query Match: 1	169 TGCC 92 IleP 226 TGTG	Oy 235AGGACAAGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTT 288 132 ProLeuArgllePheLeulleIleAlaAsnThrMetAlaPheGlnAsnAspValTyrGlu 151 Oy 289 ACCCCAAGGAATATAGATCATGACCTCAGGAAATCCATTTGGAGTGTTCCACC 342	ע ו	RESULT 9 A82094 thiamin biosynthesis lipoprotein ApbE VC2289 [imported] - Vibrio cholerae (strain N16961 C;Species: vibrio cholerae C;Species: vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 C;Accession: A82094 C;Accession: A82094 C;Accession: A82094 C;Accession: A82094 C;Accession: A82094 C;Accession: A82094 C;Accession: A82094 C;Accession: A82094 C;Accession: A82094 N.D.; Vamathevan, J.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; C,Arabernee, J.J.; Venter, J.C.; Fraser, C.M. A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID: 20406813; Paragel.	A;Accession: A82094 A;Status: preliminary A;Olecule type: DNA A;Nolecule type: DNA A;Residues: 1-367 <hel> A;Cross-references: UNIPROT:Q9KPS3; UNIPARC:UPI00000C3362; GB:AE004300; GB:AE003852; NID A;Experimental source: serogroup O1; strain N16961; biotype El Tor C;Genetics: A;Gene: VC2289 A;Map position: 1 C;Superfamily: hypothetical protein H10172</hel>	Alignment Scores: Pred. No.: Score: Score: Fercent Similarity: 4.71 Length: 367 Score: Fercent Similarity: 41.48 Conservative: 21 Best Local Similarity: 26.9\$ Mismatches: 42 Query Match: 2.3\$ Indels: 9	US-10-664-025-43_COPY_53_511 (1-459) x A82094 (1-367)

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214 CTTGTTCGTGATTGTGCCATCAGGACAAGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAA 273 50	Alignment Scores: At 199 Length: 204 Bred. No.: Conservative: 27 Best Local Similarity: 41.8\$ Conservative: 27 Best Local Similarity: 41.8\$ Mismacches: 46 Gaps: 2 Animalarity: 41.8\$ Mismacches: 46 Best Local Similarity: 24.7\$ Mismacches: 46 Gaps: 2 Animalarity: 24.7\$ Mismacches: 46 US-10-664-025-43_COPY_53_511 (1-459) x H95188 (1-204) Qy 64 GTGAAAATAAGTTGCTCTCTGGACTGGTTGATGCTGGAA 120 Qy 64 GTGAAAATAAGTTGCTCTCTGGACTGGTTGATGATATACTCTGGGAATGGGC 168 11 ValTyrileSerThrSerIleAspTyrLeuIleIleLeuIheAlaGinLeu 30 Qy 121AGCAGAAATCTGTATATATTTGCGGATGAATTACTGGGAATGGCC 168 11 ValTyrileSerThrSerIleAspTyrLeuIleIleLeuIleIleLeuPheAlaGinLeu 30 Qy 121AGCAGAAATCTGTATATATTTGCGGATGGATTGGGGATGGGC 168 11 SerGlnAsnLysGlnLysTrHHisileTyrAlaGlyGlnTyrLeuGlyFleu 49 Qy 169TGCCCTGCAAATCTGATATATTTTTTATATGTATATGTGGATTGTGGCATCAGGACAAGG 243

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A; Description: The sequence of C. elegans cosmid T04D1.
A;Reference number: 221292
A;Reference number: 221292
A;Accession: T31152
A;Status: pre-liminary; translated from GB/EMBL/DDBJ
A;Residues: 1-2957 cDRAV
A;Residues: 1-2957 cDRAV
A;Residues: 1-2957 cDRAV
A;Cross=references: UNIPROT:061845; UNIPARC:UPI000007A573; EMBL:AF067617; PIDN:AAC17559
C;Genetics:
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A;Title: Cloning and characterization of zona pellucida genes and cDNAs from a variety **
A;Reference number: $70399
A;Accession: $70399
A;Accession: $70399
A;Accession: $70399
A;Accession: $70399
A;Caces-references: UNIPARC: UNIPARC: UPI000013C463; EMBL: U05778; NID:9458272; PI:
C;Superfamily: sperm-binding glycoprotein ZP3; ZP domain homology <ZPH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2056 ValHisAspProvalTyrAsnLysLeuAsnTrpThrLysArgGluGluGluPhelle 2075
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C;Species: Felis silvestris catus (domestic cat)
C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: S70399
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2096 ThrilePheLysThrLeuSerProlleLeuGluLysLysThrAspGluAspCysHisGlu
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A;Introns: 122/3; 293/3; 515/3; 1205/2; 1577/1; 2221/3; 2776/1; 2864/3
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Conservative:
Mismatches:
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Matches:
                     R,Davidson, S.; Wohldmann, P.
submitted to the EMBL Data Library, May 1998
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                                                      hypothetical protein F4P12.250 - Arabidopsis thaliana
hypothetical protein F4P12.250 - Arabidopsis thaliana
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T45895
R;Blocker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat, A;Reference number: Z23016
A;Reference number: Z23016
A;Accession: T45895
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-256 <BLO>
A;Cross-references: UNIPROT:Q9LFG4; UNIPARC:UP100000A485C; EMBL:AL132966
A;Experimental source: cultivar Columbia; BAC clone F4F12
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| ProGluCysLeuSerAsnHisLeuLysIlePheGluTrpLysGlyTyrArgGlyArgLys
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTTTGGACCGGTGCTGAACCTC
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---GluGluLysGluIleValArgTyrIleLeuAlaAsnSerLysCysLeuArgArgIle
ProTyrPheAlaSerLeuAspTrpSerGlnThrLeuValAlaLeuLeuValPhe 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 CATGTGAAAATAAGTTGC-------TCTCTGGACTGGTTG
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Mismatches:
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A;Introns: 2/3; 53/1; 122/3; 152/3
A;Note: F4P12.250
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76.00
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21 TyrProProThrThrGluAspLysThrHisProSerLeuProSerSerProSerVal 40
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MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Felingold E.A., Grouee L.H., Derge J.G.,

A Altschul S.F., Zeeberg B.S., Wagner L., Schamen C.M., Schuler G.D.,

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A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B Hownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Roank S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R Nitlanon D.K., Muzny D.M., Sodergren B.J., Lu X., Glabbs R.A.,

Falbey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

R Hitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

B R Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R Generation and initial analysis of more than 15,000 full-length human
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein FLJ36198.
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                             063EM2_BACCZ
050T2_MOUSE
MACF1_MOUSE
04PLL5_MOUSE
06FLS_CANGA
073C23_BACC1
081TW1_BACAN
0801M1_NPWC
071AK8_DANCI
0804D8_BUPAR
072B14_DESVH
072B14_DESVH
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ID Q86WS3 HUMAN

AC Q86WS3 HUMAN PRELIMINARY;

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DT 01-JUN-2003 (TrEMBLrel. 24,

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BYPOTHERICAL METAZOA;

CENKARYOTA; METAZOA; CONTOTAGE

OC SUKARYOTA; METAZOA; CHORDAC

OC NCEL TAXID=9606;

RN NUCLEOTIDE SEQUENCE.

RA ALBUSHORS R.L., Fehingold E. RA

RA Klaushers R.L., Fehingold E. RA

ALGENINE-22388257; PubMed=124

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Q9upn3
Q5vw20
Q95y10
          GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                     using frame_plus_n2p model
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                            TISSUE-restis;
Director MGC Project;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC048121; AAH36121.1; -; mRNA.
EMBL, BC036256; AAH36256.1; -; mRNA.
Ensembl; ENSGG0000149507; Homo sapiens.
Hypothetical protein.
SEQUENCE 158 AA; 17971 MW; EEB43D6FB8ABB1FF CRC64;
                      NIH MGC Project;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ36198.
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Matches:
Conservative:
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TISSUE=Festis;
PubMed=14702039; DOI=10.1038/ng1285;
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QBN9U6;
                                                                                NUCLEOTIDE SEQUENCE
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Best Local Similarity:
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TISSUE=Testis;
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RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikawa E.,
RA Gunza Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninoniya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Yamazaki M., Ninoniya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe S., Yosida M., Hotuta T.,
RA Nomura Y., Togiya S., Komai P., Hara R., Takeuchi K., Arita M.,
RA Nomura Y., Matennawa H., Ichinara T., Shiohata N., Sano S.,
RA Noshikawa Y., Matennawa H., Ichinara T., Shiohata N., Sano S.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Pujimori Y., Komiyama M., Tashinch H., Tanigami A., Pujiwara T.,
RA Anazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami T.,
RA Autimori Y., Komiyama M., Tashinco M., Kawakami B.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaih A., Pujiwara T.,
RA Kawabata A., Hikiji T., Nogatake N., Inagaih Y., Sagaki M.,
RA Houmura K., Nawakami T., Nogatake N., Inagaih Y., Ramashita R.,
RABABINA Sugano J., Satoh T., Shirai Y., Takabashi Y., Nakagawa K.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takabashi Y., Nawagano S.,
RA Nakaiki K., Nawakami T., Nomura N., Kikuchi H., Masunob Y., Yamashita R.,
RABABI T., Otyama M., Hata H., Watanabe M., Kahashi Y., Nawashita R.,
ROMPILE sequencing and characterization of 21,243 full-length human R.,
RABABI S., Satoh V., Shirai Y., Takabashi T., Yonashita R.,
ROMPILE Sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGGATACATACATATGTATATGAGTTTATATATCTTGTTCGTGATTGTGGCATCAGGACA
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EEB43D70A8A391E8 CRC64;
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Ensembl; ENSG0000149507; Homo
SEQUENCE 158 AA; 17942 MW;
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Best Local Similarity:
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417

357

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STRAIN=CSTBL/6J. TISSUE=Placenta;

X MEDLINE=21085660; PubMed=1127851; DOI=10.1038/35055500;

X MEDLINE=21085660; PubMed=1127851; DOI=10.1038/35055500;

X Mawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Komno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Richi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

A Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Barsh G.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
61 ThrGlnIleHi8AlaHi8GlnTyrAspPheIleTyrProValSerHisCysGlyIleArg
                                                                                                                                                                  ACAAGGGTAGTTTCTGAGGAAACTCTCTTTTTCAAACCGAGCTGTACTTTACCCCAAGG
                                                                                      AATATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTG
                                                                                                                                                                                                                           TGGCTTACACCAGTTTCTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTATTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hemberger M.C., Himmelbauer H., Ruschmann J., Zeitz C., Fundele R.H.; "CDNA subtraction cloning reveals novel genes whose temporal and spatial expression indicates association with trophoblast invasion."; Dev. Biol. 0:0-0(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CS7BL/6J; TISSUE=Placenta; MEDLINE=9279255; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninol P., Hayashizaki Y.; Hidh-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
EPCS26 (FLACI) (Mus musculus adult female placenta cDNA, RIKEN full-length enriched library, clone:1600019P04 product:placental specific Name=Placi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20453190; PubMed=10995572; DOI=10.1006/geno.2000.6302; Cocchia M., Huber R., Pantano S., Chen E.Y., Ma P., Forabosco A., Ko M. S., Schlessinger D.; Pantano B., Chen E.Y., Ma P., Forabosco A., "PLACI, an Xq26 gene With placenta-specific expression."; Genomics 68:305-312(2000).
                                                                                                                                                                                                                                                                                                                                ||||||::: ||| AspPheGluAlaThrProGluGluLeuGlyLeuLeu 152
                                                                                                                                                                                                                                                                                                        GACTTTCAGACACAGCAGAAGAGTTAGGATTATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                   173 AA
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Alausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,
And Brotchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
A. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
B. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B. Bakas S.A., McKennan K.J., Malek J.A., Gunzaren P.H.,
A. Wilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Fahey J., Helton B., Ketreman M., Madan A., Rodrigues S., Sanchez A.,
Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzzywinski M.I., Skalska U., Smailus D.E.,
Monterfield Y.S.N., Krzzywinski M.I., Skalska U., Smailus D.E.,
Monter Chan And Initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 AGC---AGAAATCTGTATATTTTGCGGATGAATTACATCTGGGAATGGGCTGCCCTGCA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 AATCGGATACATACATATGTATATGAGTTTATATATCTTGTTCGTGATTGTGGCATCAGG 237
                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CATGTGAAAATAAGTTGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAA
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                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Oocytes;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH MGC Project;
Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC099498; AAH99498.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
SEQUENCE 164 AA; 18849 MW; 49ADE19216BE8606 CRC64;
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                                                                                                                                                                              Last sequence update)
Last annotation update)
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Mismatches:
TTTCAGACAACAGCAGAAGAGTTAGGATTATTA 453
                  Matches:
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431.50
72.4%
55.9%
52.2%
                                                                                                                 Q4FZG8_MOUSE PRELIMINARY;
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                                                                                              MOUSE
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RC STRAIN-CSTBL/647 TISSUE=Placenta;

RA OAGAZAKI Y. FULUND M., Kabukawa T., Adachi J., BOND H., Kordo S.,

RA OAGAZAKI Y., FULUND M., Kaito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Mikaido II., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Adarelli R., Hilli D.P., Bult C., Hume D.A., Queckenbush J.,

RA Badarelli R., Hilli D.P., Bult C., Hume D.A., Queckenbush J.,

RA Schriml L.M., Kanapin A., Mateuda H., Batalov S., Beisel K.W.,

RA Balla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Balla E., Dragani T.A., Fletcher C.F., Forrest A., Gough J.,

RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RAMAIA A., Kawaji H., Kawasawa Y., Kedilerski R.M., King B.L.,

RAMAIA A., Kawaji H., Kawasawa Y., Kedilerski R.M., King B.L.,

RADGOLT D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Magobina T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sandelin A., Schneider C., Semple C.A., Sectou M., Shimada K.,

Sandelin A., Schneider C., Semple C.A., Sectou M., Shimada K.,

Sandelin A., Schneider C., Semple C.A., Sectou M., Sangarun N.,

RA Wilming L.G., Wynnahaw Boris A., Yanagisawa M., Yang I., Yang I.,

RA Wilming L.G., Wynnahaw T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Saco K.,

Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

Hara A., Hashizume W., Imotani K., Ithia M., Kagawa I.,

Myazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

Hara A., Hashizume W., Imotani K., Ithia M., Shinagawa A.,

Banishi A., Yashai K., Sasaki D., Shibata K., Shinagawa A.,

Hara A., Hashizume W., Imotani K., Ithia K., Ithia M., Shinagawa A.,

Banishin M., Shinachis Y., Ithia M., Waterston R., Lander E.S., Rogers J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUB=Placenta; MBDLINE=20499374; PubMed=110421S9; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birney E., Hayashizaki Y., "Analysis of the mouse transcriptome based on functional annotation of
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakwa T., Bono H., Carninci P., Fukuda S., Pukunishi Y., Furuno M.
Hanagaki T., Hara A., Hayateu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.
Okazaki Y., Okido T., Owa C., Salto H., Salto R., Sakai K., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T.
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                                                                           Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
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79 TCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAAAGCAGAAATCTGTATATA 138
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                       Yoshino M.,
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires; Rodentia, Sciurognathi;
Muridae, Murinee, Mus.
STRAIN=C57BL/6J; TISSUE=Embryo; MEDLIAD1013/pnas.242603899; MEDLINE=2238825; PubMed=1247932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Zoeberg B., Buetow K.H., Schaefer G.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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42
33
45
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Placental specific protein 1.
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Indels:
                                                                                                                                                                                                                                    Length:
Matches:
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234.00
61.5%
34.4%
28.3%
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Q80WW3;
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NUCLEOTIDE SEQUENCE
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Best Local Similarity:
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Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Mathy J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Schmutz J., Myers R.M., Schnerch A., Schein J.E., Schantz J., Myers R.M., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Marra M.A., Schein J.E., Marra M.A., Schein J.E., Schein J.E.
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Last sequence update)
Last annotation update)
FLJ90605) (Placenta-specific 1).
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Strausberg R.;
Strausberg R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC051666; AAM51666.1; -; mRNA.
MGI; MMI:12926287; Placl.
G0; G0:0005615; C:extracellular space; TAS.
SEQUENCE 173 AA; 19573 WW; 79DDC0179BD730B0 CRC64;
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Matches:
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Q9HBJO;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Length Human cDNAs Encoding Secretion or Membrane Proteins from Oligo-
Capped cDNA Libraries.";
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Otsuki T., Ota T., Nishikawa T., Hayashi K., Suzuki Y., Yamamoto J., Wakamatsu A., Kimura K., Sakamoto K., Hatano N., Kawai Y., Ishii S., Saito K., Kojima S., Sugiyama T., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Nagai K., Sugano S.,
                                                                                                                                                                                                                                                 MEDLINE=20453190; PubMed=10995572; DOI=10.1006/geno.2000.6302; Cocchia M., Huber R., Pantano S., Chen E.Y., Ma P., Forabosco A., Ko M.S., Schlessinger D.; "PLACI, an Xq26 gene With placenta-specific expression."; Genomics 68:305-312(2000).
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EMBL; AF234654; AAG22596.1; -; mRNA.
EMBL; AK075086; BAC11392.1; -; mRNA.
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
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EMBL; BC066327; AAH66327.1; -; mRNA.
Ensembl; ENSG0000170965; Homo sapiens.
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NUCLEOTIDE SEQUENCE.
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RIDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rlausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Stapleton M., Soares M.B., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Bosak S.A., McEwan P.M., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.W., Roferman K.J., Malek J.A., Hullyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
Pahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
Mhiting M., Nadan A., Young A.C., Shevchenko Y., Bolffard G.G.,
Butkeeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
Butterfield X.S.N., McTouchman J.M., Butterfield Y.S.N., Marzywinski M.I., Skalska U., Smallus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
Butterfield X.S.N., Krzywinski M.I., Schalka U., Smallus D.E.,
Butterfield X.S.N., Krzywinski M.I., Schalka U., Smallus D.E.,
Butterfield Y.S.N., Krzywinski M.I., S.M., Mander M.A., Shallus D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 AGTIGCICTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAAAGCAGAAATCTG 132
                                                                                                                                                                                                                                                                                                                                                                          253 GAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAATATAGATCATGAC 312
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                                                                         72
                                                                                                                                                                                                                                                              49 CysValHisPheHisGluLeuHisLeuGlyLeuGlyCysProProAsnHisValGlnPro 68
                                                                                                                                              9 LeuMetIleLeuLeuThrSerAlaPheSerAlaĠlySerGlyGlnSerProMetThrVal 28
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                                                                     GTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCTGAGAACCTCCATGTGAAAATA
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 TATGTATATGAGTTTATATATCTTGTTCGTGATTGTGGCATCAGGACAAGGGTAGTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         313 CCTCAGGAA-----ATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGGCTTACA
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EMBL; BC097979; AAH97979.1; -; mRNA.
SEQUENCE 173 AA; 19546 MW; 9CB11878F671CEEF CRC64;
US-10-664-025-43_COPY_53_511 (1-459) x Q9HBJ0_HUMAN (1-212)
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Rattus norvegicus (Rat).
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                                                                                                                                                                                            34 ITGATTTGGACCGGT---GCTGAGAACCTCCATGTGAAAAAAAAGTTGCTCTCTGGACTGG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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MEDLINE=99279253; Pubmed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
10-DMAY-2006 (TrEMBLrel. 30, Last annotation update)
Initiate factor 3 (Oocyte-secreted protein 1 precursor) (In vitro fertilized eggs cDNA, RIKEN full-length enriched library, clone:7420700J01 product:INITIATE FACTOR 3, full insert
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Mismatches:
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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CTRAIN-C57BL/63; TISSUE=In vitro fertilized eggs;

X MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
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Genome Res. 10:1617-1630(2000).
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STRAIN-CSTBL/65.TISSUB=In vitro fertilized eggs;
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Rutuda S., Puruno M., Hanagaki T., Hara A., Habilzume W.,
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EMBL, AR050982; BAB47553.1; -; mRNA.
EMBL, AR050982; BAB47553.1; -; mRNA.
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MGI; MGI:2149290; Oospl.
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  172 CCTGCAAATCGGATACATACATAT-----GTATATGAGTTTATATATGTTCTTGT 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 GAGAACCTCCATGTGAAAATAAGTTGCTCTGGACTGGTTGATGGTCTCAGTTATCCCA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 GTTGCAGAAAGCAGAAATCTGTATATATTGCGGATGAATTACATCTGGGAATGGGCTGC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                  43 Thrile---PheHisAsnilePheMetGluProAspGluValPheLeuGlyIleGlyCys 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 TTAGAAGICTTGATGCTCCTCGCTGTCTTG-------ATTTGGACCGGTGCT 51
                                                                                                                                                        NUCLEOTIDE SEQUENCE.
MEDLINE=22222142; PubMed=12237121; DOI=10.1016/S0006-291X(02)02194-0; Mano H., Nakatani S., Aoyagi R., Ishii R., Iwai Y., Shimoda N., Jincho Y., Hiura H., Hirose M., Mochizuki C., Yuri M., Im R-H., Funada Wada U., Wada M.;

"IP3, a novel cell-differentiation factor, highly expressed in the murine liver and ovary.";

Biochem. Biophys. Res. Commun. 297:323-328(2002).

EMBL; AB086437; BAC11848.1; -; mRNA.

Ensembl; ENSWUSG00000041857; Mus musculus.

MGI:2149290; Oospil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2P3 MESAU STANDARD; PRT; 422 AA.
P23491;
01-NOV-1996 (Rel. 20, Created)
01-NOV-1996 (Rel. 33, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
20na pellucida sperm-binding protein 3 precursor (Zona pellucida glycoprotein ZP3) (Sperm receptor) (Zona pellucida protein ZP3) (Sperm receptor) (Zona pellucida protein C).
Name=ZP3; Synonyms=ZPC;
Mesocricctus auratus (Golden hamster).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Burchis; Muroidea; Cricetidae; Cricetinae; Mesocricctus.
                                                                                  Name=Oospi; Synonyms=IF3 2;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223 GATTGTGGCATCAGGACAAGGGTAGTTTCTGAGGAAACTCTCCTT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 SerCysGlyIleAlaAsnLys----SerGluSerSerPheLeu 92
                                                                                                                                                                                                                                                                             GO:0005615; C:extracellular space; TAS.
UENCE 92 AA; 10597 MW; FC458C6E10005FDA CRC64;
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                                         01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                       92 AA.
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103.00
48.4%
30.5%
                      QEK4N9 MOUSE PRELIMINARY;
Q8K4N9;
                                                                                                                               Muridae; Murinae; Mus.
                                                                          Initiate factor 3 2.
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                                                                                                                                         NCBI_TaxID=10090;
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DB:
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RESULT 9
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                            SUBGRILITY FORMULE.

SUBCELULAR LOCATION: Type I membrane protein. Extracellular matrix upon proteolytic cleavage.

SUBCELULAR LOCATION: Type I membrane protein. Extracellular matrix upon proteolytic cleavage.

TISSUE SPECIFICITY: Occytes.

DEVELOPMENTAL STAGE: Growing occytes.

DEVELOPMENTAL STAGE: Growing occytes.

DEVELOPMENTAL STAGE: Growing occytes.

PROMAIN: The ZP domain is involved in the polymerization of the ZP proteins to form the zona pellucide the transmembrane segment to yield the secreted ectodomain incorporated in the zona pellucida.

PRIN: N-glycosylated (By similarity) he proteins may play an important role in the postfertilization block to polyspermy (By important role in the postfertilization block to polyspermy (By
                                                            Kinloch R.A., Ruiz-Seller B., Wassarman P.M.;
"Genomic organization and polypeptide primary structure of zona pellucida glycoprotein hZB2, the hamster sperm receptor.";
Dev. Biol. 142:414-421(1990).
Dev. Biol. 142:414-421(1990).
Dev. Biol. 142:414-421(1990).
Dev. Biol. 142:414-421(1990).
Perovente post-fertilization polyspermy, is composed of three to prevente post-fertilization polyspermy, is composed of three to four glycoproteins, 2P1, ZP2, ZP3, and ZP4. ZP3 is essential for sperm binding and zona matrix formation.

-!-SUBUNIT: Polymers of ZP2 and ZP3 organized into long filaments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 By similarity.
Zona pellucida sperm-binding protein 3.
Removed in mature form (By similarity).
Extracellular (Potential).
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InterPro; IPR001507; Endoglin/CD105.
Pfam; PF00100; Zona pellucida; 1.
SMART; SR00023; ZPELLUCIDA.
SMART; SR000241; ZP: 1.
PROSITE; PS00682; ZP 1; 1.
PROSITE; PS51034; ZP 2; 1.
PROSITE; PS51034; ZP 2; 1.
PROSITE; PS51034; ZP 2; 1.
PROSITE; PS51034; ZP 2; 1.
PROSITE; PS51034; ZP 2; 1.
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TISSUE=Ovary;
MEDLINE=91078540; PubMed=2257975;
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CATGTGAAAATAAGTTGCTCTCTGGAC---TGGTTGATGGTCTCAGTTATCCCA---- 111
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|ThrTrpValProPheSerThrThrValSerSerGluGluLysLeuValPheSerLeuArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tetraodon nigroviridis (Green puffer).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthomorpha; Acanthomorpha; Acanthomorpha; Percomorpha; Tetraodontiformes; Tetradontoidea; Tetraodontidae; Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         322 ATCCATTTGGAGTGTTCCACCTCTAGG--------
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 3 SCAF11271, whole genome shotgun sequence.
ORFNames=GSTENG0009437001;
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Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
Cruaud C., Duprat S., Brottier F., Coutanceau J.P., Gouzy J.,
Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nubsbaum C., Kahn D., Robinson-Rechavi M.,
Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Wincker P., Lander E.S., Weissenbach J., Roset Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordarlaceae, Neurospora.
NCBI_TaxID=5141,
[1]
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-!- CATTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry whis preliminary data.

EMBL; CAAE01011271; CAF93676.1; -; Genomic_DNA.
SEQUENCE 408 AA; 44840 MW; CA8A9142A7302BDZ CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Matches:
Conservative:
Mismatches:
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Name=3H10.130;
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Coshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K., A. Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K., A. Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., A. Arita M., Musashino K., Yaumanoto J., Isano Y., A. Kawai-Hio Y., Satio K., Mishikawa T., Yamura K., Yamashita H., Murakawa K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Ranehori K., Sugiyama A., Kawakami B., Suzuki Y., Sugiyama A., Kawakami B., Suzuki Y., Sumano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Submitted (JUL-2003) to the EmBL/GenBank/DDBJ databases.

EmBL, AK127519; BAC87016.1; -; mRNA.

BERI, AK127519; BAC87016.1; -; mRNA.

GO; GO:0005856; C:cytoskeleton; IEA.

GO; GO:000779; Factin binding; IEA.

GO; GO:000779; Factin binding; IEA.

GO; GO:000779; Factin binding; IEA.

RITERPO; IPR001715; Calponin-like.

InterPro; IPR002017; Spectrin.

PEam; PP000170; Spectrin.

SRART; SM00150; SPEC; 2.

PROSITE; PS50021; CH; 1.
632 tIlePheSerThrPheCys---TrpHisAsnGluAspHisTyr---AlaTyrSerAlaAs 650
                                                                                    ||| ||| ||| ||| 650 nTyrGlnHisPheGlyAlaThrLysThrTrpTyrGlyIleProGlyGluAspAlaGluLy 670
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SerAspVallleMetTyrIleGlnGluCysGluGlyLeuIleArgGlnLeuGlnValAsp 650
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                                                                                                                                                                                                                                                                                                                                                                                                     05-JUJ-2004 (TrEMBLrel. 27, Created)
05-JUJ-2004 (TrEMBLrel. 27, Last sequence update)
05-JUJ-2004 (TrEMBLrel. 27, Last annotation update)
15-JUJ-2004 (TrEMBLrel. 27, Last annotation update)
14-JUJ-2004 (TrEMBLrel. 27, Last annotation update)
15-JUJ-2004 (TrEMBLrel. 27, Last annotation update)
16-JUJ-2004 (TrEMBLrel. 27, Last annotation update)
16-JUJ-2004 (TrEMBLrel. 27, Last annotation)
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16-JUJ-2004 (TrEMBLRel. 27, Last a
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593 AsnProTyrSerThrAspProTrpAsnLeuAsnLeuLeuProLeuHisPro-GluSerLe 612
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612 uPheArgTyrIleLysThrAspIleSerGlyMetThrValProTrpValTyrValGlyMe 632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253 CAGAAACTACCCTTGTCC-----TGATGCCACAAT-----CACGAAGAAGATATA 209
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573 AlaAspIleHisCysThrThrHisGlySerGlyPheProThrValGluLysAsnProAsn 592
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                                                                                                                                                                Graman Neurospora genome project;
Submitted (NOV-2001) to the EMBL/Genbank/DDBJ databases.
Branch: ALS1342; CAC28652.2; -; Genomic_DNA.
Brit: ALS1342; T4842.2; -; Genomic_DNA.
Brit: ALS1342; CAC28652.2; -; Genomic_DNA.
Brit: ALS1342; LAM2.
R GO; GO:0006352; C:Intracellular; IEA.
GO; GO:0006352; C:Intracellular; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
R InterPro; IPR001304; Lectin C.
InterPro; IPR001304; Lectin C.
InterPro; IPR001304; Lectin C.
InterPro; IPR001304; TF_JmjN.
R InterPro; IPR001304; TF_JmjN.
InterPro; IPR001304; TF_JmjN.
InterPro; IPR001304; TF_JmjN.
InterPro; IPR001304; TF_JmjN.
InterPro; IPR001304; TF_JmjN.
InterPro; IPR001306; INF.
InterPro; IPR001306; INF.
InterPro; IPR001306; INF.
InterPro; IPR001306; INF.
InterPro; IPR001306; INF.
INF.
INF. SMART; SM0051; BRIGHT; I.
INF. SMART; SM0051; JmjN; I.
INF. SMART; SM00545; JmjN; I.
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                              Holland
                              Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Nyakatura G., Mewes H.W., Mannhaupt G.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PSSI011; ARID; 1.
PROSITE; PS06615; C TYPE LECTIN 1; UNKNOWN 1.
PROSITE; PS01359; ZF PHD 1; UNKNOWN 2.
PROSITE; PS01359; ZF PHD 2; 2.
SEQUENCE 1736 AA; 195653 MW; 6299E2F6BC2AA074 CRC64;
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   NUCLEOTIDE SEQUENCE
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Res. 4:345-349(1997)
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SMR; Q9UPN3; 68-301
                                from human brain."
                                                                      SEQUENCE REVISION.
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    691 HisPheThrSerLeuGluLeuValProProSerThrLeuThrThrHisLeuLysAla 710
238 ACAAGGGTAGTTTCTGAGGAAACTCTCTTTTTCAAACCGAGCTGTACTTTACCCCAAGG 297
                                                  298 AATATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACC---TCTAGGAAA--- 351
                                                                                                       -----TCAGTGTGGCTTACACCAGTTTCT-----ACTGAGAATGAAATAAAATTG 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20001959; PubMed=10529403; DOI=10.1006/bbrc.1999.1518; Okuda T., Matsuda S., Nakatsugawa S., Ichigotani Y., Iwahashi N., Takahashi M., Ishigaki T., Hamaguchi M.; "Molecular cloning of macrophin, a human homologue of Drosophila kakapo with a close structural similarity to plectin and dystrophin."; Biochem. Biophys. Res. Commun. 264:568-574(1999).
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                          MACF1 HUMAN STANDARD; PRT; 5430 AA.

QUUND3; O75033; Q8MXY2; Q9H540; Q9UKPO; Q9ULG9;

Q1-NT3; O75033; Q8MXY2; Q9H540; Q9UKPO; Q9ULG9;

Q1-FEB-2005 (Rel. 46, Last sequence update)

13-SEP-2005 (Rel. 48, Last annotation update)

Microtubule-actin crosslinking factor 1, isoforms 1/2/3/5 (Actin cross-linking family protein 7) (Macrophin 1) (Trabeculin-alpha) (620 kDa actin-binding protein) (ABP620).

Name=MACF1; Synonyms=ABP620, ACF7, KIAA0465, KIAA1251;
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DNA Res. 6:337-145(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE (ISOFORM 1).

MUCLEOTIDE SEQUENCE (ISOFORM 1).

BURDLINE-SO026884; PubMed=1.0559237;

SUN Y., Zhang U., Kaeft S.-K., Auclair D., Chang M.-S., Liu Y.,

Sutherland R., Salgia R., Griffin J.D., Perland L.H., Chen L.B.;

Wholecular cloning and characterization of human trabeculin-alpha,

giant protein defining a new family of actin-binding proteins.";

J. Biol. Chem. 274:33522-33530(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE OF 182-4812 (ISOFORM 2), AND ALTERNATIVE SPLIC MEDLINE=21833812; PubMed=11845288; DOI=10.1007/800335-001-3037-3; Gong T.-W.L., Beafill C.G., Lomax M.I.; MAACF1 gene structure: a hybrid of plectin and dystrophin."; Mamm. Genome 12:852-861(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98116662; PubMed=9455484;
Seki N., Ohira M., Nagase T., Ishikawa K.-I., Miyajima N.,
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GluPro 712
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Machiama D., Nomara N., Obara O., Nagaer C., The Communication of CDNA clones in size-fractionated cDNA libraries from human brain, 1970.

Machiama D., Nadaziki N., Yamakawa H., Kikuno R., Obara O., Nagaer T.; Nadaziki N., Yamakawa H., Kikuno R., Obara O., Nagaer T.; Nadaziki N., Yamakawa H., Kikuno R., Obara O., Nagaer T.; Nadaziki N., Yamakawa H., Kikuno R., Obara O., Nagaer T.; Nadaziki N., Yamakawa H., Kikuno R., Obara O., Nagaer T.; Nadaziki N., Nadaziki N., Nadaz
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426 LeuGluLeuLeuLeuGlnIleAlaAsnLysIleGlnAsnGlyAlaLeuAsnCysGluGlu 445
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0.1-FEB-2005 (TYEMBLICEL. 29, Last sequence update)
13-SEP-2005 (TYEMBLICEL. 1), Last annotation update)
Microtubule-actin crosslinking factor 1.
Name-MACF1; ORFNames-RP11-69E11.1-001;
Homo sapiens (Human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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446 LysLeuThrLeuAlaLysAsnThrLeuGln---------
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AL442071; CAH73668.1; -; Genomic_DNA.
EMBL; AL137853; CAI21814.1; -; Genomic_DNA.
EMBL; AL355277; CAI16417.1; -; Genomic_DNA.
EMBL; AL355477; CAI16417.1; -; Genomic_DNA.
EMBL; AL37853; CAH73668.1; JOINED; Genomic_DNA.
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      Alignment Scores:
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Potential.
Potential.
R InterPro; IPR001715; Calponin act bd.
R InterPro; IPR011992; EF-Hand Type.
R InterPro; IPR002048; EF-Hand Type.
R InterPro; IPR00310452; SH3.
R InterPro; IPR00310452; SH3.
R InterPro; IPR001452; SH3.
R InterPro; IPR001452; SH3.
R InterPro; IPR001452; SH3.
R Ffam; PF00036; efhand; 2.
R Pfam; PF00036; efhand; 2.
R Pfam; PF00036; EF-hand; 1.
R SMART; SM00043; EF-hand; 1.
R SMART; SM00043; EF-hand; 1.
R SMART; SM00150; SPEC; 33.
R R ROSITE; PS00019; ACTININ 1; 1.
R R ROSITE; PS00012; ACTININ 1; 1.
R R ROSITE; PS00012; ACTININ 2; 1.
R R ROSITE; PS00018; EF-HAND 1; 2.
R R ROSITE; PS50012; EF-HAND 1; 2.
R R ROSITE; PS50013; ACTININ 2; 1.
R ROSITE; PS50013; ACTININ 2; 1.
R ROSITE; PS50013; ACTININ 2; 1.
R ROSITE; PS50013; ALTENIN 2; 2.
R ROSITE; PS50014; EF-HAND 1; 2.
R ROSITE; PS50014; EF-HAND 1; 2.
R ROSITE; PS50014; EF-HAND 1; 2.
R ROSITE; PS50014; EF-HAND 1; 2.
R ROSITE; PS50014; EF-HAND 1; 2.
R ROSITE; PS50014; EF-HAND 1; 2.
R ROSITE; PS50014; EF-HAND 1; 2.
R ROSITE; PS50014; EF-HAND 1; 2.
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R ROSITE; PS50014; EF-HAND 1; 2.
R ROSITE; PS50014; EF-HAND 1; 2.
R ROSITE; PS50014; EF-HAND 1; 2.
R ROSITE; PS50015; RIJ; FALES NEC.
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Spectrin 34.
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Spectrin 36.
Spectrin 37.
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Spectrin 2.
Spectrin 3.
Spectrin 4.
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Spectrin 9.
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Spectrin 15.
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127 AATCTGTATATATTTGCGGATGAATTACATCTGGGAATGGGCTGCCCTGCA----- 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 AAAATAAGTTGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAAAGCAGA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 AATCGGATACATACATATGTATATGAGTTTATATATGTTGTTGTGGTGATTGTGGCCATCAGG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 ACAAGGGTAGTTTCTGAGGAAACTCTCTTTTTCAAACCGAGCTGTACTTTACCCCAAGG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 AATATAGATCATGACCTCAGGAAATCCATTTGGAGTGTTCCACC---TCTAGGAAA--- 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 TTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCTGAGAACCTCCATGTG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00018; EF HAND; 2.
PROSITE; PS00659; GLYCOSYL HYDROL F5; UNKNOWN 1.
SEQUENCE 5430 AA; 620418 MW; 4C0CB72BDFBF9777 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-664-025-43_COPY_53_511 (1-459) x Q5VW20_HUMAN (1-5430)
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              EMBL; AL365277; CAH73668.1; JOINED; GENOMIC_DNA. BYBL; AL365277; CAH73668.1; JOINED; GENOMIC_DNA. BYBL; AL365277; CAH721844.1; JOINED; GENOMIC_DNA. BYBL; AL365277; CAH21844.1; JOINED; GENOMIC_DNA. BYBL; AL37853; CAH16477.1; JOINED; GENOMIC_DNA. BYBL; AL355477; CAH16417.1; JOINED; GENOMIC_DNA. BYBL; AL355477; CAH16417.1; JOINED; GENOMIC_DNA. BYBL; AL356277; CAH70156.1; JOINED; GENOMIC_DNA. BYBL; AL37853; CAH70156.1; JOINED; GENOMIC_DNA. BYBL; AL37853; CAH70156.1; JOINED; GENOMIC_DNA. BYBL; AL37853; CAH70156.1; JOINED; GENOMIC_DNA. BYBL; AL356277; CAH70156.1; JOINED; GENOMIC_DNA. BYBL; AL365277; CAH70156.1; JOINED; GENOMIC_DNA. BYBL; AL365277; CAH70156.1; JOINED; GENOMIC_DNA. SYR; QSVW20; 68-301. CAH70156.1; JOINED; GENOMIC_DNA. GO; GO:0005509; F:calcium ion binding; IEA. GO; GO:0005509; F:calcium actin bd. InterPro; IPRO01715; Calponin act_bd.
InterPro; IPRO01715; Calponin act_bd.
InterPro; IPRO01715; Calponin act_bd.
InterPro; IPRO01715; Calponin act_bd.
InterPro; IPRO01715; Galponin act_bd.
InterPro; IPRO01715; Galponin act_bd.
InterPro; IPRO01715; Galponin act_bd.
InterPro; IPRO0187; Glyco_hydro_5.
InterPro; IPRO0187; Spectrin.
Pfam; PF00187; GAS2; 1.
Pfam; PF00187; Spectrin, 27.
Pfam; PF00187; Spectrin, 27.
Pfam; PF00187; CH: 2.
Pfam; PF00187; CH: 2.
Pfam; PF00185; Spectrin, 27.
ProDom; PF000012; EF-Dand; 1.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
   Genomic_DNA
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SWART; SW00033; CH; 2.
SWART; SW00054; EFh; 2.
SWART; SW00150; SPEC; 3.
FROSITE; PS00019; ACTININ_1; 1.
PROSITE; PS00019; ACTININ_2; 1.
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Db 531 HisPheThrSerLeuGluLeuValProProSerThrLeuThrThrHisLeuLysAla 550
Qy 397 GATCCT 402
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Db 551 GluPro 552
Search completed: May 9, 2006, 10:09:19
Job time: 122.9 secs
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo:

1 (bases 1 to 512)
S Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.
EST and encoded human protein
Patent: JP 2002010789-A 36 15-JAN-2002;
GENSET CORP
OS Homo sapiens (human)
PN JP 2002010789-A/36
PP 07-AUG-2000 JP 200280989
PR 05-AUG-1999 US 60/147499
PR 05-AUG-1999 US 60/147499
PR JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI
                                                                                                                   AX748179 Sequence
AK093517 Homo sapi
AX588689 Sequence
BD110503 EST and e
AR414950 Sequence
BD119756 EST and e
AR414203 Sequence
BD119756 EST and e
AK941203 Sequence
BD10979 EST and e
AK941203 Sequence
CC09498 Mus muscu
BD109279 EST and e
AK917056 Sequence
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                                                                                   Homo sapi
Homo sapi
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JP 2002010789-A/36
JP 20020107090-A/36
07-AUG-2000
05-AUG-1999 US 60/147499
JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C12NS/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00,
 CQ737424 SBD109278 BD109278 AX413725 AX577405 CS072271 AX5774405 AX60226 BC048121 BD275948
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BD127476 E
CQ783102 S
AK075086 H
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JP 2002010789-A/36.
Homo sapiens (human)
Homo sapiens
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PC C12N5
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ACCESSION
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TITLE
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-MODEL=frame+ p2n.model -DEV=xlp
-MODEL=frame+ p2n.model -DEV=xlp
-G=Abss/ABSSWEB spool/US10664025/runat_08052006_173641_29351/app_query.fasta_1
-DB=GenEmbl -QFWT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX-Eblosum62 -TRANS=human40.cdi -LIST4-45
-UNITS=bits -START=1 -END=-1 -MATRIX-Eblosum62 -TRANS=human40.cdi -LIST4-65
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UOTFWT=papto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US1064025_@CGN 1 1 7724 @runat 08052006_173641_29351 -NCPU=6 -ICPU=3
-NO_WMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGCLOG -DEV_TIMEOUT=170
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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AR412406 Sequence
AX969240 Sequence
                                                                                            (without alignments)
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                                                                              9, 2006, 13:15:42 ; Search time 4123.8 Seconds
                                                                                                                                                                                                                                                                          11766282
          GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                     nucleic search using frame plug p2n model
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                                                                                                                                                                                                                                                    5883141 seqs, 28421725653 residues
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Listing first 45 summaries
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AR412406
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
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Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
EST's and encoded human proteins
Patent: US 6639063-A 43 28-OCT-2003;
WOX;
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                                                                             Key Location/Qualifiers CDS 53. 511
sig_peptide 53. 103. Location/Qualifiers 1. 512 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
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Sequence 43 from patent US 6639063.
AR412406 AR412406.1 GI:40167516
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                                                                                          1 MetAlaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAlaGluAsnLeu
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                                                                                                                                                                                                                                                                                             41 SerArgAenLeuTyrIlePheAlaAspGluLeuHisLeuGlyMetGlyCysProAlaAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dumas Milne Edwards,J.B., Jobert,S. and Giordano,J.Y. ESTs and encoded human proteins
Patent: EP 1104808-A 43 06-JUN-2001;
Genset (FR)
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/note="unnamed protein product"
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AX969240
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1. .512
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                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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477 151 0 0 0

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 642)
S Edwards, J. B. D. M., Jobert, S. and Giordano, J. E.

EST and encoded human protein
D Patent: JP 2002010789-A 1355 15-JAN-2002;
GENSET CORP
OS Homo sapiens (human)
PN JP 2002010789-A/1355
PD 15-JAN-2002
PP 07-AUG-2000 JP 2000208099
PR 05-AUG-1999 US 60/147499
PI JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI
                                                                                                                                                                                                                              81 ArgValValSerGluGluThrLeuLeuPheGlnThrGluLeuTyrPheThrProArgAsn 100
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Matches:
Conservative:
Mismatches:
Indels:
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     DNA"
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JP 2002010789-A/1355.
Homo sapiens (human)
Homo sapiens
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PC C12N5
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VLMLLAVLIWTGA/EN"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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PE Corporation (NY) (US)
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Sequence 23358 from Patent WO02068579.
CQ737424 GI:42335713
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Location/Qualifiers
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PAT 18-SEP-2002

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1. 642
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AX970559
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Unclassified.
Unclassified.
1 (bases 1 to 642)
Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
EST's and encoded human proteins
Patent: US 6639063-A 1362 28-OCT-2003;
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Indels:
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AR413725.
AR413725.1 GI:40168835
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          Von Heijne matrix
score 10.699998092651
seq VLMLLAVLIWTGA/EN
Key 53. .526
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Query Match:
DB:
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AR413725
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PAT 15-JAN-2004
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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ESTs and encoded human proteins
Patent: EP 1104808-A 1362 06-JUN-2001;
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VLMLLAVLIWTGA/EN"
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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gespy polymicleotides and polypeptides and uses thereof
Patent: WO 02060466-A 2 08-AUG-2002;
GENSET (FR)
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Sequence 2 from Patent WO02060466.
AX574405
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Query Match:
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VLMLLAVLIWTGA/EN"
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                                                                                                                                                                                              Dumas Milne Edwards, J.B., Bougueleret, L. and Jobert, S. Full-length human cDMAs encoding potentially secreted proteins Patent: WO 201042451-A 19 14-JUN-2001; Serono Genetics Institute S.A. (FR) Location/Qualifiers
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BC036256 1502 bp mRNA linear PRI 28-JUL-2005
Homo sapiens hypothetical protein FLJ36198, mRNA (cDNA clone
MGC:43628 IMAGE:5270384), complete cds.
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1 (bases I to 1502)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wang, J., Wang, J., Hsieh, F.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
and death
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Matches:
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Indels:
Proteins associated with cell growth, Patent: WO 02072830-4 16 19-SEP-2002; Incyte Genomics, Inc. (US) Location/Qualifiers
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Homo sapiens hypothetical protein FLJ36198, mRNA (cDNA clone MGC:57403 IMAGE:5266642), complete cds.
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                US-10-664-025-3903 (1-153) x BC036256 (1-1502)
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Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramon, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Kodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnorch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki

CDNA Library Preparation: (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Whe site: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 74 Row: k Column: 9
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 42476002. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MALEVIMILAVLIWTGAENLHVXISCSLDWLMVSVIPVAESRNL
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                                                                                                                                                                                                                                                                                                                                                                           NIH MGC Project
Direct Submission
Submitted (31-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                 human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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PAT 17-JUL-2003
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36 CGGATACATACATATGTATATGAGTTTATATATCTTGTTGTGATTGTGCCATCAGGACA 425
                                                                                                                               LeuThrProValSerThrGluAsnGluIleLysLeuAspProSerProPheIleAlaAsp 140
                                                                                                                                                                                                           Euteleostomi;
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Brianyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

E 1 (bases 1 to 1898)
S Birse, C.B., Mouret, P.A., Florence, K.A., Ruben, S.M.,
Komatsoulis, G.A., Ni, J., Ebner, R., M.D., Lafleur, Olsen, H.S.,
Shi, Y., Soppet, D.R., Rosen, C.A. and Young, P.E.
62 Human secreted proteins
Fatent: JP 2002543771-A 26 24-DEC-2002;
Human Genome Schences Inc
OS Homo sapiens
PN JP 2002543771-A/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PD 24-DEC-2002
PF 06-APR-2000 JP 2000611564
PR 09-APR-1999 US 60/128693,26-APR-1999 US 60/130991 PI
charles e birse,paul a mouret,kimberly a florence,steven m PI
                                                                                                          101 IleAspHisAspProGlnGluIleHisLeuGluCysSerThrSerArgLysSerValTrp
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Key Location/Qualifiers
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lafleur,henrik s olsen,
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1. 1898
Acrganism="Hono sapiens"
//nol_type="genomic DNA"
/do_xref="taxon:9606"
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62 Human secreted proteins.
BD275948
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JP 2002543771-A/26.
Homo sapiens (human)
Homo sapiens
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JP 2002543771-A/26
24-DEC-2002
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Query Match:
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                              NIH MGC Project

Direct Submission

L Submission

L Submitted (04-MAR-2003) National Institutes of Health, Mammalian
Submitted (04-MAR-2003) National Institutes of Health, Mammalian
Gene Collection (MCC), Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: http://mgc.nci.nih.gov

Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLML)

DNA Sequencing by: Institute for Systems Biology

http://www.systemsbiology.org

contact: amadan@systemsbiology.org

Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 106 Row: j Column: 14 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 42476002. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="walevimidavijumgaenihvkiscsidmimusvipvaesrni
Yifadbihilgogcpanrihtyvyefiylvrdcgirtrvvsbettleqtbiytetprtid
HDPQBIHLECSTSRKSVWLTPVSTENEIKLDPSPFIADFQTTAEBLGILSSSPNLI"
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                                                                                                                                                                                        Shiraki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCTGAGAACCTC 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 CATGTGAAAATAAGTTGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAA 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein LOC219990"
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| db_xref="GeneID:219990"
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Matches:
Conservative:
Mismatches:
Indels:
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186. 662
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Cta, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sakine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishi, Shibahara, T., Tanaka, T., Ishi, Shibahara, T., Tanaka, T., Ishi, Shiratori, A., Sado, H., Hosoiri, T., Kawai, Y., Nakamura, Y., Nagahari, K., Murakani, K., Yasuda, T., Ishida, K., Kadaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Carai, H., Kikawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Huracka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watsunabe, N., Huracka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watsunabe, N., Hara, M., Tanasa, T., Kusano, J., Kanehori, K., Takahashi, Fuji, A., Takau, Y., Susuki, M., Matsunabe, S., Sosida, M., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shohata, N., Satoh, N., Takami, S., Shohata, N., Sano, S., Moriya, S., Moniyama, H., Satoh, N., Takami, S., Shohata, N., Sano, S., Moriya, S., Senoh, A., Mizoguchi, H., Kawatanabe, K., Kumagai, A., Itakura, S., Puliwara, T., Yamazaki, M., Watanabe, T., Kumagai, A., Itakura, S., Puliwara, T., Pulimori, Y., Kumagai, A., Itakura, S., Puliwara, T., Watanabe, T., Moriyama, A., Takama, A., Takemo, M., Ohmori, Y., Kumagai, T., Matanumi, Y., Matanabe, T., Matanabe, M., Komatan, H., Ikana, Y., Okamoro, S., Okitani, R., Kawakami, T., Matanumi, Y., Matanabe, M., Mata, H., Matanabe, M., Kawakami, K., Hira, Y., Mizuo, T., Morinaga, M., Sasaki, M., Takakami, Y., Matanabe, M., Komatau, T., Matanabe, M., Komatau, K., Ohmura, K., Nawa, M., Hata, H., Watanabe, M., Komatsu, T., Matanabe, M., Komatsu, T., Matanabe, M., Komatsu, T., Matanabe, M., Kawakami, Y., Wawashi, K., Yamashi, K., Yamashi, K., Yamashi, Y., Wasashi, K., Yamashi, Y., Wanani, K., Yada, T., Matanabe, M., Watanabe, T., Nomura, W., Kikuchi, H., Matanabe, T., Nawai, K., Yamashi, Y., Wanani, K., Yamashi, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1492 bp mRNA linear PRI 30-JAN-2004
Homos appiens cDNA FLJ36198 fis, clone TEST12028242, weakly similar
AK093517
                                                                                                                                                                                        81 ArgValValSerGluGluThrLeuLeuPheGlnThrGluLeuTyrPheThrProArgAsn 100
                                                                                                                                                                                                                                                                          | IleAspHisAspProGlnGluIleHisLeuGluCysSerThrSerArgLysSerValTrp 120
                           352 ATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTG 411
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                         61 ArgileHisThrTyrValTyrGluPheIleTyrLeuValArgAspCysGlylleArgThr
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Oligo capping; fis (full insert sequence).
Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                               HisValLyslleSerCysSerLeuAspTrpLeuMetValSerVall1eProValAlaGlu 40
                                                                                                       ArgValValSerGluGluThrLeuLeuPheGlnThrGluLeuTyrPheThrProArgAsn 100
                                                                                                                                                                                                                                                                                           314
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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                                                                                                                                                               61 ArgileHisThrTyrValTyrGluPheIleTyrLeuValArgAspCysGlyIleArgThr
                                                                                                                                                                                                                                                                        255 AGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Figure, 1-10. The sequences Part - 1-10. The sequences Partner: EP 1308459-A 1704 07-MAY-2003; Helix Research Institute (JP); Research Association for Biotechnology (JP)
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Indels:
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AX748179.1 GI:32132567
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Homo sapiens
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LOCUS
DEFINITION
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VERSION
KEYWORDS
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Location/Qualifiers
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                                                                                                                                                                                                                                       3 (bases 1 to 1492)
Brogai, .. and Yamamoto, J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
                  Ono,Y., Hotuta,T., Hiraoka,S., Murakawa,K., Takiguchi,S.,
Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M.,
Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M.,
Wakamatsu,A., Ishii,S., Yamama,T., Irie,R., Kawat-Hio,Y.,
Saito,K., Nishikawa,T., Kimura,K., Matsuo,K., Nakamura,Y.,
Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Takahashi-Fujii,A.,
Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.,
NEDO human cDNA sequencing project
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 AGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT 351
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  Ishibashi,T., Kanehori,K., Yosida,M., Watanabe,S., Ishida,S.
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                               352 ATAGATCATGACCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGGG
IleAspHisAspProGlnGluIleHisLeuGluCysSerThrSerArgLysSerValTrp
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Search completed: May 9, 2006, 14:49:44 Job time : 4129.8 secs

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Adb3550 Human sec
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Aba25212 Pr
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Aai15997 H
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Aai38038 H
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AAH64148
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AAK92136
AAK93954
ADL30381
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AAK93399
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AAV87718
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ACF57863
ABAZ5212
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AAT38038
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AAH64743
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Abk90053 DNA encod
Abs78646 Human cDN
Aac69528 Human sec
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                                                                                                     9, 2006, 13:15:10 ; Search time 795.6 Seconds
              GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                        nucleic search, using frame plus p2n model
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Listing first 45 summaries
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ABK90053
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Human

BP.

ABK90053 standard; DNA; 1337

ABK90053

(first entry)

05-NOV-2002

ABK90053;

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The invention relates to full length GENSET human nucleic acids encoding potentially secreted proteins. The nucleic acids and the polypeptides they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GENSET gene expression. For example, they be used to treat disorders associated with decreased GENSET gene expression by rectifying mutations or deletions in a patient's gene expression by rectifying mutations or deletions in a patient's gene expression by rectifying mutations or deletions in a patient's patients own production of GENSET polypeptides. Conversely, antisense nucleic acid molecules may be administered to down regulate GENSET expression. The sense and antisense nucleic acids may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic assays to detect and quantitate the presence of similar nucleic assays to detect and quantitate the presence of similar nucleic assays to detect and quantitate the presence of similar nucleic assays to destorative therapy. The GENSET polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of GENSET polypeptide the expression and activity. The present sequence is a GENSET pucleic acid of
                                                                                                                                                                           Full length GENSET human nucleic acids encoding potentially secreted proteins, useful in gene therapy and vaccination against a variety of diseases, and for diagnosis of those diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Page 579; 921pp; English
WPI; 2001-367870/38
                                                    P-PSDB; AAG89140
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Sequence 691 BP; 198 A; 126 C; 151 G; 216 T; 0 U; 0 Other;

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1 MetAlaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAlaGluAsnLeu
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151
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    461
42 AIGGCGTIAGAAGICTIGAIGCTCCTCGCTGTCTIGAITITGGACCGGTGCTGAGAACCTC 101
                                                                                                                  102 CATGTGAAATAAGTTGCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAA 161
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                                                                                                                                                                                                162 AGCAGAAATCTGTATATATTTGCGGATGAATTACATCTGTGGGAATGGGCTGCCCTGCAAAT
                                                                                                                                                                                                                                                                                                                                                                                                      282 AGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT
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Human; GSSP3; circulating blood glucose level; insulin sensitivity; body mass; serum glucose regulation; body weight loss; obesity; metabolic-related disorder; impaired glucose tolerance; stroke; insulin resistance; hyperlipidaemia; atherosclerosis; hear disease; hypertension; syndrome C; type I diabetes; type II diabetes; microangiopathy; retinopathy; neuropathy; nephropathy; ocular lesion; polycystic ovarian syndrome; acanthosis nigrican; leprechaunism; lipoatrophy; physical performance; exercise; dyslexia; schizophrenia; attention-deficit disorder; hyperactivity disorder; psychiatric disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            microanglopathy, retinopathy, neuropathy, nephropathy, polycystic ovarian syndrome, ocular lesions, microanglopathic lesions, or syndromes such as acanthosis nigricans, leprechaunism and lipoatrophy). The polypeptides are also useful to improve physical performance during work or exercise, and to treat dyslexia, attention-deficit disorder, attention-deficit/hyperactivity disorder, and psychiatric disorders such as schizophrenia. The present sequence encodes human GSSP3 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide, and polynucleotide sequences that encode it. The GSSP3 polypeptide reduces circulating blood glucose levels, increases insulin sensitivity, and/or reduces body mass. The GSSP3 polypeptide and polynucleotide sequences are useful in serum glucose regulation, fatty acid metabolism, body weight loss, and prevention of body weight gain. Compositions comprising GSSP3 polypeptides are useful for controlling blood glucose levels, for treating metabolic-related diseases or disorders (e.g. obesity, impaired glucose tolerance, insulin resistance, hyperlipidaemias, atherosclerosis, heart disease, hypertension, stroke, syndrome C, type I or II diabetes, diabetes related complications,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reducing circulating glucose levels or increasing insulin sensitivity, useful for reducing body mass or preventing body weight gain, comprises administering composition comprising GSSP3 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yen-Potin F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention relates to the isolation of human GSSP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1337 BP; 457 A; 214 C; 240 G; 426 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chicca J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                "GSSP3 polypeptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 95-96; 97pp; English
                                                                                                        DNA encoding human GSSP3 polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; ss; gene; cell growth; differentiation; death; CGDD; cancer; cell proliferative disorder; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; paroxysmal nocturnal haemoglobinuria; psoriasis; polycythaemia vers; primary thrombocytopsenia; developmental disorder; renal tubular acidosis; anaemia; mental retardation; epilepsy; AIDS; neurological disorder; Alzheimer disease; Parkinson's disease; asthma; reproductive disorder; alzheimer disease; Parkinson's disease; asthma; inflammatory disorder; infertility; autoimmune disorder; gout; allergy; autoimmune thyroiditis; context dermatitis; Crohn's disease; infection; diabetes mallitus; glomerulonephritis; irritable bowel syndrome; multiple gclerosis; osteoporosis; pancreatitis;
                                                                                                                                                                      53 ATGCCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGTGCTGAGAACCTC
                                                                                                                                                MetalaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAlaGluAenLeu
                                                                                                                                                                                                            HisValLysIleSerCysSerLeuAspTrpLeuMetValSerValIleProValAlaGlu
                                                                                                                                                                                                                                   113 CATGTGAAATAAGTTGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAA
                                                                                                                                                                                                                                                                        SerArgAsnLeuTyrIlePheAlaAspGluLeuHisLeuGlyMetGlyCysProAlaAsn
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                                Matches:
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                                                                                           Gaps:
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Best Local Similarity:
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Alignment Scores:
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The invention relates to an isolated polypeptide comprising CGDD1-12 (cell growth, differentiation and death), a naturally occurring amino acid sequence at least 90% identical to CGDD, a biologically active CCC acid sequence at least 90% identical to CGDD, a biologically active fragment or an immunogenic fragment. Also included are the comprising a promoter sequence operably linked to the CGDD comprising a cell transformed with the recombinant polynucleotide, an anticody, screening for compounds which bind to/modulate or are antibody, screening for compounds which bind to/modulate or are compliants of CGDD or alter the expression of CGDD polynucleotide and account antibody, screening for compounds which bind to/modulate or are compliants of CGDD polynucleotide microarray. The polypeptides, polynucleotide and a cGDD polynucleotide microarray. The polypeptides, polynucleotide and account and antagonists are useful for diagnosing, treating or comprises of CGDD reventing disorders associated with aberrant expression of CGDD, particularly cell proliferative (e.g. arteriosolerosis, atherosolerosis, cirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia cycles, particularly cell proliferative (e.g. arteriosolerosis, polycythaemia cycles; paroxysmal nocturnal haemoglobinuria, polycythaemia cycles; cirrhosis, proriasis, primary thromobocytopaemia or cancer), development of disorders (e.g. renal tubular acidosis, anaemia or mental retardation), neurological disorders (e.g. Alzheimer disease, parkinson's disease or cyclesis, productis, contact dermatitis, crohn's disease, parkinson's disease or cyclesis, cacquired immunodeficiency syndrome) allergies, asthma, autoimmune cyclement, and the area also useful in the assessment of the effects of conferce and produced or account of the effects of conferce and produced or account of the effects of conferce and produced or account of the effects of conferce and produced or account of the effects of a conferce of produced or account of the effects of a conferce 
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Burford N;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human proteins associated with cell growth, differentiation death, useful for diagnosing, treating or preventing autoimmune inflammatory disorders (e.g. AIDS, allergy or anemia), cancer, atherosclerosis or hepatitis.
                                                                                                                                                                                                                                                                                  Lu Y, Warren BA, Elliott VS,
Tang TY, Lal PG, Duggan BM,
an UK, Khare R, Walia NK;
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Xu Y, Gietzen KJ, Tang
Richardson TW, Tran UK,
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                                 09-FEB-2001; 2001US-0268111P.
23-FEB-2001; 2001US-027115F.
08-MAR-2001; 2001US-0274503P.
09-MAR-2001; 2001US-0274552P.
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           AGCAGAAATCTGTATATTTTGCGGATGAATTACATCTGGGAATGGGCTGCCCTGCAAAT
                                                                             81 ArgValValSerGluGluThrLeuLeuPheGlnThrGluLeuTyrPheThrProArgAsn
                                             209 CGGATACATACATATGTATATGAGTTTATATATATCTTGTTCTTGTGTTTGTGGCATCAGGACA
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                                 ArgileHisThrTyrValTyrGluPheIleTyrLeuValArgAspCysGlyIleArgThr
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Shi Y;
Birse CE;
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Florence KA,
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Olsen HS, Ebner
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rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms of the breast or liver; (c) cardiovascular disorders e.g. cardiac arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e) angiogenesis; (f) nervous system disorders e.g. Alzheimer's disease; (g) infections caused by bacteria, viruses and fungi; and (h) ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis
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The present invention relates to novel human secreted proteins (ABR41633-ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins can their coding sequences are useful for the preparation of a diagnostic or pharmaceutical composition for diagnosing or treating a cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary artistisclerosis and mycazdial ischaemia), neural disorders, immune system disorders, pulmonary disorders, renal disorders, immune system disorders and/or cancerous diseases and conditions, for conditions and epithelial cell proliferation, to treat inflammation or infection, for treating thrombosis and arteriosclerosis, for treating or preventing neural damage which occurs in neuronal disorders or preventing neural damage which occurs in neuronal disorders or preventing neural damage which occurs in neuronal disorders or containing or neurodegenerative conditions such as Alzaimer's diseases and bane contained and periodontal resembation and aid in tissue transplants or bone grafts, to prevent skin aging or hair loss, to transplants or bone grafts, to prevent skin aging or hair loss, to organs before transplantation or for supporting cell culture of primary corgans before transplantation or for supporting cell culture of primary corgans before transplantation or for supporting cell culture of primary cells metabolism. Note: The sequence data for this patent was published in celetronic format and is available from WIPO at
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                                                                                                                                                                                                                                                           secreted proteins, useful for detecting, preventing, prognosticating, treating and/or ameliorating cardiovascular
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                                                                                                                                                                                                                                                                                                                                       Claim 21; SEQ ID NO 309; 1881pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                           Novel human secreted proteins,
                                                     21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
                                                                                                                                                                                                                                                                                                  disorders such as arrhythmia.
                  19-MAR-2002; 2002WO-US009785.
                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
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protein genes, and ABP00011-ABP00299 represent the proteins they encode.

Divotein genes, and ABP00011-ABP00299 represent the proteins they encode.

ABZ71479-ABZ714740 represent human secreted protein genomic fragments. The invention also encompasses antibodies specific for the secreted proteins, continued in drug screening, and recombinant vectors and host cells comprising a nucleic acid of the invention. The secreted proteins, nucleic acids encoding them, antibodies or antibody fragments specific for the secreted proteins, and modulators of protein activity are useful for diagnosing, treating, ameliorating or preventing digestive disorders. Such conditions include disorders of the mouth, coesophagus, stomach, small intestine, large intestine, liver, billary tract and pancreas, and include cancers of these organs and tissues. The secreted proteins and their nucleic acids may also be used in the secreted proteins and their nucleic acids may also be used in the creatment of immune disorders, inflammation, inflection, chromosome coff the invention may be used for chromosome identification, chromosome mapping, in gene therapy, for identifying individuals from minute
                                                                  LeuThrProValSerThrGluAsnGluIleLysLeuAspProSerProPheIleAlaAsp 140
                                                                                                                                                                   CTTACACCAGTTTCTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTATTGCTGAC 434
255 AGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; secreted protein, digestive disorder; gastrointestinal disorder; mouth; oesophagus; stomach; small intestine; large intestine; liver; biliary tract; pancreas; cancer; tumour; hyperproliferative disorder; immune disorder; inflammation; infection; wound healing; drug screening; chromosome identification; chromosome mapping; cycostatic; antiinflammatory; immunosuppressive; vulnerary; gene therapy; gene; ss.
                                       IleAspHisAspProGlnGluIleHisLeuGluCysSerThrSerArgLysSerValTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human secreted proteins and nucleic acids, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating e.g. gastrointestinal diseases and disorders, or cancers.
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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Ruben SM;
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                                                                                                                                                       MetalaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAlaGluAsnLeu
biological samples, as hybridisation probes, and as molecular weight markers. The present sequence represents a human secreted proteinencoding cDNA clone of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Secreted protein; gene therapy; antidiabetic; diabetes; human; ss.
                                      Sequence 1898 BP; 595 A; 315 C; 332 G; 654 T; 0 U; 2 Other;
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19-JUL-2001; 2001US-0306171P.
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The invention relates to isolated nucleic acid molecules ADB91065-
ADB91448 and ADB91835-ADB91911 encoding human secreted proteins ADB91449-
ADB91843. Also disclosed is a recombinant vector comprising a
polynucleotide of the invention, and a recombinant host cell comprising
the recombinant vector. The polypeptide of the invention is useful in
the recombinant vector. The polypeptide of the invention is useful in
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the recombinant vector. The polypeptide of the invention is useful in
the recombinant vector. The polypeptide of the invention is useful in
the cases activity of the polypeptide. The polypeptide with a
binding partner, and determining whether the binding partner increases or
decreases activity of the polypeptide. The polypeptide of polynucleotide,
antibody or its fragment, agonist or antagonist are useful for preparing
antibody or its fragment for diagnosing or treating diabetes or
conditions related to diabetes. The present sequence is that of the human
immunoglobulin Fc portion used to generate fusion proteins, increasing
the stability of the fused protein as compared to the secreted protein
conly. Note: The sequence data for this patent did not form part of the
printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Nucleic acid encoding a human secreted protein is useful in diagnosing treating diabetes or conditions related to diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel human secreted polypeptide comprising a defined sequence given in the specification. The polypeptide, nucleic acid molecule, antibody, agonist or antagonist of the invention may be useful for preparing a composition for diagnosing or treating a haemopoletic or haematologic disorder such as anaemia, autoimmune disorders such as rheumatoid arthritis, inflammation, Grave's disease, disorders including parthinson's disbetes, systemic lumps erythematomus or glomerulonophritis, neurodegenerative disorders including Parkinson's disease and Alzheimer's disease, wounds and hyperproliferative disorders including atherosclerosis or cancer, as well as bacterial, viral, fungal or parasitic infections. The polypeptide may also be used during gene therapy procedures and for identifying a binding partner by contacting the polypeptide with a binding partner and determining whether the binding partner increases or decreases the activity of the polypeptide. The current sequence is that of the human secreted protein-related DNA of the invention.
                                                                                                                                  antianaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid; antidiabetic; immunosuppressive; dermatological; nephrotropic; antidathritoring antiparkinsonian; neuroprotective; nootropic; antibacterial; virucide; fungicide, antiparastic; antiarteriosclerotic; vulnerary; cytostatic; haempooietic; haematologic; anaemia; autoimmune disorder; heumatologic; anaemia; autoimmune disorder; systemic lupus erythematosus; glomerulonephritis; neurodegenerative; systemic lupus erythematosus; glomerulonephritis; neurodegenerative; Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis; cancer; bacterial; viral; fungal; parasitic infection; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human secreted polypeptide for diagnosing, preventing or treating hematopoietic or hematologic disorders (e.g. anemia), autoimmune disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or atherosclerosis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 595 A; 315 C; 332 G; 654 T; 0 U; 2 Other;
                                                                                                    - SEQ ID 356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 27; SEQ ID NO 356; 2272pp; English.
                                                                                                    Human secreted protein-related DNA
 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
ADC73723 standard; DNA; 1898
                                                                                                                                                                                                                                                                                                                                                                                                                            19-MAR-2002; 2002WO-US008277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA, Ruben SM;
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                                                                                                                                                                                                                                                                                        human; gene; ds
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                                                                 01-JAN-2004
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1898 151 0 0 0

Conservative: Mismatches: Length: Matches:

3.19e-89 789.00 100.0% 100.0% 98.7%

Percent Similarity: Best Local Similarity: Query Match:

Alignment Scores:

Indels:

US-10-664-025-3903 (1-153) x ADC73723 (1-1898)

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134
                                                                                                                                                                                                                                                IleAspHisAspProGlnGluIleHisLeuGluCysSerThrSerArgLysSerValTrp 120
                                                                                                                                                                                                                                                                                                Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                194
                                                                                                                                                                    254
                                                                                                                                                                                            ArgValValSerGluGluThrLeuLeuPheGlnThrGluLeuTyrPheThrProArgAsn 100
                                                                                                                                                                                                            AGGGTACTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT 314
                                                                                                                                                                                                                                                                         ATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGG 374
          74
                                    HisValLysIleSerCysSerLeuAspTrpLeuMetValSerValIleProValAlaGlu 40
                                                                                      9
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                                                  SerArgAsnLeuTyrIlePheAlaAspGluLeuHisLeuGlyMetGlyCysProAlaAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; 88; gene; pharmaceutical; diagnostic; gene therapy;
tissue regeneration; cell regeneration; membrane protein;
signal transduction-related protein; transcription-related protein;
osteoporosis; neurological disease; cancer; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= "Clone TESTI20282420 protein"
                                                                                                                                                                                                                                                                                                                                                       151
                                                                                                                                                                                                                                                                                                                                                                    TTTCAGACACAGCAGAAGAGTTAGGATTATTA 467
                                                                                                                                                                                                                                                                                                                                                     PheGlnThrThrAlaGluGluLeuGlyLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cDNA encoding clone TESTI20282420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
52. .528
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADB63550 standard; cDNA; 1492 BP
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RES ASSOC BIOTECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-NOV-2001; 2001JP-00379298.
25-JAN-2002; 2002US-00350978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-450961/43.
P-PSDB; ADB65520.
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(REAS-) 1
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The invention discloses a polynuclectide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel colypeptides. Also claimed is a polypeptide encoded by the polynuclectide or its partial peptide, an antibody binding to the polypeptide or peptide of the polynuclectide, immunologically assaying the polypeptide or peptide of the polynuclectide by contacting the polypeptide or peptide of the manipody of the encoded protein, and observing the binding between the two, a transformant carrying the polynuclectide in peptide or expressible manner and an antisense polynuclectide. The oligonuclectide is useful as a primer for synthesising the polynuclectide in a a probe for detecting the polynuclectides and encoded proteins are useful as pharmaceutical agents and many disease-related proteins are useful as pharmaceutical agents and many disease-related of genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell regeneration. Membrane proteins, signal transduction-related proteins, cof generation of used so indicacors for diseases (e.g. osteoporosis, encoding them can be used as indicacors for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours. The cDNA may be used to regulate the activity or expression of the encoded protein or treat diseases. The sequence presented is a cDNA of the invention. Note: Some of the sequence activity or expression of the invention. Note: Some of the sequence is based on sequence information supplied by the European Patent Office.
polynucleotides and polypeptides, useful for developing a diagnostic ter or medicines for regulation of their expression and activity, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1492 BP; 452 A; 250 C; 272 G; 518 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                  Claim 1; Page; 222pp; English.
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785.00
99.3%
99.3%
                                                                                                   targets of gene therapy.
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1 MetAlaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAlaGluAsnLeu 1492 150 0 0 0 US-10-664-025-3903 (1-153) x ADB63550 (1-1492) Gaps: Percent Similarity: Alignment Scores: Query Match: DB: Best ò 셤 셤 ò g ò ò

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The present invention relates to novel GENSET polynucleotides (ABZ36404-ABZ36911) encoding polypeptides (ABP75963-ABP76368). The polynucleotides and polypeptides are useful in screening and diagnostic assays for abnormal GENSET expression and/or biological activity. They are also useful for screening of compounds for treating or preventing GENSET-related disorders, such as heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, central nervous system (CNS), cardiovascular or gastrointestinal effects of the toxicity. The polynucleotides are useful for constructing or expanding chromosome maps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New GENSET polynucleotides and polypeptides, useful for treating heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, CNS, cardiovascular or gastrointestinal effects of the
                                                                                                                                                                                                          Cytostatic; antiinflammatory; nootropic; neuroprotective; cardiant; gastroincestinal; gone therapy, GRNET; heavy metal toxicity; cancer; inflammatory disease; immune disorder; neuromuscular; toxicity; central nervous system; cardiovascular; gastrointestinal; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Giordano J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jobert
TTTCAGACAACAGCAGAAGAGTTAGGATTATTA 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dumas Milne Edwards J,
                                                                                                                                                                           564.
                                                                                                                                                                           Human GENSET coding sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12; Page 579; 735pp; English.
                                                                   BP.
                                                                                                                                                                                                                                                                                                                                                                                                      18-APR-2001; 2001WO-IB000914.
                                                                                                                                                                                                                                                                                                                                                                                                                                        18-APR-2001; 2001WO-IB000914.
                                                                   ABZ36691 standard; cDNA; 497
                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bejanin S, Tanaka H,
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                                                                                                                                                                                                                                                                                                                                    WO200283898-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GEST ) GENSET
                                                                                                                                      21-FEB-2003
                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                   24-OCT-2002.
                                                                                                      ABZ36691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    toxicity
                                                   ABZ3669
                                    RESULT
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497 148 0 0 0 Matches: Conservative: Mismatches: Length: Indels: US-10-664-025-3903 (1-153) x ABZ36691 (1-497) 2.78e-88 775.00 100.0% 100.0% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Н Query Match: ð

Sequence 497 BP; 127 A; 99 C; 117 G; 154 T; 0 U; 0 Other;

HisValLys1leSerCysSerLeuAspTrpLeuMetValSerVallleProValAlaGlu 40 22 21 112 g ò 셤 ò a

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120
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                                 291
                                                            ArgValValSerGluGluThrLeuLeuPheGlnThrGluLeuTyrPheThrProArgAsn 100
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Arg11eHisThrTyrValTyrGluPhe11eTyrLeuValArgAspCysGly1leArgThr
                    CGGATACATACATATGTATATGAGTTTATATATATCTTGTTGGTGATTGTGGGCATCAGGACA
                                                                                    AGGGTAGTTTCTGAAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT
                                                                                                                      IleAspHisAspProGlnGluIleHisLeuGluCysSerThrSerArgLysSerValTrp
                                                                                                                                             LeuThrProValSerThrGluAsnGluIleLysLeuAspProSerProPheIleAlaAsp
                                                                                                                                                                                                     CTTACACCAGTTTCTACTGAGAATGAAATAAAATTGGATCCTAGTCCTTTTTATTGCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytostatic; antiinflammatory; nootropic; neuroprotective; cardiant; gastrointestinal; gene therapy; GENSET; heavy metal toxicity; cancer; inflammatory disease; immune disorder; neuromuscular; toxicity; central nervous system; cardiovascular; gastrointestinal; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 500 BP; 129 A; 100 C; 113 G; 155 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jobert S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human GENSET coding sequence SEQ ID 563.
                                                                                                                                                                                                                                                PheGlnThrThrAlaGluGluLeu 148
                                                                                                                                                                                                                                                                                495
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                                                                                                                                                                                                                                                                  ВР
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                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                          ABZ36690 standard; cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                     (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200283898-A1
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                              232
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Length:

2.29e-85

Alignment Scores: Pred. No.:

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IleAspHisAspProGlnGlulleHisLeuGluCysSerThrSerArgLysSerValTrp 120
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                                                                                                                                                                                      251
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                                                                                                                        HisVallysIleSerCysSerLeuAspTrpLeuMetValSerValIleProValAlaGlu
                                                                                                                                      CATGTGAAAATAAGTTGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAA
                                                                                                                                                               SerArgAsnLeuTyrllePheAlaAspGluLeuHisLeuGlyWetGlyCysProAlaAsn
                                                                                                                                                                              ArgileHisThrYalTyrGluPheIleTyrLeuValArgAspCysGlyIleArgThr
                                                                                                                                                                                                                                                                     312 AGGGTAGTTTCTGAGGAAACTCTCTCTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT
                                                                                                                                                                                                                              252 CGGATACATACATATGTATATGAGTTTATATATCTTGTTCGTGATTGTGGCATCAGGACA
                                                                                                                                                                                                                                                                                                                ATAGATCATGACCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Full length GENSET human nucleic acids encoding potentially secreted proteins, useful in gene therapy and vaccination against a variety of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             secreted protein; gene therapy; vaccine; treatment; dlagnosis;
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 Matches:
Conservative:
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                                                             (1-500)
                                           Gaps:
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                                                           US-10-664-025-3903 (1-153) x ABZ36690
                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein cDNA,
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06-MAR-2000; 2000US-0187470P
752.00
100.0%
100.0%
94.1%
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TTTCAGACA 500
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P-PSDB; AAG89145.
          Percent Similarity:
Best Local Similarity:
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portal hypertension;

lomerulonephritis; digestive disease;

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potentially secreted proteins. The nucleic acids and the polypeptides they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GENSET gene expression. For example, they be used to treat disorders associated with decreased GENSET gene expression by rectifying mutations or deletions in a patient's gene expression by rectifying mutations or deletions in a patient's gene expression by rectifying mutations or deletions in a patient's gene patients own production of GENSET polypeptides. Conversely, antisense nucleic acid molecules may be administered to down regulate GENSET expression. The sense and antisense nucleic acids may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence to determine which patients may be in need of restorative therapy. The GENSET polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of GENSET polypeptide expression and activity. The present sequence is a GENSET nucleic acid of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 Argacerragaagrerrgargerecresergrerragarragaecegragaagaacere 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATGIGAAATAAGTIGCICICICIGGACIGGITGAIGGICICAGTIAICCCAGIIGCAGAA 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGATACATACATATGTATATGAGTTTATATATCTTGTTCGTGATTGTGCGCATCAGGACA 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HisValLysIleSerCysSerLeuAspTrpLeuMetValSerValIleProValAlaGlu 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgileHisThrTyrValTyrGluPheIleTyrLeuValArgAspCysGlyIleArgThr 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fragment of a BAC clone that encodes a human secreted protein Seq532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         multiple myeloma; reproductive system disorder; prostatitis; injudical hernia; musuloskeletal disease; systemic lupus erythematosus; gout; cardiovascular disease; arrhythmia; hypernatraemia; fetal disease; fetal alcohol syndrome; Down's syndrome; excretory disease; runtinary incontinence; renal disorder; neural; sensory disease; Alzheimer's disease; meningtis; respiratory disease; emphysema; occupational lung disease; endocrine disease; diabetes;
                                                                                  invention relates to full length GENSET human nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 SerArgAsnLeuTyrIlePheAlaAspGluLeuHisLeuGlyMetGlyCysProAlaAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MetAlaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAlaGluAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 470 BP; 137 A; 87 C; 107 G; 139 T; 0 U; 0 Other;
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Matches:
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diseases, and for diagnosis of those diseases.
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                                          Claim 7; Page 583; 921pp; English.
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429.00
100.0%
100.0%
53.7%
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Best Local Similarity:
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This invention relates to novel polymucleotides encoding human secreted proteins. Specifically, it refers to the vectors, host cells, recombinant and synthetic methods for producing human polymucleotides, polymetides can darkthetic methods for producing human polymucleotides, polymetides can antibodies. Furthermore, it relates to escreening methods to identify agonists and antagonists that can be used to inhibit or enhance the production and function of the secreted proteins. The present invention describes these compositions as useful for diagnosing, treating or production and multiple myeloma, reproductive system disorders including prostatitis and inguinal hermia, musculoskeletal diseases including systemic lupus erythematosus and gout, cardiovascular disease including systemic lupus erythematosus and gout, cardiovascular disease including strathymia and hypernatraemia, mixed fetal diseases including fetal alcohol syndrome and bown's syndrome, excretory disease including curinary incontinence and renal disorders, neural or sensory disease including curinary incontinence and corupational lung disease, endocrine diseases including cortal hypertension and irritable bowel syndrome and connective tissue or portal hypertension and irritable bowel syndrome and connective tissue or epithelial diseases including scleroderma and espidermolysis bullosa. As such, there are various activites such as extostatic, antianemic, antiarthritic, antiasthmatic, anti-HIV, immunosuppressive,
           irritable bowel syndrome; epithelial disease; scleroderma; epidermolysis bullosa; cytostatic; antianemic; antiantitic; antiantitic; antiantestimatic; anti-HIV; immunosuppressive; antiinflammatory; antipschmatic; antibecrail; osteopathic; dermatological; antiout; inflammatory; antipscripting; cardiant; noctropic; antipscripting; cardiant; noctropic; antilipemic; nephrotropic; uropathic; neuroprotective; antiparkinsonian; tranquilizer; antidabetic; anabolic; hypertensive; vulnerary; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acids and polypeptides, useful for diagnosing, treating, preventing or ameliorating diseases or disorders e.g. cancer, anemia, arthritis, asthma, inflammatory bowel disease or Alzheimer's
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Ebner R, Olsen H;
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Yu G, Florence C,
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97US-0061536P.
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98WO-US021142.
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2000US-0244591P.
                                                                                                                                                                                                                                                                           30-OCT-2001; 2001US-00984429
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Ferrie AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BREWER L A.
DUAN R D.
RUBEN S M.
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OLSEN H.
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                                                                                                                                                                Homo sapiens.
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08-APR-1999;
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Young PE,
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(OLSE/)
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(GREE/)
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Qy 81 ************************************	Oy 81 *** *** *** *** *** <	81 1141 AAGTGTGTATTCCTCATCTGTTACTCCAAATATCTTCCACTGAAACT 82ValValSerGluGluThrLeuLeuPheGlnThrGluLeuTyrPheI 1201 TAGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACGGGGCTGTACTTTTA	Qy 101 IleAspHisAspProGlnGluIleHisLeuGluCysSerThrSerArg 116	ABK90052; 05-NOV-2002 (first entry) Human GSSP3 genomic sequence. Human; GSSP3; circulating blood glucose level; insulin sens: body mass; serum glucose regulation; body weight loss; obes: metabolic-related disorder; impaired glucose tolerance; stre		XX PN WO200260466-A2. XX XX XX XX F 01-FEB-2002; 2002WO-IB001333.	02-FEB-2001; (GEST) GENSE Salter-Cid L, Bihain B;
antiinflammatory, antipsoriatic, antibacterial, c dermatological, antigout, immunomodulator, antibacterial, antipout, immunomodulator, antibacterial, antiparkinsonian, tranquilizer, antidiabetic, and vulnerary. This polynucleotide is a DNA fragment encodes a human secreted protein of the invention of electronic format from the US patent office at the www.seqdata.uspto.gov/sequence.html; Document ID: X Sequence 5013 BP; 1442 A; 909 C; 826 G; 1836 T; 0 lignment Scores: 6.29e-30 Length: core: 21.8\$ Conservative:	ty: 21.8% 40.7% 12 x ADJ12678 (1-153) x ADJ12678 8T1eSerCysSerLeuAsp7 AATAAGTTGCTCTCTGAACA	ArgasnleutyrilePhealaAspGluleuHisleuGlyMetGlyCysProAlaAsnArg	Qy 81	Qy 81	421 ATTATATTTTACTAAATATTAGCAGACTGCTTTAAATTTTGTGTGATTCTTCTAATGTGG 81	Db 541 AIGTTCCAIGAGAATTTGTGTAAATATATAGTGGATTTTCATTGAAATGTGTATGT 600 Qy 81	Qy 81

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Furthermore, the nucleic acids and polypeptides may also be used to identify molecules that modulate or inhibit neurogenesis, cell differentiation and proliferation, haemopoiesis, wound healing and anglogenesis, as well as in gene therapy. Finally, the nucleic acids be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The current sequence is that of
The present invention relates to the isolation of human GSSP3

polypeptide, and polynucleotide sequences that encode it. The GSSP3

polypeptide reduces circulating blood glucose levels, increases insulin

sensitivity, and/or reduces body mass. The GSSP3 polypeptide and

caid metabolism, body weight loss, and prevention of body weight gain.

Compositions comprising GSSP3 polypeptides are useful for controlling

blood glucose levels, for treating metabolic-related diseases or

clasorders (e.g. obesity, impaired glucose tolerance, insulin resistance,

thyperlipidaemias, atherosclerosis, heart disease, hypertension, stroke,

syndrome C, type I or II diabetes, diabetes related complications,

cyndrome, ocular lesions, microangiopathic lesions, or syndromes such as

carathosis nigricans, leprechaunism and lipoatrophy). The polypeptides

carathosis nigricans, leprechaunism and lipoatrophy). The polypeptides

canthosis nigricans, leprechaunism and lipoatrophy). The polypeptides

and to treat dyslexia, attention-deficit disorder, attention-

deficit/Apperactivity disorder, and psychiatric disorders such as

chizophrenia. The present sequence encodes human GSSP3 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5444 GIGAAAATAAGTIGCTCTCGGACTGGTIGATGGTCTCAGTTATCCCAGTIGCAGAAAGC 5503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5504 AGAAATCTGTATATATTTGCGGATGAATTACATCTGGGAATGGGCTGCCCTGCAAATCGG 5563
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                                      Reducing circulating glucose levels or increasing insulin sensitivity, useful for reducing body mass or preventing body weight gain, comprises administering composition comprising GSSP3 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 IleHisThrTyrValTyrGluPheIleTyrLeuValArgAspCysGlyIleArgThrArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 ValLyslleSerCysSerLeuAspTrpLeuMetValSerVallleProValAlaGluSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 ArgAsnLeuTyrIlePheAlaAspGluLeuHisLeuGlyMetGlyCysProAlaAsnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10115 BP; 2860 A; 1941 C; 1815 G; 3475 T; 0 U; 24 Other;
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Matches:
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Mismatches:
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                                                                                                                       Disclosure; Page 90-95; 97pp; English.
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325.00
100.0%
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WPI; 2002-608487/65
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Alsobrook JP, Alvarez E, Anderson DW, Baron M, Boldog FL;
Burgess CE, Casman SJ, Chapoval A, Dhanabal M, Edinger SR, Eisen A;
Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;
Grosse WM, Guo X, Hackett C, Ji W, Kekuda R, Khramtsov NV;
Lepley DM, Li L, Macdougall JR, Malyankar UM, Mazur A, Mcqueeney K;
Mezes PS, Miller CE, Millet I, Mishra VS, Padigaru M, Patturajan M;
Pena CEA, Peyman JA, Rastelli L, Rieger DK, Shenoy SG, Shimkets RA;
Smithson G, Starling G, Spytek KA, Stone DJ, Tchernev VT, Twomlow N;
Vernet CAM, Zerhusen BD, Zhong M;
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cell differentiation; proliferation; haemopoiesis;
                                         therapy; chromosome mapping;
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                                     wound healing; angiogenesis; gene thutissue typing; human; 88; gene; NOV.
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2001US-0336600P.
2001US-0338285P.
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2001US-0341477P.
2001US-0341540P.
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2001US-0344903P.
2002US-0373288F.
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17-MAY-2002; 2002US-0381495P.
28-MAY-2002; 2002US-0383534P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-MAY-2002; 2002US-0383744P.
29-MAY-2002; 2002US-0383829P.
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P-PSDB; ADE28663.
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       neurogenesis;
                                                                                                                                                   Homo sapiens.
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17-DEC-2001;
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17-APR-2002;
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US-10-664	-025	US-10-664-025-3903 (1-153) x ADE28662 (1-838)
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ò	25	SerCysSerLeuAspTrpLeuMetValSerValIleProValAlaGluSerArgAsnLeu 44
qq	184	.84 CTGTGCTCCATAGACTGGTTCATGGTCACAGTGCACCCCTTCATGCTAAACAACGATGTG 243
È	45	TyrilePheAlaAspGluLeuHisLeuGlyMetGlyCysProAlaAsnArgIleHisThr 64
qq	244	::: 44 TGTGTACACTTTCATGAACTACACTTGGGCCTGGGTTGCCCCCCAAACCATGTTCAGCCA 303
ò	65	TyrValTyrGluPhelleTyrLeuValArgAspCysGlyileArgThrArgValValSer 84
ą	304	::: :::
È	85	85 GluGluThrLeuLeuPheGlnThrGluLeuTyrPheThrProArgAsnIleAspHisAsp 104
ą _Q	364	GAGGACATGGTTATCTACAGCACTGAGATACACTACTCTTCTAAGGGCACG 414
È	105	ProGlnGluIleHisLeuGluCysSerThrSerArglysSerValTrpLeuThr 122
qq	415	

Search completed: May 9, 2006, 13:30:07 Job time: 801.6 secs

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Title: Perfect score:

Sequence:

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Sequence 21, Appl
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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: PATENT PM
US-09-949-016-15949
US-09-949-016-11874
US-09-184-418C-95
US-10-290-579A-95
US-10-290-579A-96
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US-09-270-767-999
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NAME/KEY: CDS
LOCATION: 53.-511
NAME/KEY: sig_peptide
LOCATION: 53.-103
OTHER INFORMATION: VON Heijne matrix
OTHER INFORMATION: score 10.699999095651
OTHER INFORMATION: seq_VLMLLAVLIWTGA/EN
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Sequence 43, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local Similarity:
    Alignment Scores:
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  SEQ ID NO 43
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Sequence 1362, Ap
Sequence 1704, Ap
Sequence 2587, Ap
Sequence 15700, A
Sequence 1363, Ap
Sequence 5361, Ap
Sequence 5361, Ap
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                    GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-621-976-1362
US-10-104-047-1704
US-09-621-976-1587
US-09-621-976-15700
US-09-949-016-5361
US-09-949-016-5361
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
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Delop 6.0, Delext
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112 CATGTGAAATAAGTTGCTCTCTGGACTGGTTGATGGCCTCAGTTATCCCAGTTGCAGAA 171
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                                                                                           40
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                                                                                         HisValLysIleSerCysSerLeuAspTrpLeuMetValSerValIleProValAlaGlu
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US-10-664-025-3903 (1-153) x US-09-621-976-1362 (1-642)
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Patent No. 6943241

GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE

TITLE FOF INVENTION: No. 6943241e1 full length cDN

FILE REFERENCE: H1-A0105

CURRENT APPLICATION NUMBER: US/10/104,047

CURRENT FILING DATE: 2002-03-25

PRIOR FILING DATE:

PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 PheGlnThrThrAlaGluGluLeuGlyLeuLeu 151
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1704
LENGTH: 1492
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; ORGANISM: Homo sapiens
US-10-104-047-1704
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US-10-104-047-1704
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                                                                                                                                          21 HisValLysIleSerCysSerLeuAspTrpLeuMetValSerVallleProValAlaGlu 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1362, Application US/09621976

Patent No. 639063

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Glordano, J.Y.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.

FILE REFERENCE: GENSET. 054PR2.

CURRENT APPLICATION UNMER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 1362

LENGTH: 642
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                US-10-664-025-3903 (1-153) x US-09-621-976-43 (1-512)
 Indels:
Gaps:
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LOCATION: 53..526
NAME/KEY: sig_peptide
LOCATION: 53..103
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 10.699999802551
OTHER INFORMATION: seq VIMILAVLIWIGA/EN
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Best Local Similarity:
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US-09-621-976-1362
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                                                                                                                                     RESULT 5
US-09-621-976-15700

i Sequence 15700, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: JODERT, S.
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; FILE REPERENCE: GENNET.054PR2
; CURRENT APPLICATION UNBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 15700
; LENGTH: 372
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Mismatches:
Indels:
Gaps:
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Matches:
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; LOCATION: 351
; OTHER INFORMATION: n=a,
US-09-621-976-15700
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-09-621-976-1363
; Sequence 1363, App
; Patent No. 6639063
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Pred. No.:
                 293
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                                                                                                                                                                                                                                                                                               Sequence 2587, Application US/09621976
Patent No. 639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPERENCE: GENSET. 054PR2;
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2887
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Matches:
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ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity:
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; LOCATION: 372..539
US-09-621-976-2587
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US-09-621-976-2587
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i Sequence 5361, Application US/09949016
i Patent No. 6812339
i GENERAL INFORMATION:
i APPLICANT: VENTER, J. Craig et al.
i TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
i TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
i TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
i CURRENT APPLICATION NUMBER: 06/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PELLOR DATE: 2000-10-20
i PRIOR PELLOR DATE: 2000-10-03
i PRIOR PELLOR DATE: 2000-10-03
i PRIOR PELLOR DATE: 2000-10-03
i PRIOR PELLOR DATE: 2000-09-08
i WUMBER OF SEQ ID NOS: 207012
i SOFTWARE: FastSEQ for Windows Version 4.0
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82
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                               APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTE and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION UNMBER: US/09/621,976
CURRENT APPLICATION UNMBER: US/09/621,976
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 1363
LENGTH: 469
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Matches:
Conservative:
Mismatches:
Indels:
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 137..454
NAME/KEY: 812_peptide
CCATION: 137..187
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 10.699998092651
CUTHER INFORMATION: seq VLMLLAVLIWTGA/EN
US-09-621-976-1363
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               APPLICANT: Dumas Milne Edwards, J.B.
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Best Local Similarity:
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 GENERAL INFORMATION
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US-09-949-016-17103

US-09-949-016-17103

Sequence 17103, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WIMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTHARE: PESEUSEQ for Windows Version 4.0

LENGTH: 96690
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314 CTGATGATCCTCACCTCTGCGTTTTCAGCCGGTTCAGGACAAAGTCCAATGACTGTG 373
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Conservative:
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Best Local Similarity:
Query Match:
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Query Match:
DB:
              TYPE: DNA
ORGANISM: Human
US-09-949-016-5361
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Sequence 15949, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: WENTER, J. Craig et al.
TITLE OF INVENTION:
PITLE OF INVENTION:
PITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
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                                                                                                 85 GluGluThrLeuLeuPheGlnThrGluLeuTyrPheThrProArgAsnIleAspHisAsp 104
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                                                                                                                         460 CACGCCTACCAGTTCAC-TACCGTGTTACTGAATGTGGCATCAGGGCCAAAGCTGTCTCT
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15949
LENGTH: 23222
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Best Local Similarity:
Query Match:
DB:
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US-09-949-016-15949
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                                                         SerCysSerLeuAspTrpLeuMetValSerVallleProValAlaGluSerArgAsnLeu
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US-10-664-025-3903 (1-153) x US-09-949-016-17103 (1-96690)
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Matches:
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APPLICANT: Volkmuth, Wayne
APPLICANT: Walker: Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
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OTHER INFORMATION: a, t, c, g, or other
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Patent No. 6426186
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OTHER INFORMATION: Incyte ID No.
NAME/KEY: unsure
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SEQ ID NO 55
LENGTH: 1098
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                                                                                                                                                                      APPLICANT: Hahn, Beatrice
APPLICANT: Gao, Feng
APPLICANT: Gao, Feng
APPLICANT: Gao, Feng
APPLICANT: Shaw, George
TITLE OF INVENTION: CLONES AND SEQUENCES FOR NON-SUBTYPE B ISOLATES (
TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS TYPE 1
FILE REFERENCE: D6287
CURRENT APPLICATION NUMBER: US/09/184,418C
CURRENT FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 112
SEQ ID NO 95.
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Mismatches:
Indels:
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US-09-184-418C-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Human immunodeficiency virus type 1
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Matches:
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Patent No. 6897301
GENERAL INFORMATION:
APPLICANT: Hahn, Beatrice
APPLICANT: Gao, Feng
APPLICANT: Shaw, George
                                                                                   Sequence 95, Application US/09184418C Patent No. 6492110 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                    Sequence 11874, Application US/09949016

Facet No. 6812339
GENERAL INFORMATION
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUWAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUWAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR APPLICATION NUMBER: 60/231,768
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 11874
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TITLE OF INVENTION: CLONES AND SEQUENCES FOR NON-SUBTYPE B ISOLATES OF HUMAN TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS TYPE 1
FILE REFERENCE: DG297D
CURRENT APPLICATION NUMBER: US/10/290,579A
CURRENT FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: US 09/184,418
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 270
SEQ ID NO 95
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US-09-184-418C-96
US-09-184-418C-96
Sequence 96, Application US/09184418C
Patent No. 6492110
GENERAL INFORMATION:
APPLICANT: Hahn, Beatrice
APPLICANT: Gao, Feng
TITLE OF INVENTION: CLONES AND SEQUENCES FOR NON-SUBTYPE B ISOLATES OF HUMAN
TITLE OF INVENTION: IMMUNOBERICIENCY VIRUS TYPE 1
FILE REPRENCE: D6287
CURRENT APPLICATION NUMBER: US/09/184,418C
CURRENT FILING DATE: 1999-11-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     329 TATAAGAAATTAAGAAGGAAAGGAAAATAGACTGGTTAATCAAAAGAATAAGTGAGAGA 388
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543 -GATACCATCCTATTTTGTGCATCAGATGCTAAAGCATATGATACAGAAGTGCAT---- 596
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609 AGTATACTATGGAGTACCTGTGTGGAAAGATGCA------
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                             TYPE: DNA
ORGANISM: Human immunodeficiency virus type 1
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Sequence 96, Application US/10290579A

Patent No. 6897301
GENERAL INFORMATION:
APPLICANT: Hahn, Beatrice
APPLICANT: Shaw, George
APPLICANT: Shaw, George
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APPLICANT: Shaw, George
TITLE OF INVENTION: IMMUNOBERICIENCY VIRUS TYPE 1
FILE REFERENCE: D6287D
CURRENT APPLICATION NUMBER: US/10/290,579A
CURRENT PILING DATE: 1999-11-02
PRIOR FILING DATE: 1999-11-02
CEO. TO NO. 65
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190 TATAAGAAATTAAGAAGGAAAAGAAAAGAAAGAATGAGAGAGA 249
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04 -GATACCATCCTATTTTTGTGCATCAGATGCTAAAGCATATGATACAGAAGTGCAT---- 457
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                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                   ; OTHER INFORMATION: isolate=94CY017.41; gene=rev
US-09-184-418C-96
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; OTHER INFORMATION: isolate=94CY017.41; gene=rev
US-10-290-579A-96
TYPE: DNA
ORGANISM: Human immunodeficiency virus type 1
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US-10-290-579A-96
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310 AGGGGCATCTTGATTTTGGGGATGTTAATAATGTGTAAAGCTACAGATTTGTGGGTCAC 369
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250 GCAGAAGACAGTGGCAATGAGAGTGATGGGGACACACAGAGGAACTATCAGCACTTGTGGAG 309
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                                                                                                                              19 AsnLeuHisValLysIleSerCysSerLeuAspTrpLeuMetValSerValIleProVal 38
                                                                                                                                                                  39 AlaGlu------SerArgAsnLeuTyrIlePheAlaAsp 49
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         Length:
Matches:
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Sequence 19, Application US/09731872
Fatent No. US20020102604A1
Fatent No. US20020102604A1
Fatent No. US20020102604A1
Fatent InPoRMATION:
FAPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Dubert, Severin
APPLICANT: Dubert, Severin
FILE REFERENCE: 78 US3.REG
FILE REFERENCE: 78 US3.REG
CURRENT APPLICATION NUMBER: US/09/731,872
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR FILING DATE: 1999-12-08
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 482
SOFTWARE: Patent.pm
SEQ ID NO 19
                                                                                                                   Sequence 24, Appl
Sequence 24, Appl
Sequence 53, Appl
Sequence 13, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 202, Appl
Sequence 196, Appl
Sequence 196, Appl
Sequence 1978, Appl
Sequence 1878, Appl
Sequence 1878, Appl
Sequence 2733, Appl
Sequence 2733, Appl
Sequence 5976, Appl
Sequence 95, Appl
Sequence 95, Appl
Sequence 96, Appl
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Sequence 20168, A
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Sequence 2215, Ap
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Sequence 691324,
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Sequence
9 US-10-472-533-175
6 US-11-104-047-1704
3 US-09-184-224
3 US-09-24
3 US-09-24
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3 US-09-24
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3 US-09-24
4 US-10-43-836
6 US-10-47-36-65
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7 US-10-287-971-39
8 US-10-47-021-36
6 US-10-47-021-36
7 US-10-287-971-41
9 US-10-996-952-4
3 US-09-96-952-4
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6 US-10-136-996-956
10 US-11-135-597-95
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US-09-925-065A-691324
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LOCATION: 42.515
NAME/KEY: sig_peptide
LOCATION: 42.52
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: secre 10.7019149319754
OTHER INFORMATION: seq_VLMLLAVLIWTGA/EN
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ORGANISM: Homo sapiens
                  RESULT 1
US-09-731-872-19
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Sequence 19, Appl
Sequence 2, Appli
Sequence 16, Appli
Sequence 27, Appl
Sequence 27, Appl
                                                                                                                                                                                                                                           May 9, 2006, 14:40:21 ; Search time 1012.5 Seconds (without alignments) 1874.392 Million cell updates/sec
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1 MALEVLMILAVLIWTGAENL.....PSPFIADFQTTAEELGILIF
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1: /cgn2_6/ptodata/1/pubpna/USO1_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO98_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO98_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO08_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USIOR_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USIOR_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/USIOR_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USIOR_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USIOR_PUBCOMB.seq:*
                                           GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                 using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-731-872-19
US-09-876-997-19
US-10-643-836-19
US-10-467-046-2
US-10-677-535-16
US-10-050-74-27
US-10-798-512-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9793542 seqs, 4134689005 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
Xgapop 10.0 , Xgapext
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Maximum DB seq length: 200000000
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Result No.

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Sequence 19, Application US/10643836
; Sequence 19, Application Wolfolds 19, Sequence 19, Application Wolfolds 19, Application No. US20050096458A1
; GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Douguelert, Lydie
APPLICANT: Douguelert, Lydie
APPLICANT: Douguelert, Lydie
APPLICANT: Douguelert, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED FROTEINS
FILE REFERENCE: 78.023.REG
CURRENT APPLICATION NUMBER: US/09/731,872
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR APPLICATION NUMBER: US 60/187,470
SPRIOR APPLICATION NUMBER: US 60/187,470
PRIOR APPLICATION NUMBER: US 60/187,470
SPRIOR APPLICATION NUMBER: US 60/187,470
PRIOR                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        401
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Matches:
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; OTHER INFORMATION: SCORE 10.7019149919754
; OTHER INFORMATION: Seq VLMLLAVLIWTGA/EN
US-09-876-997-19
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ORGANISM: Homo sapiens
                                                                                                                                             Percent Similarity:
Best Local Similarity:
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NAME/KEY: CDS
LOCATION: 42..515
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Sequence 19, Application US/09876997

Publication No. US20030152921A1

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Jobert, Lydie

APPLICANT: Jobert, Lydie

APPLICANT: Jobert, Lydie

APPLICANT: Jobert, Lordie

APPLICANT: Jobert, Lordie

APPLICANT: Jobert, Lordie

APPLICANT: Jobert, Lordie

APPLICANT: Jobert, Lordie

CURRENT APPLICATION: VUMBER: US/09/876,997

CURRENT APPLICATION NUMBER: US 60/187,470

PRIOR APPLICATION NUMBER: US 60/187,470

PRIOR APPLICATION NUMBER: US 60/169,629

PRIOR APPLICATION NUMBER: US 60/169,629

PRIOR FILING DATE: 1999-12-08

NUMBER OF SEQ ID NOS: 482

SEQ ID NO 19

LENGTH 691

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Mismatches:
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ORGANISM: Homo sapiens
FRATURE:
NAME/KEX: CDS
LOCATION: 42..515
NAME/KEX: sig_petide
LOCATION: 42..92
OTHER INFORMATION: Von Heijne matrix
                                              3.48e-105
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Query Match:
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APPLICANT: YUE, Henry; YAO, Monique G.
APPLICANT: YUE, Henry; YAO, Monique G.
APPLICANT: BAUGRN, Craig H.; LU, Yan
APPLICANT: WARREN, Baldiget A.; ELLIOTT, Vicki S.
APPLICANT: TANG, TANG, TANG, Lib.
APPLICANT: TANG, TOWN Y.; LAL, Preeti G.
APPLICANT: DUGGAN, Brendan M.; BURFORD, Neil
APPLICANT: TRAN, Uyen K.; KHARE, Reena
APPLICANT: TRAN, Uyen K.; KHARE, Reena
APPLICANT: CHAMLA, Narinder K.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
FILE REFERENCE: PF-0903 USN
                                                                                                                                                                                                                                                                                   81 ArgValValSerGluGluThrLeuLeuPheGlnThrGluLeuTyrPheThrProArgAsn 100
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Matches:
Conservative:
Mismatches:
Indels:
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CURRENT FILING DATE: 2003-08-08
PRIOR APPLICATION NUMBER: PCT/US02/03715
PRIOR FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/268,111
PRIOR FILING DATE: 2001-02-09
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789.00
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100.0%
98.7%
      ; FEATURE:

; NAME/KEY: CDS

; LOCATION: (53)..(103)

; FEATURE:

; NAME/KEY: sig peptide

; LOCATION: (104)..(526)

US-10-46-2
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Best Local Similarity:
Query Match:
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US-10-467-535-16
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NAME/KEY: sig_peptide
LOCATION: 42..92
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: SCORE 10.7019149919754
OTHER INFORMATION: SEQUENTIALAVLIWTGA/EN
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TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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   ; FEATURE:
; NAME/KEY: 819_;
; LOCATION: 42...
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US-10-643-836-19
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Publication No. US20040152164A1
GENERAL INFORMATION:
TITLE OF INVENTION: 62 Human Secreted Proteins;
FILE REFERENCE: PZ039P1
CURRENT APPLICATION NUMBER: US/10/798,512;
CURRENT APPLICATION NUMBER: US/09/684,524;
PRIOR FILING DATE: 2000-10-10
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PRIOR APPLICATION NUMBER: 60/128, 693
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: 60/130, 991
PRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 344
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 27
LENGTH: 1898
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ORGANIZAM: Homo sapiens
FEATURE:
I LOCATION: (1398)
COTHER INFORMATION: n equal
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COTHER INFORMATION: n equal
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Matches:
Conservative:
Mismatches:
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Publication No. US20030050442A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 62 Human Secreted Proteins
FILE REFRENCE: P2039P1
CURRENT FILING DATE: 2002-01-18
FRIOR APPLICATION NUMBER: 09/684,524
FRIOR PILING DATE: 2000-10-10
FRIOR PILING DATE: 2000-10-10
FRIOR FILING DATE: 2000-01-01
FRIOR FILING DATE: 2000-04-06
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NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 5284076CB1
US-10-467-535-16
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 PRIOR APPLICATION NUMBER: US 60/271,175
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: US 60/274,503
PRIOR PILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 16
LENGTH: 1480
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789.00
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98.7%
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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US-10-050-704-27
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TITLE OF INVENTION: No. US20030236392Alel full length cDNA
FILE REFERENCE: H1-A0105
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Matches:
Conservative:
Mismatches:
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PRIOR APPLICATION NUMBER: US 60/331,287
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-1
SOFTWARE: PATENT ON NUMBER: US 60/277,340
SOFTWARE: PATENT ON SEQ ID NOS: 650
SEQ ID NO 175
LENGTH: 1898
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NAME/KEY: misc_feature
LOCATION: (1398)..(1398)
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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Matches:
Conservative:
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Indels:
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Sequence 175, Application US/10472533
Publication No. US20050197285A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Human Secreted Proteins
FIER REFERENCE: PS906PCT
CURRENT APPLICATION NUMBER: US/10/472,533
PRIOR APPLICATION NUMBER: PCT/USO0/08979;
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/128,693
PRIOR FILING DATE: 1999-04-09
PRIOR PILING DATE: 1999-04-26
PRIOR PRIOR DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 344
SOFTWARE: PATENTIN UND 27
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98.7%
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FEATURE:
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NAME/KEY: SITE
LOCATION: (1428)
CHER INFORMATION: n
US-10-798-512-27
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Best Local Similarity:
Query Match:
DB:
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LOCATION: (1398)
OTHER INFORMATION:
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Sequence 24, Application US/09876997

Sequence 24, Application US/09876997

Publication No. US2003015291A1

GENERAL INFORMATION:

APPLICANT: Unamas Milne Edwards, Jean Baptiste

APPLICANT: Dunas Milne Edwards, Jean Baptiste

APPLICANT: Bougueleret, Lydie

APPLICANT: Bougueleret, Lydie

APPLICANT: Jobert, Severin

TITLE OF INVENTION: FULL-ENGTH HUMAN cDNAS ENCODING POTENTIALLY SECRETED PROTEINS

FILE REFERENCE: 78 US4 CIP

CURRENT APPLICATION NUMBER: US/09/876,997

CURRENT APPLICATION NUMBER: US 60/187,470

PRIOR FILING DATE: 2000-10-06

PRIOR FILING DATE: 2000-03-06

PRIOR FILING DATE: 1200-03-06

PRIOR FILING DATE: 1200-03-06

NUMBER OF SEQ ID NOS: 482

SEQ ID NO 24

SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 CATGIGAAAATAAGTIGCTCTCTGGACTGGTGATCTCAGTTATCCCAGTTGCAGAA 256
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                  Matches:
                                                                                                                                             LOCATION: 137..187
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: SCORE 10.7019149919754
OTHER INFORMATION: SEG VLMLLAVLEWIGA/EN
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NAME/KEY: 819 peptide
LOCATION: 137..187
OTHER INFORMATION: Von Heijne matrix
                                                                                                                                                                                                                                                                                      1.72e-52
429.00
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53.7%
                       TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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ORGANISM: Homo sapiens
                                                                                   NAME/KEY: CDS
LOCATION: 137...454
NAME/KEY: 81g_peptide
LOCATION: 137...187
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Best Local Similarity:
Query Match:
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  LENGTH: 470
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Sequence 24, Application US/09731872

Patent No. US20020102604A1

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Bougueleret, Lydie

APPLICANT: Bougueleret, Lydie

APPLICANT: Gobert, Severin

FILE REFERENCE: 78.US3.REG

CURRENT FILING DATE: 2000-12-07

FRIOR PAPLICATION NUMBER: US 60/169,629

PRIOR FILING DATE: 1999-12-08

PRIOR FILING DATE: 2000-03-06

NUMBER OF SEQ ID NOS: 482

SOFTWARE: Patent.pm

SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 ArgValValSerGluGluThrLeuLeuPheGlnThrGluLeuTyrPheThrProArgAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 ATGGCGTTAGAAGTCTTGATGCTCCTCGCTGTCTTGATTTGGACCGGGCCTGAGAACCC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 CATGTGAAAATAAGTTGCTCTCTGGACTGGTTGATGGCCTCAGTTATCCCAGTTGCAGAA 171
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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CURRENT APPLICATION NUMBER: US/10/104,047 CURRENT FILING DATE: 2002-03-25 PRIOR APPLICATION NUMBER: PRIOR FILING DATE:
                                                                                                                                                                                                                                                                 4.45e-104
785.00
99.3$
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                                                                             NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1704
LENGTH: 1492
                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-104-047-1704
                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-09-731-872-24
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197 CATGTGAAATAAGTTGCTCTCTGGACTGGTTGATGCTCTCAGTTATCCCAGTTGCAGAA 256
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Matches:
Conservative:
Mismatches:
Indels:
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PUDLICATION No. US20040010132A1
GENERAL INFORMATION:
JAPPLICATION No. US20040010132A1
GENERAL INFORMATION:
JAPPLICATIN Rosen et al.
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REFERENCE: PS2018P2
CURRENT FILING DATE: 2001-10-30
FRIOR APPLICATION NUMBER: 06/244,591
FRIOR APPLICATION NUMBER: 06/244,591
FRIOR FILING DATE: 1999-10-08
FRIOR FILING DATE: 1999-10-08
FRIOR FILING DATE: 1999-10-09
FRIOR FILING DATE: 1997-10-09
FRIOR APPLICATION NUMBER: 60/061,536
FRIOR FILING DATE: 1997-10-09
FRIOR APPLICATION NUMBER: 60/061,532
FRIOR FILING DATE: 1997-10-09
FRIOR APPLICATION NUMBER: 60/061,532
FRIOR FILING DATE: 1997-10-09
FRIOR APPLICATION NUMBER: 60/061,532
FRIOR FILING DATE: 1997-10-09
FRIOR APPLICATION NUMBER: 60/061,532
FRIOR FILING DATE: 1997-10-09
FRIOR APPLICATION NUMBER: 60/061,532
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325.50
21.8%
21.8%
Best Local Similarity: 100.0%
Query Match: 53.7%
DB:
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ORGANISM: Homo sapiens
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Best Local Similarity:
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Fublication No. US20050096458A1

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Jobert, Severin

IIILE REPERBNCE: 78.US3.REG

CURRENT FILING DATE: 2003-08-19

PRIOR FILING DATE: 2003-08-19

PRIOR FILING DATE: 1999-12-08

PRIOR FILING DATE: 2000-03-06

PRIOR PILING DATE: 2000-03-06

NUMBER OF SEQ ID NOS: 482

SOFTWARE: Patent.pm

SEQ ID NO 24

LENGTH: 470

TYPE: DNA
                                                                                                                                                                                                                                                                                                21 HisValLysIleSerCysSerLeuAspTrpLeuMetValSerValIleProValAlaGlu 40
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Matches:
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Mismatches:
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Matches:
Conservative:
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    ; OTHER INFORMATION: score 10.7019149919754
; OTHER INFORMATION: seq VLMLLAVLIWTGA/EN
US-09-876-997-24
                                                                                                                                                                                                                    Gaps:
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LOCATION: 137..454
PEATURE:
NAME/KEY: sig_peptide
LOCATION: 137..187
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Best Local Similarity:
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US-10-643-836-24
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244 TGTGTACACTTTCATGAACTACACTTGGGCCTGGGTTGCCCCCCAAACCATGTTCAGCCA 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 SerCysSerLeuAspTrpLeuMetValSerVallleProValAlaGluSerArgAsnLeu 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 TyrValTyrGluPhelleTyrLeuValArgAspCysGlylleArgThrArgValValSer 84
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Matches:
Conservative:
Mismatches:
Indels:
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Job time : 1017.5 secs
PRIOR FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 397
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 39
LENGTH: 838
                                                                                                                                                                                                                                  3.61e-22
225.50
60.8%
33.3%
                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                               ; LOCATION: (100)..(735)
US-10-287-971-39
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### APPLICATION NUMBER: 0/4024

### TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD FILE REPERENCE: 21402-480B.

### CURRENT APPLICATION NUMBER: 0/9/997, 425

### RIOR APPLICATION NUMBER: 0/9/997, 425

### RIOR PILING DATE: 2001-11-29

### RIOR PILING DATE: 2001-11-29

### RIOR FILING DATE: 2001-10-22

### RIOR PILING DATE: 2001-11-05

### RIOR FILING DATE: 2001-11-05

### RIOR FILING DATE: 2001-11-05

### RIOR FILING DATE: 2001-11-06

### RIOR FILING DATE: 2001-11-06

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### RIOR FILING DATE: 2001-11-06

### RIOR PILING DATE: 2001-11-06

### RIOR PILING DATE: 2001-11-09

### RIOR PILING DATE: 2001-11-09

### RIOR APPLICATION NUMBER: 60/333, 262

### RIOR APPLICATION NUMBER: 60/406, 181

### RIOR APPLICATION NUMBER: 60/406, 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5444 GTGAAATAAGTTGCTCTCTGGACTGGTTGATGGTCTCAGTTATCCCAGTTGCAGAAAGC 5503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5504 AGAAATCTGTATATATTTGCGGATGAATTACATCTGGGAATGGGCTGCCCTGCAAAATCG5 5563
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Indels:
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LOCATION: (8293)...(8293)
OTHER INFORMATION: n is a, c, g,
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LOCATION: (8334)...(8336)
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NAME/KEY: misc feature
LOCATION: (8342)...(8349)
OTHER INFORMATION: n is a, c, g,
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US-10-287-971-39
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Sequence 1704, App
Sequence 564, App
Sequence 563, App
Sequence 61, App
Sequence 60, Appl
Sequence 260, App
Sequence 260, App
Sequence 257, App
Sequence 257, App
Sequence 254, App
                                                                                                                                                                                                                                                                                                                         Sequence 1224309,
Sequence 1224309,
Sequence 1136381,
Sequence 1175389,
Sequence 1022, Ap
Sequence 691324,
Sequence 1022, Ap
Sequence 1022, Ap
Sequence 1022, Ap
Sequence 574920,
Sequence 574920,
Sequence 574919,
Sequence 574919,
                                                                                                                                                                                                               Sequence 256, App
Sequence 24510, A
Sequence 24510, A
Sequence 83, Appl
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Sequence 272, App
Sequence 73, Appl
Sequence 898046,
Sequence 11514, A
Sequence 114751,
Sequence 728160,
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Sequence 610900,
Sequence 1218750,
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Sequence 1220067
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 Description
                            B US-11-072-512-1704

1 US-10-475-075-564

1 US-10-475-075-564

1 US-10-475-075-564

1 US-10-475-075-563

1 US-10-112-908-61

2 US-11-112-908-61

2 US-10-995-561-256

2 US-10-995-561-256

2 US-10-995-561-256

2 US-10-995-561-256

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; Sequence 1704, Application US/11072512
; Sequence 1704, Application No. US20060029945A1
; GENERAL INFORMATION:
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APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YUKI
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TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
NAGAHARI, KENJI
DB
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NAGAI, KEIICHI
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-Q=/abss/ABSSWEB_spool/US10664025/runat_08052006_173656_29587/app_query.fasta_1-DB=Published_Applications_NA_New -QFMT=fastap -SUFTX=p2n.rnpbn -MINNATCH=0.1_LOOPCL=0 -LOOPEXT=0 -UNITS=b1ts -START==10-END=1 -MATRIX=b108um62
-TRANS=human40.cdi -LIST=45 -DOCALICN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL_OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0-MAXIEN=200000000 -HOST=abss08
                                                                                                    May 9, 2006, 14:45:03 ; Search time 682.2 Seconds (without alignments) 1370.049 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -USER=US10664025 @CGN 1 1 981 @runat 08052006 173656 29587 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DBV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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| SIDSS/ptodata/1/pubpna/USO8_NEW_PUB.seq1:*
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          GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                     - nucleic search, using frame_plus_p2n model
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SUMMARIES

* Query

Result

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:

YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database

9306428 segs, 2036268586 residues

Searched:

0.5 7.0 7.0

BLOSUM62 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

US-10-664-025-3903 799

Title: Perfect score:

Sequence:

protein

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Run on:

Scoring table:

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RESULT 3

US-10-475-075-563

US-10-475-075-563

Sequence 563, Application US/10475075

Publication No. US20060053498A1

GENERAL INFORMATION:

APPLICANT: Bejanin, Stephane

APPLICANT: Tanaka, Hiroaki

APPLICANT: Jobert, Severin

APPLICANT: Jobert, Severin

APPLICANT: Jobert, Severin

APPLICANT: Giordano, Jean-Baptiste

APPLICANT: Giordano, Jean-Yves

APPLICANT: Giordano, Jean-Yves

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APPLICANT: Giordano, Jean-Yves
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerArgAsnLeuTyrIlePheAlaAspGluLeuHisLeuGlyMetGlyCysProAlaAsn 60
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Matches:
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NAME/KRY: CDS
I LOCATION: 52..495
FEATURE:
NAME/KRY: sig_peptide
CCATION: 52..102
COTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 10.699998092651
CTHER INFORMATION: seq VLWLLAVLIWTGA/EN
US-10-475-075-564
  PRIOR APPLICATION NUMBER: PCT/IB01/00914
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 918
SEGTWARE: Patent.pm
SEQ ID NO 564
LENGTH: 497
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Best Local Similarity:
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Publication No. US20060053498A1
GENERAL INFORMATION.

APPLICANT: Bejanin, Stephane
APPLICANT: Dunas Milne Edwards, Jean-Baptiste
APPLICANT: Jobert, Severin
APPLICANT: Glordano, Jean-Yves
TITLE OF INVENTION: Full-Length human cDNAs encoding potentially secreted proteins
FILE REFERENCE: G-081US03PCT
CURRENT APPLICATION NUMBER: US/10/475,075
CURRENT FILING DATE: 2003-10-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 CGGATACATACATATGTATATGAGTTTATATATCTTGTTCGTGATTGTGGCATCAGGACA 291
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Matches:
Conservative:
Mismatches:
Indels:
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TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT PELLING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2005-03-07
PRIOR PILING DATE: 2001-125
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOUTHARE: PALENTIN VET. 2.1
SEQ ID NO 1704
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785.00
99.3%
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US-11-072-512-1704
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Best Local Similarity:
Query Match:
DB:
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US-10-475-075-564
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Pred. No.:
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APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OP INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
TITLE OP INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
TITLE OP INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 181
LENGTH: 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316 CTGATGATCCTCCTCTCTGCGTTTTCAGCCGGTTCAGGACAAAGTCCAATGACTGTG 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  376 CTGTGCTCCATAGACTGGTTCATGGTCACAGTGCACCCTTCATGCTAAACAACGATGTG 435
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Mismatches:
Indels:
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US-11-112-908-61/C
US-11-112-908-61/C
Sequence 61, Application US/11112908
Publication No. US20050260659A1
GENERAL INFORMATION:
APPLICANT: Harris, Cole
TILLE OF INVENTION: Lisa M.
TILLE OF INVENTION: Breast Cancer Biomarkers
FILE REFERENCE: 04-164-US
CURRENT PAPLICATION NUMBER: US/11/112,908
CURRENT PAPLICATION NUMBER: US 60/564,758
PRIOR FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: US 60/575,978
PRIOR FILING DATE: 2004-06-01
PRIOR FILING DATE: 2004-06-01
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-11-30
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 61
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60.04
33.34
28.04
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: 819 peptide
LOCATION: 72.122
OTHER INPORMATION: Von Heijne matrix
OTHER INFORMATION: 8core 10.699998092651
OTHER INFORMATION: 8cq VLMLLAVLIWTGA/EN
CURRENT APPLICATION NUMBER: US/10/475,075
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: PCT/IB01/00914
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 918
SEQ ID NO 563
LENGTHARE: Patent.pm
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Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
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; OTHER INFORMATION: n = a, g, c
US-10-475-075-563
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TTTCAGACA 500
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                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                            FEATURE:
NAME/KEY: CDS
LOCATION: 72..500
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NAME/KEY: Unsure
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US-10-821-234-181
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53687 TCGGCTATTCAAGTACAATGCACCCAGTTTTGGTTCTGTGCCAGGATTAAACCCACGATA 53628
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Sequence 262, Application US/10995561

Sequence 262, Application US/10995561

Publication NO. US20050272054A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: DETECTION AND USES THEREOF

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT PILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SEQ ID NOS: 85702

SEQ ID NOS: 86702

SEQ ID NOS: 86702
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                                                                                               Conservative:
Mismatches:
Indels:
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                         Alignment Scores:
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Matches:
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Publication No. US20050260659A1
GENERAL INFORMATION:
GENERAL INFORMATION:
THOROMATION:
TILLE OF INVENTION:
TILLE REFERENCE: 0-164-US
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT FILING DATE: 2005-04-22
PRIOR APPLICATION NUMBER: US 60/564,758
PRIOR APPLICATION NUMBER: US 60/564,758
PRIOR PILING DATE: 2004-04-23
PRIOR PILING DATE: 2004-04-23
PRIOR PILING DATE: 2004-11-30
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PRIOR PILING DATE: 2004-11-37
SOFTWARE: PRIOR DATE: 2004-11-37
SOFTWARE: PALENTION NUMBER: US 60/633,826
PRIOR PILING DATE: 2004-11-37
SOFTWARE: PALENTIN NUMBER: US 60/633,826
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SOFTWARE: PALENTIN VARIENTIN                                                                                                                                         11.5
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147210 GATAGAGGTG 147201
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                       TYPE: DNA
ORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
US-11-112-908-60
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US-11-112-908-60/c
LENGTH: 159497
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1264 CTCCAGATCCTGCGGGATGAGAATTACTACCAGCTAGAAGAGCTGGCTTTTTAGGGTCATG 1323
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                    AsnArglleHisThrTyrValTyrGluPhelleTyrLeuValArgAspCysGlylleArg 79
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS (
TITLE OF INVENTION: DATECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995, 561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: PASLESEQ for Windows Version 4.0
LENGTHARE: DASC
                                                                                    80 ThrargValValSerGluGluThrLeuLeuPheGlnThrGluLeuTyrPheThrProArg
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1336 AAACTGACACTAGCTAAGAATACACTGCAG----
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Best Local Similarity:
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US-10-995-561-257
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CTGGAATTGCTACAGATTGCAAACAAAATCCAGAATGGTGTTTGAACTGTGAAGAA 1335
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1411 TCAGATGTCATATGTAGAGTGTGAAGGTGTCATCAGGCAGCTGCAGGTGGAT 1470
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Publication No. US20050272054A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
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LeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAlaGluAsnLeuHisVal
                                                               LyslleSerCysSerLeuAspTrpLeuMetValSerVallleProValAlaGluSerArg
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LENGTH: 17292
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US-10-995-561-260
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                         -----SerValTrpLeuThrProValSer-----ThrGluAsnGluIleLysLeu
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                                                                                                                                           ; Sequence 254, Application US/10995561
; Publication No. US20000272054A1
; GENERAL INFORMATION:
    APPLICANT: CARGILL, Michele et al.
    TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
    TITLE OF INVENTION: DETECTION AND USES THEREOF
    FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FESTESEQ for Windows Version 4.0
; SEQ ID NO 254

LEMOTH: 17507
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Best Local Similarity:
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ORGANISM: Homo
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Publication No. US20050272054A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
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Fublication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
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US-10-995-561-258
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1651 GAACCC 1656
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Best Local Similarity:
Query Match:
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LENGTH: 17610
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619 ------CTGTTCAGAGAGGGTGTCTCTAATTCGCACAAAGATGCTGCTT 666
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; Publication No. US20050287531A1
; GENERAL INFORMATION:
    GENERAL INFORMATION:
    APPLICANT: MMI GENOMICS, INC.
    APPLICANT: RERR, Richard
    APPLICANT: RERR, Richard
    APPLICANT: RERR, Richard
    APPLICANT: RERR, Richard
    APPLICANT: RERR, Richard
    APPLICANT: RAPIN, Dennis
    APPLICANT: FANTIN, Dennis
    TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
    FILE REFERENCE: MAILING-1
    CURRENT APPLICATION NUMBER: US/10/750,623
    CURRENT PLING DATE: 2003-12-31
    FRIOR PILING DATE: 2002-12-31
    NUMBER OF SEQ ID NOS: 64922
    SOFTWARE: PALEATIN version 3.1
    SEQ ID NO 24510
    LENGTH: 3996
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; ORGANISM: Bovine 19866880767338
US-10-750-623-24510
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Query Match:
         , ORGANISM: Bovine
US-10-750-185-24510
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1276 CTGGAATTGCTGCTACAGATTGCAAAATCCAGAATGGTGCTTTGAACTGTGAAGAA 1335
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1591 CATTICACTIGAATIGGIICCACCCTCTACTITAACCACCACTCATGAAAGCA 1650
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Fublication No. US20050260603A1
GENERAL INFORMATION:
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FANTIN,
Demnia
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT APPLICATION NUMBER: US/10/750,185
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Mismatches:
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Matches:
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 256
LENGTH: 17642
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; ORGANISM: Homo sapiens
US-10-995-561-256
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US-10-750-185-24510
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LENGTH: 3996
TYPE: DNA
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92 ThrGluLeuTyrPheThrProArg-AsnIleAspHisAspProGlnGluIleHisLeuGl 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 GluAsnLeuHisValLysIleSerCysSerLeuAspTrpLeuMet------ValSer 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 AspCysGlyIleArgThrArg-----ValValSerGluGluThrLeuLeuPheGln
PRIOR FILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: EP 04090380.9
PRIOR FILING DATE: 2004-03-0
PRIOR FILING DATE: 2004-04-01
PRIOR FILING DATE: 2004-04-01
Remaining Prior Application data removed - See File Wrapper or PALM.
SEQ ID NO 83
                                                                                                                                                                                                                                                          OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||| |||||||:::::: 721 CAGGTAGAATATATATATATGCTCCATGAGAGGACTGTGGGAAAGACTCCGCTTGCC 780
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                                                                                          28
                                                                                                                                                                         29 AspTrpLeuMetValSerValIleProValAlaGluSerArgAsnLeuTyrIlePheAla 48
                                                                                                                                                                                                                                                          49 Asp-----GluLeuHisLeuGlyMetGlyCysProAlaAsnArglleHisThrTyr 65
                                                                                                                                                                                                                                                                                                                                             66 ValTyrGluPhelleTyrLeuValArgAspCysGlyIleArgThrArgValValSerGlu 85
                                                                                       9 LeuAlaValLeuIleTrpThrGlyAlaGluAsnLeuHisValLysIleSerCysSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 ThrGluAsnGluIleLysLeuAspProSerProPheIle 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           781 rerecaggireactgeceaececacciereceracera 819
                                              US-10-664-025-3903 (1-153) x US-10-750-623-24510 (1-3996)
                                                                                                                                                                                                              526 CACTGGGTCCCACACCCCGGACCCAAAAGGAAA----
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CURRENT APPLICATION NUMBER: US/11/011,332A

CURRENT FILING DATE: 2004-12-13

PRIOR APPLICATION NUMBER: US 10/517,741

PRIOR APPLICATION NUMBER: US 10/517,741

PRIOR PILING DATE: 2003-10-01

PRIOR FILING DATE: 2003-10-01

PRIOR FILING DATE: 2003-10-01

PRIOR FILING DATE: 2003-10-01

PRIOR FILING DATE: 2003-01-07

PRIOR PELING DATE: 2003-01-07

PRIOR PLING DATE: 2003-04-17

PRIOR PILING DATE: 2003-04-17

PRIOR PELING DATE: 2004-04-12-13

PRIOR PELING DATE: 2004-12-13

PRIOR PELING DATE: 2004-12-13

PRIOR PELING DATE: 2004-12-13

PRIOR PELING DATE: 2004-12-13

PRIOR PELING DATE: 2003-11-11

PRIOR PELING DATE: 2004-12-13

PRIOR PELING DATE: 2004-12-13

PRIOR PELING DATE: 2004-12-13
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Sequence 83, Application US/11011332A

Publication No. US20060024684A1

GENERAL INFORMATION:
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Koenig, Thomas
Maier, Sabine
Martens, John
Model, Fabian
Nimmrich, Inko
Rujan, Tamas
Schmitt, Manfred
Lesche, Ralf
Dietrich, Dimo
Mueller, Volkmar
Kluth, Antje
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Hartmann, Oliver
Adorjan, Peter
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APPLICANT:
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OM protein -

Run on:

Sequence:

Searched:

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Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
CDNA Library Preparation: Michael J. Brownstein (LLNL)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAMIGS row: e column: 09

High quality sequence stop: 624.

Location/Qualifiers

rce
1. .626
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603204535F1 NIH_MGC_97 Homo saplens cDNA clone IMAGE:5270384 5',
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BG067944 H3059H12-
CR86054 CR86054 Mous
CO798699 AGENCOURT
AU045772 AU045772
BF709198 MI-P-AXO-
BF709198 MI-P-AXO-
BF709198 MI-P-AXO-
BF709198 MI-P-AXO-
BF709198 MI-P-AXO-
BF70919 MI-P-AXO-
BF70919 MI-P-AXO-
BY736907 BF7080907
CR367041 B41759 MA
CF367041 GENCOURT
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CF933109 AGENCOURT
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                        AISS4902 t
BG081002 B
BY731676 I
CO810251 A
AII38881 C
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BG202365 F
CB298889 2
BX110037 E
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                     AA608835

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CO810251

AI138881

AI13881

BB557840

AI028204

CO798599

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AI028203

BF708131

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BI463012.1 GI:15253668
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mRNA sequence.
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431.5
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AUTHORS
TITLE
JOURNAL
COMMENT
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-MODEL=frame+_p2n.model -DEV=x1h
-MODEL=frame+_p2n.model -DEV=x1h
-G=/abss/RBE spool/UR1066464025/runat 08052006_173646_29404/app_guery.fasta_1
-DB=EST -QFWT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPECL=0 -LOOPEXT=0
-UNITS=bbts -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UOTFWT=PAD- -NORM=SAT -HEADESIZE=500 -MININEN=0 -MAXEN=20000000000 -HOST=abss07
-USER=US10664025_6CGN 1 1 6731 @runat 08052006 173546_29404 -NCPU=6 -ICPU=3
-NO MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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BG772527 602720619
B1520154 603071295
BX118111 BX118111
B1459538 603200545
AW664990 hi98h06.x
BE972717 601652136
                                                                                                                              9, 2006, 13:30:21 ; Search time 5379.3 Seconds (without alignments) 1996.103 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                           MALEVLAMLLAVLIWTGAENL......PSPFIADFQTTAEELGLLIF
              GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                              using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                         41078325 segs, 23393541228 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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Maximum Match 100%
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BG772527
B1520154
BX118111
B1459538
AW664990
BE972717
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Maximum DB seq length: 200000000
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Database :

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Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninoi (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Http://mage.llnl.gov

Plate: LLAMIO770 row: e column: 05

High quality sequence stop: 773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /.doinglib="NIHUMGC 97"
//clonellib="NIHUMGC 97"
//note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI: Site_2: SalI-XhoI glueggi); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTTTTN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primert library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMM/NHGHI, National Institutes of Health). Note: this is a NIH_MGC Library."
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                    NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab host="DH10B"
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DB:
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/organism="Homo sapiens"

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/lab_host="DH10B"
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/clone_lib="MNH MGC_97"
/clone_lib="MnH MGC_97"
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/clone_lib="Jog-dr_brimed using primed groups testis yetcolor primed using primer is 2.2 kand normalized to ROT 5. This is a primer is 2.2 kand normalized to ROT 5. This is a primer using the Captrapher method (Carninci, in preparation). Library constructed using the Captrapher method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is
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Homo sapiens
Eukaryora; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40
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VERSION
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Radeloff, U., Schneider, D. and Korn, B.

Human Unigeneset - RZPD3

Londact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

RZPD INAG9898D122574.

RZPDILB: I.M.A.G.E. CDNA Clone Collection;

Human Unigeneset - RZPD3 (RZPDLIB NO.972)

http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response7libNo-972 Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 101

Fax: +49 30 32639 101
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/lab_host="bHl0B"
/lab_host="bHl0B"
/cone_lib="Soares_testis_NHT"
/note="Vector: pTTT3D-Pac (Pharmacia) with a modified
polylinker; Site_l: Not I; Site_2: Eco RI; lst strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BX118111 Soares_testis_NHT Homo sapiens cDNA clone IMAGp998D122574 i_IMAGE:1030619, mRNA sequence.
                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                389
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150 AGCAGAAATCTGTATATTTGCGGATGAATTACATCTGGGAATGGGCTGCCCTGCAAAT 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                                          210 CGGATACATACATATGTATATGAGTTTATATATCTTGTTCGTGATTGTGGCATCAGGACA
                                                                                                                                             81 ArgValValSerGluGluThrLeuLeuPheGlnThrGluLeuTyrPheThrProArgAsn
                                                                                                                                                                       270 AGGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAT
                                                                                                                                                                                                                                            IleAspHisAspProGlnGluIleHisLeuGluCysSerThrSerArgLysSerValTrp
                                                                                                                                                                                                                                                                                          330 ATAGATCATGACCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGTGTGG
                                              61 Arg1]eHisThrTyrValTyrGluPhelleTyrLeuValArgAspCysGlylleArgThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGp998D122574 ; IMAGB:1030619"
                                                                                                                                                                                                                                                                                                                                                                                                                                          PheGlnThrThrAlaGluGluLeuGlyLeuleu 151
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TTTCAGACAACAGCAGAAGAGTTAGGATTATTA 482
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Infe Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
CDNA Sequencing by: Incyte Genomics, Inc.
CLONE distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
CLONE distribution: MGC clone distribution information can be http://image.lln.gov
Rlade.cover.cov
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 878)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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Mismatches:
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                  141 PheGlnThrThrAlaGluGluLeuGlyLeuLeu 151
                                              US-10-664-025-3903 (1-153) x BI520154 (1-878)
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789.00
100.0%
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98.7%
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Homo sapiens
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Best Local Similarity:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

E 1 (bases 1 to 778)
S NIH-MGC http://mgc.nci.nih.gov/.

IN NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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and Bco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "
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                                                                                                                                                                                                                                                                                                                                           26 CysSerLeuAspTrpLeuMetValSerValIleProValAlaGluSerArgAsnLeuTyr 45
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146
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Matches:
Conservative:
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Indels:
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AW664990 GI:7457534 EST.
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Matches:
Conservative:
Mismatches:
Indels:
           column: 11
                                                             /organism="Homo sapiens"
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          Plate: LLAM11672 row: i column
High quality sequence stop: 674.
Location/Qualifiers
                                                                                                 /clone="IMAGE:5266642"
/lab_host="DH10B"
                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                        a NIH MGC Library."
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743.00
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http://image.llnl.gov
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BE972717 516 bp mRNA linear EST 04-OCT-2000
   254 AATGAAATAAAATTGGATCCTAGTCCTTTTATTGCTGACTTTCAGACAACAGCAGAAGAG 195
                                                                                                                                                                                                                                                                                                                      Hominidae, Homo.

I (bases 1 to 516)

S NIH-MGC http://mgc.nci.nih.gov/.

I (bases 1 to 516)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LIML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

http://magg-llnl.gov

Plate: LLCM777 row: h column: 09

High quality sequence stop: 505.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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670.00
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97.7%
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                                                       LeuGlyLeuLeu 151
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                                                                                                                                                                                          mRNA sequence.
BE972717
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                                                                                                                                                           Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.
High qualify sequence stop: 460.

Location/Qualifiers

1. 619

/organism="Homo sapiens"
/mol_type="mRNN"
/db xref="taxon:966"
/clone="IMAGE:2980379"
/lab host="PHHIDS"
/clone="IMAGE:2980379"
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/clone="Organ: poled; Vector: pr773D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHLI9W, testis NH7, and B-cell
NCI CGAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAR purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. Clones 297480-302087, 682632-687239,
726408-728711, and 729086-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        374 CTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAATATAGATCATGACCCTCAGGAA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 AsnGluIleLysLeuAspProSerProPheIleAlaAspPheGlnThrThrAlaGluGlu 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 LeuAspTrpLeuMetValSerVallleProValAlaGluSerArgAsnLeuTyrllePhe 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 AlaAspGluLeuHisLeuGlyMetGlyCysProAlaAsnArglleHisThrTyrValTyr 67
                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                Hominidae, Homo.

1 (bases 1 to 619)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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Indels:
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97.2%
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 sapiens (human)
                                                                                                                                  Tumor Gene Index
Unpublished (1997)
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Best Local Similarity:
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/Bach mater DH10B"
/lab hoster DH10B"
/clone lib="Soares testis NHT"
/note="Vector: pryT3D-pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; lst strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                430 bp mRNA linear EST 02-MAR-1998
af03h06.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1030619
AA608835
                                                                               507 GICTIGAITIGGACCGGIGCIGAGAACCICCAIGIGAAAAIAAGIIGCICICIGGACIGG 448
                                                                                                                                                    268
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                                                                                                                                                                                                                                                                                                                                                                                                                     267 CAAACCGAGCTGTACTTTACCCCAAGGAATATAGATCATGACCCTCAGGAAATCCATTG 208
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Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,D., More,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NII human EST Project
Unpublished (1997)
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                                                                                                                           LeuMetValSerValIleProValAlaGluSerArgAsnLeuTyrIlePheAlaAspGlu 50
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Washington University School of Medicine
444 Forest Parkway, Box 8501, St. Louis, MO 63108
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Final: est@watson.wustl.edu
This clone is available royalty-free through LiNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 629 Std Error: 0.00
Seq primer: -40013 fwd. FT from Amersham
High quality sequence stop: 424.
                                                                                                                                                                                                                                                                                                      TyrLeuValArqAspCysGlyIleArgThrArgValValSerGluGluThrLeuLeuPhe
                                                                                                                                                                                                                                                                                                                               327 TATCTTGTTCGTGATTGTGGCATCAGGACAAGGGTAGTTTCTGAGGAAACTCTCCTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
US-10-664-025-3903 (1-153) x AW572898 (1-508)
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Homo sapiens
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AA608835/c
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/clone lib="Soares NFL T GBC S1"
/note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbH119W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239,
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                                                                                                                                                                                                                                                                                 479
                                                                                                                                                                             360 AGGTAGTTTCTGAGGAAACTCTCCTTTTTCAAACCGAGCTGTACTTTACCCCAAGGAAC 419
81 ArgValValSerGluGluThrLeuLeuPheGlnThrGluLeuTyrPheThrProArgAsn 100
                                                                                                                                                                                                                                      101 -IleAspHisAspProGlnGluIleHisLeuGluCysSerThrSerArgLysSerValTr 120
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1 (bases 1 to 508)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tuncor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -400p from Gibco
High quality sequence stop: 451.
Location/Qualifiers
1..508
                                                             61 ArgileHisThrTyrValTyrGluPheIleTyrLeuValArgAspCysGlyIleArgThr
                                                                                                                                                                                                                                                                      420 TATAGATCATGACCCTCAGGAAATCCATTTGGAGTGTTCCACCTCTAGGAAATCAGGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AWS72898 508 bp mRNA linear ES1
hf17c01.xl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2932128 3', mRNA sequence.
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Homo sapiens
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COMMENT
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ACCESSION VERSION KEYWORDS

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FEATURES

ORIGIN

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Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacis), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "
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1 (Dases 1 to 480)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 656 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 458.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          TyrLeuValArgAspCysGlyIleArgThrArgValValSerGluGluThrLeuLeuPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                             91 GlnThrGluLevTyrPheThrProArgAsnIleAspHisAspProGlnGluIleHisLeu
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/mol type="mkm"
/db xref="taxon:9606"
/clone="INAGE:2090452"
/lab_host="DH10B"
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100.0%
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Homo sapiens
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Unpublished (1997)
                                                                                                                                                                                                Best Local Similarity:
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AUTHORS
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/clone_lib="Soares_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL)9W, testis NHT, and B-cell NCI CGAP GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H3059H12-5 NIA Mouse 15K CDNA Clone Set Mus musculus CDNA clone H3059H12 5', mRNA sequence.
BG081002
BG081002.2 GI:40015217
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1 (bases 1 to 598)
Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X., Grahovac,M.J., Pantano,S., Sano,Y., Plao,Y., Nagaraja,R., Doi,H., Wood,W.H. III, Becker,K.G. and Ko,M.S.H.
Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
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Other_ESTs: H3059H12-3
Contact: George J. Kargul
                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
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64.4%
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Laboratoryr for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Vokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
T-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
Fax: 81-45-503-9216
                                                                                                                                                                                 120 TrpLeuThrProValSerThrGluAsnGluIleLysLeuAspProSerProPheIleAla 139
                                                                                                                                                                                                                                                  401 rescrirareccactarcrascasascarccaaaaccrerraasascrerrirarsact 460
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia;
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                    341 AAITATTGTTTGGAACTTCAGATAGTCCCTTTGCAGTGTTCTGCCTCTCGGAAGTCTGTG
                                      AsnileAspHisAspProGlnGluIleHisLeuGluCysSerThrSerArgLysSerVal
                                                                                                                                                                                                                                                                                                                               140 AspPheGlnThrThrAlaGluGluLeuGlyLeuLeu 151
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Mus musculus
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BY731676
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/clone is among a rearrayed set of 15,247 clones from it clones is among a rearrayed set of 15,247 clones from it clones from it clones from it clones from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, or extraembryonic part of E7.5 embryos, and E1.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse development of DNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during praimplanteation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7:5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
                       National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdnaedgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details. Plate: H3059 row: H column: 12 Seq primer: -21M13 Reverse High quality sequence stop: 598 POLYA-NO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sex="Clones arrayed from a variety of cDNA libraries"
dev stage="Clones arrayed from a variety of cDNA
libraries"
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Conservative:
Mismatches:
Indels:
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/db_xref="taxon:10090"
/clone="H3059H12"
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/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/strain="C57BL/6J"
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Laboratory of Genetics
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/clone lib="NIH MGC 257"

/note="Organ: Occyte; Vector: pExpress-1; Site_1: EcoRV;
Site_2: NOTI; CDNA was primed using oligo-dr primer:

5:-pGACTAGTTCTAGATGGGGGGGGCGGCC(T) 25-3; and cloned into
the EcoRV/Not1 sites of pExpress-1. Size-selection >0.5 kb
resulted in an average insert size of 1.0kb. This is a
normalized library (primary library is NIH MGC 256) and
was constructed by Express Genomics (Frederick, MD). Note:
this is a NIH MGC library"
                                                                                                                                                                                                                                                                                                                                                                                                    EST 06-AUG-2004
                                                                                                                                                                                                           ||||||| ||||::||||||||| ::: ||| || ||| |||:: TGGCTTATGCCACTATCTACTGAGGAGGATCCCAGTAAGAGTCCCTTTATGACT 465
                                                                                                                                                                                   TrpLeuThrProValSerThrGluAsnGluIleLysLeuAspProSerProPheIleAla 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LE 1 (bases 1 to 862)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Genomics

National Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-romail.nih.gov

Tissue Procurement: Dr. Kathleen Horner, Stanford University

CDNA Library Preparation: Express Genomics

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioceince Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDAM179 row: h column: 07

High quality sequence stop: 654.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                     100 AsnileAspHisAspProGlnGlulleHisLeuGluCysSerThrSerArgLysSerVal
                                                                                                                         ThrArgValValSerGluGluThrLeuLeuPheGlnThrGluLeuTyrPheThrProArg
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/mol_type="mRNA"
/db_xref="taxon:10090"
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/lab host="DH10B TonA"
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Mus musculus
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KEYWORDS
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper selected cDNAs to prepare full-length cDNA libraries for trapper selected cDNAs to prepare full-length cDNA libraries for trapper selected cDNAs to genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 ACTCAGATACACGCACATCAATATGATTTCATATACCCTGTTTCTCACTGTGGGATCAGG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 HisyalLysIleSerCysSerLeuAspTrpLeuMetValSerValIleProValAlaGlu 40
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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85
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/dev_stage="2 days pregnant adult"
/lab_host="DH10B"
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Matches:
Conservative:
Mismatches:
Indels:
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/db_xref="taxon:10090"
/clone="E330031A07"
                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="female"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Rukaryota; Metazoa; Chordata; Craniata; Glires; Rodentia;
Sciurognathi; Murcidea; Muridae; Murinae; Mus.
1 (bases 1 to 642)
1 (bases 1 to 642)
2 Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
Sono,H., Sasaki,Y., Okido,T., Satto,R., Sakai,C., Sakai,K.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Wouse ESTS (Arakawa,T., et al. 2001)
Unpublished (2001)
Unpublished (2001)
Con Aug 1, 2000 this sequence version replaced gi:9644206.
Contact: Yoshinde Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
Sciences Center(GSC), Yokohama Institute
Sciences Center(GSC), Yokohama Institute
Tel: 81-45-503-9222
                                                                               /note="Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; lst strand cDNA was prepared from that obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB557840 RIKEN full-length enriched, 2 days pregnant adult female ovary Mus musculus cDNa clone E330031A07 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40
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Mus musculus
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Email: cgapbs-r@mail.nih.gov

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

cDNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 395 Std Error: 0.00

Seq primer: -40ml3 fwd. Er from Amersham.

Location/Qualifiers
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Homo sapiens cDNA clone IMAGE:1737606
                                                                                                                                                                                                                                                                                                                                                                            247
                                                                                                                                                                                                                                                                                                                                                                                                                                                248 ACAAAGGTTATCTCAAATGAAATCGTCTGTTTTGAAACCGAGATGTACTTTCGTCCAAGG 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 AsnIleAspHisAspProGlnGluIleHisLeuGluCysSerThrSerArgLysSerVal 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        368 TGGCTTATGCCACTATCTACTGAGGAGGATCCAAAACCTGTTAAGAGTCCCTTTATGACT 427
                                                                                                                                                                                                 68 GACGTGGATGTAAGTTGTTCTCAGGACTGGATGACGGTCAGTGTTAGTGCGTTTTCCCAG 127
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                                                                                        21 HisValLyslleSerCysSerLeuAspTrpLeuMetValSerValIleProValAlaGlu 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae; Homo.
1 (bases 1 to 331)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                 MetAlaLeuGluValLeuMetLeuLeuAlaValLeuIleTrpThrGlyAlaGluABnLeu
                                                                                                                                                                                                                                                                                                                                                            188 ACTCAAATACACGCACATCAATATAGATTTCATATACCCTGTTTCTCACTGTGGCATCAGG
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/clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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/db_xref="taxon:9606"
                         US-10-664-025-3903 (1-153) x CO810251 (1-862)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Euarchonto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A1138881
31
gd99c04.x1 Soares_testis_NHT
3', mRNA sequence.
AI138881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI138881.1 GI:3644853
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
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AI138881/c
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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TITLE
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COMMENT
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Eas: 81-46-503-912.

East: 81-46-503-912.

East: 81-46-503-912.

Carmicle, P., Shibata, Y. Haytelland, N., Sughata, Y., Shibata, Y. Haytelland, Shibata, Y., Inch.M., Known, H., Okazaki, Y., Murmanten, M., and Hayahizaki, Y. Toh, M., Anno, H., Okazaki, Y., Murmanten, M., and Hayahizaki, Y. Haytelland, Shibata, Y., Sh
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Alignment Scores: 6.77e-38 Length: 642

Pred. No.: 395.50 Marches: 83

Score: 395.50 Marches: 24

Best Local Similarity: 54.2* Mismatches: 44

Query Match: 2
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US-10-664-025-3903 (1-153) x BB557840 (1-642)

Gaps:

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315
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                                                        196 AACTCAGATACACGCACATCAATATGATTTCATATACCCTGTTTCTCACTGTGGCATCAG 255
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                                             53
                                                                                          4
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                                                                                                                                                                              gAsnIleAspHisAspProGlnGluIleHisLeuGluCysSerThrSerArgLysSerVa
                                                                                                                                  9ThrArgValValSerGluGluThrLeuLeuPheGlnThrGluLeuTyrPheThrProAr
                                                                                                                                                 GAATTATTGGTATTGGAACTTCAGATAGTCCCTTTGCAGTGTTCTGCCTCTCGGAAGTCTGT
                                             40 uSer---ArgAsnLeuTyrIlePheAlaAspGluLeuHisLeuGlyMetGlyCysProAl
                                                                                       59 aAsnArgileHisThrTyrValTyrGluPheileTyrLeuValArgAspCysGlyIleAr
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Search completed: May 9, 2006, 15:10:09 Job time : 5382.3 secs

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	GenCore version 5.1.8 Copyright (c) 1993 - 2006 Biocceleration Ltd.	
OM protein - pr	OM protein - protein search, using sw model	
Run on:	May 9, 2006, 10:10:22; Search time 105.3 Seconds (without alignments) 638.414 Million cell updates/sec	
Title: Derfect score:	US-10-664-025-3903	
Sequence:	1 MALEVIAMLIAVIIWTGAENLPSPFIADFQTTABELGLLIF 153	

2443163 Total number of hits satisfying chosen parameters: 2443163 segs, 439378781 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Minimum DB seq length: 0 Maximum DB seq length: 200000000 Scoring table:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003s:* geneseqp2003s:* geneseqp2004s:* A_Geneseq_21:* 1: geneseqp1980s:* 2: geneseqp1990s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STRMMADIES

		de			SUMMARIES	
Result		Query				
No.	Score	Match	Match Length	80	ជា	Description
7		98.7	158	4	AAG89140	Aaq89140 Human sec
7	789	98.7	158	Ŋ	ABG97353	Abg 97353 Human CGD
м	789	98.7	158	Ŋ	ABG31324	Human
4	789	98.7	158	9	ABR47931	1 Human
S	789	98.7	158	9	ABR00175	5 Human
9	789	98.7	158	7	ADB91675	5 Human
7	789	98.7	158	7	ADC74338	
80	789	98.7	159	m	AAB38337	Aab38337 Human sec
σ	785	98.2	158	7	ADB65520	Adb65520 Human pro
10	775	97.0	148	9	ABP76238	
11	752	94.1	143	9	ABP76237	Human
12	429	53.7	106	4	AAG89145	Aag89145 Human sec
13	225.5	θ.	212	7	ADE28663	Ade28663 Human NOV
14	225.5	θ,	212	æ	ADM93408	Human
15	223.5	œ.	212	N	AAW73630	Aaw73630 Human sec
16	223.5	θ,	212	m	AAY94302	Aay94302 Human cor
17	223.5	œ.	212	4	AAM93517	Aam93517 Human pol
18	223.5	œ.	212	Ŋ	ABP62038	Abp62038 Human sec
19	223.5	œ.	212	ഹ	ABP61861	
20	•	28.0	212	7	ADC24649	Protei
21	223.5	œ	212	œ	ADL31210	Adl31210 Human pro
22	223.5	28.0	213	~	AAY12939	Aay12939 Amino aci
23	183.5	23.0	139	7	ABR83176	Abres176 PLAC1 int
24	161	20.5	163	7	ADE28665	Ade28665 Human NOV

Adm93410 Human NOV	Abg12048 Novel hum	Abres177 PLAC1 int	Abb21608 Protein #		Abq27342 Novel hum	Adr09311 Human pro	Human	Adp30075 Human sec			Adz85102 Full-leng		Abul8092 Protein e	Aag85042 Shrimp wh	Abb82478 Rat stear		Adi79900 Human El-	Adk46733 Streptoco	Adr95319 Novel S.	Aea59189 Streptoco	
ADM93410	ABG12048	ABR83177	ABB21608	ABG51070	ABG27342	ADR09311	ADP30076	ADP30075	AAU14603	ADJ68935	ADZ85102	AAU14697	ABU18092	AAG85042	ABB82478	ADE61071	ADI79900	ADK46733	ADR95319	AEA59189	
63 8	930 4	39 7	59 4	59 4	34 4	62 8	48 8	76 8	73 4	73 7	30 9	47 4	41 6	31 4	358 5	358 7	358 8	158 8	65 8	62 9	
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191	98.5	96.5	94	94	88.5	85.5	85.5	85.5	85.5	85.5	85.5	85.5	84	79.5	77	77	77	9/	9/	16	
25	26	27	28	29	30	31	32		34	32	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

Human; secreted protein; gene therapy; vaccine; treatment; diagnosis; Human secreted protein, SEQ ID NO: 260. AAG89140 standard; protein; 158 AA. 07-DEC-2000; 2000WO-IB001938. 08-DEC-1999; 99US-0169629P. (first entry) WO200142451-A2. Homo sapiens. 11-SEP-2001 14-JUN-2001 AAG89140; GENSET. AAG89140 ID AAG8

(GEST) GENSET.

Bougueleret L, Dumas Milne Edwards J,

Jobert S;

WPI; 2001-367870/38. N-PSDB; AAH64743.

Full length GENSET human nucleic acids encoding potentially secreted proteins, useful in gene therapy and vaccination against a variety of diseases, and for diagnosis of those diseases.

Claim 21; Page 804; 921pp; English.

The invention relates to full length GENSET human nucleic acids encoding potentially secreted proteins. The nucleic acids and the polypeptides they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GENSET gene expression. For example, they be used to treat disorders associated with decreased GENSET gene expression by rectifying mutations or deletions in a patient's gene expression by rectifying mutations or deletions in a patient's patients own production of GENSET polypeptides. Conversely, antisense nucleic acid molecules may be administered to down regulate GENSET expression by binding with the cells' own genes and preventing their

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                                                                                                                                                                                                                                                                                                                                           61 RIHTYVYEFIYLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQEIHLECSTSRKSVW 120
probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence to determine which patients may be in need of restorative therapy. The GENNET polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of GENSET polypeptide expression and activity. The present sequence is a GENSET polypeptide the invention
                                                                                                                                                                                                                                                                                                                        61 RIHTYVYEFIYLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQEIHLECSTSRKSVW 120
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Burford N;
                                                                                                                                                                                                                                                      1 MALEVLMLLAVLIWTGAENLHVKISCSLDWLMVSVIPVAESRNLYIFADELHLGMGCPAN
                                                                                                                                                                                                                                                                         1 MALEVLMLIAVIIWTGAENIHVKISCSLDWLMVSVIPVAESRNLYIFADELHLGMGCPAN
                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                      Length 158;
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TY, Lal PG, Duggan BM,
Khare R, Walia NK;
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                                                                                                                                                                                      98.7%; Score 789; DB 4; 1100.0%; Pred. No. 3.3e-81;
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                                                                                                                                                                                                100.0%; Preu. ...
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J, Tang TY,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG97353 standard; protein; 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human CGDD4, INCYTE 5284076CD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-FEB-2001; 2001US-0271175P.
08-MAR-2001; 2001US-0274503P.
09-MAR-2001; 2001US-0274552P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-FEB-2001; 2001US-0268111P-23-FEB-2001; 2001US-0271175P-
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Xu Y, Gietzen KJ,
Richardson TW, Tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                     Matches 151; Conservative
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                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                     Sequence 158 AA;
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Lu DAM,
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The invention relates to an isolated polypepties comprising valued to acid sequence at least 90% identical to CGDD, a biologically active acid sequence at least 90% identical to CGDD, a biologically active acid sequence at least 90% identical to CGDD, a biologically active acid sequence at least 90% identical to CGDD, a biologically active fragment or an immunopeance fragment. Also included are the comprising a promoter sequence operably linked to the CGDD comprising a promoter sequence operably linked to the CGDD computedetides, a cell transformed with the recombinant polymucleotide, an anti-cCGD antibody, screening for compounds which bind to/modulate or are antigaonists of CGDD or alter the expression of CGDD polymucleotide and a cCGDD polymucleotide microarray. The polypeptides, polymucleotide and a cCGDD polymucleotide microarray. The polypeptides, polymucleotide and a cCGDD polymucleotide microarray. The polypeptides, polymucleotides or alternating disorders associated with aberrant expression of CGDD, polymucleotide microarray. The polypeptides, polymucleotides, cirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycytheemia cirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycytheemia cirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycytheemia cirrhosis, psoriasis, primary thromobocytopaemia or cancer), developmental cirrhosis, hepatitis, primary thromobocytopaemia or cancer), developmental cycle, or autoinmune/inflammatory disorders (e.g. Alzheimer disease, Parkinson's disease or the mensitual cycle, or autoinmune/inflammatory disorders (e.g. Alzheimer disease, diabetes mellitus, cottact dermatitis, or utral, bacterial, fungal, parasitic, protozoal or helminthic cirrhosis, they are also useful in the assessment of the effects of exogences compounds on the expression of mucleic acid and amino acid cycle or expression of mucleic acid and amino acid cycle or expression of mucleic acid and amino acid cycle or expression of mucleic acid and amino acid cycle or expression 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                     invention relates to an isolated polypeptide comprising CGDD1-12
New human proteins associated with cell growth, differentiation and death, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), cancer, atherosclerosis or hepatitis.
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100.0%; Pred. No. 3.3e-81;
iive 0; Mismatches 0;
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                                                                                                                                    Claim 1; Page 146; 181pp; English
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ABR47931 standard; protein; 158 AA.

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The present invention relates to the isolation of human GSSP3

Dolypeptide, and polymucleotide sequences that encode it. The GSSP3

Dolypeptide reduces circulating blood glucose levels, increases insulin

sensitivity, and/or reduces body mass. The GSSP3 polypeptide and

Compositions comprising dSSP3 polypeptides and prevention of body weight gain.

Compositions comprising GSSP3 polypeptides are useful for controlling

Compositions comprising GSSP3 polypeptides are useful for controlling

Compositions comprising dSSP3 polypeptides are useful for controlling

Compositions comprising dSSP3 polypeptides are useful for controlling

Compositions comprising dSSP3 polypeptides are useful for controlling

Compositions at the reactions metabolic-related diseases or

disorders (e.g. obesity, impaired glucose tolerance, insulin resistance, hyperlipidaemias, atherosclerosis, heart disease, hypertension, stroke, syndrome C, type I or II diabbetes related complications,

Compositions in gricans, incroangiopathic lesions, or syndromes such as acanthosis ingricans, incroangiopathic lesions, or syndromes such as acanthosis ingricans, leprechaunism and lipoatrophy). The polypeptides

Composition in improve physical performance during work or exercise, and to treat dyslexia, attention-deficit disorder, attention-deficit disorder, attention-deficit disorders such as schizophrenia. The present sequence represents human GSSP3 polypeptide
lipoatrophy; physical performance; exercise; dyslexia; schizophrenia; attention-deficit disorder; hyperactivity disorder; psychiatric disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reducing circulating glucose levels or increasing insulin sensitivity, useful for reducing body mass or preventing body weight gain, comprises administering composition comprising GSSP3 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yen-Potin F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chicca J,
                                                                                                                                                                 18. .158 ____/label= Mature_GSSP3_polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                              Bour BA,
                                                                                                                                 l. .17
/label= Signal_peptide
                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 96-97; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salter-Cid L, Ebbets-Reed D,
                                                                                                                                                                                                                                                                                                                    01-FEB-2002; 2002WO-IB001333.
                                                                                                                                                                                                                                                                                                                                                             02-FEB-2001; 2001US-0266156P
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                                                                 Homo sapiens
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                                                                                                                            Peptide
                                                                                                                                                                      Protein
                                                                                                           Key
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                                                                                                                                                            61 RIHTYVYEFIYLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQEIHLECSTSRKSVW 120
                                                                                                                                       RIHTYVYEFIYLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQEIHLECSTSRKSVW 120
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                                                                   1 MALEVLMLLAVLIWTGAENLHVKISCSLDWLMVSVIPVAESRNLYIFADELHLGMGCPAN
                                                                                     0; Gaps
Query Match 98.7%; Score 789; DB 5; Length 158; Best Local Similarity 100.0%; Pred. No. 3.3e-81; Matches 151; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                           121 LTPVSTENEIKLDPSPFIADFQTTAEELGLL 151
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RESULT 4 ABR47931

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ARRABIAS) and their coding sequences (ACC50856). The proteins and their coding sequences are useful for the preparation of a diagnostic cor pharmaceutical composition for diagnosing or treating a cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary arteriosclerosis and myocardial ischaemia), neural disorders, immune system disorders, muscular disorders, reproductive disorders, immune gastrointestinal disorders, pulmonary disorders, renal disorders, for proliferative disorders and/or cancerous diseases and conditions, for coventing neural damage which occurs in neuronal disorders or infection, for treating thrombosis and arteriosclerosis, for treating or preventing neural damage which occurs in neuronal disorders or neurodegenerative conditions such as Alzheimer's disease and Parkinson's disease, to enhance bone and periodontal regeneration and aid in tissue transplants or bone grafts, to prevent skin aging or hair loss, to stimulate growth and differentiation of haemacopoietic cells and bone marrow cells when used in combination with other cytokines, to maintain organs before transplantation or for supporting cell culture of primary tissues, to increase or decrease differentiation or proliferation of embryonic stem cells, or to modulate mammalian characteristics or metabolism. Note: The sequence data for this patent was published in continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and continual and conti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human secreted proteins, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating cardiovascular disorders such as arrhythmia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention relates to novel human secreted proteins (ABR47633
                                                                                                                                                                                                  Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic; vulnerary; antiinflammatory; nootropic; neuroprotective; antianflammatory; human; cardiovascular disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 13; SEQ ID NO 822; 1881pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                     Human secreted protein, SEQ ID 822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2001; 2001US-0277340P
19-JUL-2001; 2001US-0306171P-
13-NOV-2001; 2001US-0331287P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-MAR-2002; 2002WO-US009785
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                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                        WO200295010-A2.
                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                  12-JUN-2003
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                                                  ABR47931;
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Gaps ; 0

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61 RIHTYVYEFIXLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQEIHLECSTSRKSVW 120
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                                                                    1 MALEVIANILAVIIWTGAENLHVKISCSLDWLAVSVIPVAESRNLYIFADELHIGMGCPAN
                                                                                                                                   RIHTYVYEFIYLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQEIHLECSTSRKSVW
                                          1 MALEVIANLLAVLIWIGAENLHVKISCSLDWLMVSVIPVAESRNLYIFADELHLGMGCPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secreted protein; gene therapy; antidiabetic; diabetes; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein #SEQ ID 621.
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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Conservative
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151;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                      ABZ71190-ABZ71478 represent cDNAs corresponding to 178 human secreted protein genes, and ABP00011-ABP00299 represent the proteins they encode. ABZ71479-ABZ714740 represent human secreted protein genomic fragments. The invention also encompasses antibodies specific for the secreted proteins, and recombinant vectors and host cells comprising a nucleic acid of the invention. The secreted proteins, nucleic acids encoding them, antibodies or antibody fragments specific for the secreted proteins, and modulators of protein activity are useful for diagnosing, treating, ameliorating or preventing digestive disorders. Such conditions include disorders of the mouth, cesophagus, stomach, small intestine, large intestine, liver, biliary treat and pancreas, and include cancers of these organs and tissues. The secreted proteins and their nucleic acids may also be used in the treatment of immune disorders, and to promote wound healing. Nucleic acids of the invention may be used for chromosome identification, chromosome mapping, in gene therapy, for identifying individuals from minute biological samples, as hybridisation probes, and as molecular weight in arkers. The present sequence represents a human secreted protein of the
                                                                                                                                                                                                                                                                                                                                                          Human, secreted protein, digestive disorder, gastrointestinal disorder, mouth, oesophagus, stomach, small intestine; large intestine; liver; blilary tract; pancreas, cancer; tumour; hyperproliferative disorder; immune disorder; inflammation; infection; wound healing; drug screening; chromogome identification; chromosome mapping; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human secreted proteins and nucleic acids, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating e.g. gastrointestinal diseases and disorders, or cancers.
                                                                                                                                                                                                                                                                                                                  Human gene 165 encoded secreted protein HTELS08, SEQ ID NO:464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiinflammatory; immunosuppressive; vulnerary; gene therapy.
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                       121 LTPVSTENEIKLDPSPFIADFQTTAEELGLL 151
                                            121 LTPVSTENEIKLDPSPFIADFQTTAEELGLL 151
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                                                                                                                                                                              ABR00175 standard; protein; 158
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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                                                                                                                                                                                                                                                                       (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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The invention relates to isolated nucleic acid molecules ADB91065-ADB91448 and ADB91835-ADB91911 encoding human secreted proteins ADB91449-ADB91448 and ADB91835-ADB91911 encoding human secreted proteins ADB91449-DB91844. Also disclosed is a recombinant vector comprising a polymucleotide of the invention, and a recombinant host cell comprising the recombinant vector. The polypeptide of the invention is useful in the recombinant vector. The polypeptide of the invention is useful in clentifying a binding partner by contacting the polypeptide, with a binding partner, and determining whether the binding partner increases or decreases activity of the polypeptide. The polypeptide, polymucleotide, antibody or its fragment, agonist or antagonist are useful for preparing conditions related to diabetes. The present sequence is that of the human immunoglobulin Fc portion used to generate fusion proteins, increasing conditions related protein as compared to the secreted protein conly. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Matches 151; Conserv
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                                                                                                                                                                                                                                                                                                                               antianaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   defined sequence given in the specification. The polypetide, nucleic acid molecule, antibody, agonist or antagonist of the invention may be useful for preparing a composition for diagnosing or treating a haemopoietic or haematologic disorder such as anaemia, autoimmune disorders such as rheumatologic disorder such as naemia, autoimmune disorders such as rheumatologic arthritis, inflammation, Grave's disease, alsorders including Parkinson's disease, adiabetes, systemmic lupus erythematosus or glomerulomephritis, neurodegenerative disorders including Parkinson's disease and Alzheimer' disease, wounds and hyperproliferative disorders including atherosclerosis or cancer, as well as bacterial, viral, fungal or parasitic infections. The polypeptide may also be used during gene therapy procedures and for identifying a binding partner by contacting the polypeptide with a binding partner and determining whether the
                                                                                                                                                                                                                                                                                                                                          antidabetic; immunosuppressive; dermatological; nephrotropic; antidabetic; immunosuppressive; dermatological; nephrotropic; antidaterior antidaterior antidaterior antidaterior antidaterior antidaterior antidaterior antidaterior antidaterior antidaterior antidaterior, numerary; cytostatic; haemopoletic; haematologic; anaemia; autoimmune disorder; rheumatold arthritis; inflammation; Grave's disease; diabetes; systemic lupus erythematosus; glomerulonephritis; neurodegenarative; Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis; cancer; bacterial; viral; fungal; parasitic infection; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human secreted polypeptide for diagnosing, preventing or treating hematopoietic or hematologic disorders (e.g. anemia), autoimmune disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer atherosclerosis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel human secreted polypeptide comprising
                 RIHTYVYEFIYLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQEIHLECSTSRKSVW
MALEVLMLLAVLIWTGAENLHVKISCSLDWLMVSVIPVAESRNLYIFADELHLGMGCPAN
                                                                                                           LTPVSTENEIKLDPSPFIADFQTTAEELGLL 151
                                                                                                                             Claim 16; SEQ ID NO 971; 2272pp; English.
                                                                                                                                                                                                                                                                                                    Human secreted protein - SEQ ID 971.
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                                                                                                                                                                                                               ADC74338 standard; protein; 158
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                           ADC74338;
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binding partner increases or decreases the activity of the polypeptide.
The current sequence is that of the human secreted protein of the
                                                                                                                                                                                                                                                                                                   cytostatić; cardiant; vasotropić; cerebroprotective; neuroprotective;
nootropić; antibacterial; virucide; fungicide; opthalmalogical; human;
vulnerary; gene therapy; infection; secreted protein.
                                                                                                                                                                                                                                                                         1 MALEVLMLLAVLIWTGAENLHVKISCSLDWLMVSVIPVAESRNLYIFADELHLGMGCPAN
                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                    Length 158;
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, Moore PA,
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                                                                                                                                                           98.7%; Score 789; DB 7; I
100.0%; Pred. No. 3.3e-81;
ive 0; Mismatches 0;
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n HS, Ebner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB38337 standard; protein; 159
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99US-0130991P.
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                                                                                                                                                                                                                    Matches 151; Conservative
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                                                                                                                                                                                       Local Similarity
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                                                                                                              Sequence 158 AA;
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                                                           invention.
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Young PE;
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(f) nervous system disorders e.g. Alzheimer's disease, (g) infections caused by bacteria, viruses and fungi; and (h) ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis
                                                                                                                                                                                                                                                                           Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                           RIHTYVYEFIYLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQEIHLECSTSRKSVW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell regeneration; membrane protein; signal transduction-related protein; transcription-related protein; osteoporosis; neurological disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical; diagnostic; gene therapy; tissue regeneration;
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                                                                                                                                       Length 159;
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                                                                                                                                    98.7%; Score 789; DB 3; I
100.0%; Pred. No. 3.4e-81;
iive 0; Mismatches 0;
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25-JAN-2002; 2002US-00350978.
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                                                                                                                                                                  Matches 151; Conservative
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Yamamoto J, Isono Y, )
Seki N, Yoshikawa T, (
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N-PSDB; ADB63550.
                                                                                                                                                    Similarity
                                                                                                            Sequence 159 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel polypeptides. Also claimed is a polypeptide encoded by the polynucleotide or its partial peptide, an antibody binding to the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or

Claim 1; Page; 222pp; English.

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peptide of the polynucleotide by contacting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polynucleotide. The oligonucleotide is useful as a primer for synthesising the polynucleotide. The oligonucleotide of the detecting the polynucleotide sud encoded proteins are useful as pharmaceutical agents and many disease-related proteins are useful as pharmaceutical agents and many disease-related genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell regeneration. Membrane proteins, signal transduction-related proteins, transcription-related proteins, disease-related proteins are encoding them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours. The CDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence presented is a protein of the invention. Note: Some of the sequence data for this patent is not represented in the printed or sequence information supplied by the
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isorders, and the
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99.3%; Pred. No. >...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                          Sequence 158 AA;
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The present invention relates to novel GENSET polynucleotides (ABZ154404-ABZ3641) encoding polypeptides (ABP75963-ABP76368). The polynucleotides and polypeptides are useful in screening and diagnostic assays for abnormal GENSET expression and/or biological activity. They are also useful for screening of compounds for treating or preventing GENSET-related disorders, such as heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, central nervous system (CNS), cardiovascular or gastrointestinal effects of the toxicity
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                                                                                                                                                                                                                                                         MALEVLMLIAVI IWTGAENLHVKISCSLDWLMVSVI PVAESRNIYI FADELHIGMGCPAN 60
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                                                                                                                                                                                                                                                                             1 MALEVLALLAVLIWITGAENLHVKISCSLDWLMVSVIPVAESRNLYIFADELHLGAGCCPAN
                                                                                                                                                                                                                                                                                                                             cancer;
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~~~d. No. 1.2e-79;
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                          Claim 14; Page 680; 735pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; protein; 143
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                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tanaka H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-075548/07.
                                                                                                                                                                            Sequence 148 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200283898-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-FEB-2003
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                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                          61
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The present invention relates to novel GENSET polynucleotides (AB236404-AB236911) encoding polypeptides (ABP75963-ABP76368). The polynucleotides and polypeptides are useful in screening and diagnostic assays for

Claim 14; Page 680; 735pp; English.

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abnormal GENSET expression and/or biological activity. They are also useful for screening of compounds for treating or preventing GENSET-related disorders, such as heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, central nervous system (CNS), cardiovascular or gastrointestinal effects of the toxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        potentially secreted proteins. The nucleic acids and the polypeptides they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GBNSET gene expression. For example, they be used to treat disorders associated with decreased GENSET gene expression by rectifying mutations or deletions in a patient's genome that affect the activity of GENSET or by supplementing the patients own production of GENSET or by supplementing the nucleic acid molecules may be administered to down regulate GENSET expression by binding with the cells' own genes and preventing their expression. The sense and antisense nucleic acids may also be used as DNA
                                                                                                                                                                                                                                                                              RIHTYVYBFIYLVRDCGIRTRVVSEETLLFQTBLYFTPRNIDHDPQEIHLECSTSRKSVW 120
                                                                                                                                                                                                                                                                                                      RIHTYVYBEIYLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQEIHLECSTSRKSVW 120
                                                                                                                                                                                                               69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to full length GENSET human nucleic acids encoding
                                                                                                                                                                                                             1 MALEVLMLLAVLIWTGAENLHVKISCSLDWLMVSVIPVAESRNLYIFADELHLGMGCPAN
                                                                                                                                                                                                                                      MALEVLMELAVI, INTGAENLHVKISCSLDMLMVSVI PVAESRNLYI FADELHLGMGCPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Full length GENSET human nucleic acids encoding potentially secreted proteins, useful in gene therapy and vaccination against a variety of diseases, and for diagnosis of those diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;
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                                                                                                                                         Length 143;
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                                                                                                                                       Score 752; DB 6; I
Pred. No. 4.7e-77;
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                                                                                                                                                   100.0%; Preu. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted protein, SEQ ID NO: 265.
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                                                                                                                                                                                                                                                                                                                                                    143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG89145 standard; protein; 106 AA.
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                                                                                                                                                                                                                                                                                                                                                    LTPVSTENEIKLDPSPFIADFQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins, useful in gene therar
diseases, and for diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-DEC-2000; 2000WO-IB001938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-DEC-1999; 99US-0169629P
06-MAR-2000; 2000US-0187470P
                                                                                                                                          94.18;
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                                                                                                                                                                           Matches 143; Conservative
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                                                                                                                                                         Similarity
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N-PSDB; AAH64748.
                                                                                                        Sequence 143 AA;
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                                                                                                                                          Query Match
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probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence to determine which patients may be in need of restorative therapy. The GENSET polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of GENSET polypeptide expression and activity. The present sequence is a GENSET polypeptide of
                                                                                                                                                                                                                                         1 MALEVIMILIAVI.IWTGAENI.HVKISCSLDWI.MVSVIPVAESRNI.YI.FADELHI.GMGCPAN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOVX; antidiabetic; anorectic; cardiant; hypotensive; antidiabetic; anorectic; cardiant; hypotensive; antidacterial; fungicide; protozoacide; nootropic; neuroprotective; antiparkinsonian; anticonvulsant; osteopathic; antiarthritic; antiinflammatory; dermatological; antiarthritic; antiinflammatory; dermatological; antianthmatic; antilipaendc; metabolic; diabetes; obesity; infectious; anorexia; cancer; cardiovascular; hypotrension; atheroselerosis; neurodegenerative; Alzheimer's disease; Parkinson's, epilepsy; immune; osteoarthritis; haemopoietic; inflammatory skin; asthma; dyslipidaemia; neurogenesis; cell differentiation; proliferation; haemopoiesis; wound healing; angiogenesis; gene therapy; chromosome mapping; tissue typing; human; NOV.
                                                                                                                                                                                                                       1 MALEVLMLLAVLIWTGAENLHVKISCSLDWLMVSVIPVAESRNLYIFADELHLGMGCPAN
                                                                                                                                                                                           Gaps
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                                                                                                                                                            Length 106;
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Pred. No. 1.7e-40;
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100.0%; Pred. No. 1...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                ADE28663 standard; protein; 212 AA.
                                                                                                                                                                                                                                                                                      61 RIHTYVYEFIYLVRDCGIRTRV 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human NOV12a protein - SEQ ID 40.
                                                                                                                                                                                                                                                                                                       2001US-0341477P.
2001US-0341540P.
2001US-0342592P.
2001US-0344297P.
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2002US-0383534P.
2002US-0383744P.
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2002US-0401788P.
2002US-0406353P.
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2001US-0341346P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-2004 (first entry)
                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 82; Conservative
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                                                                                                                             Sequence 106 AA;
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17-DEC-2001;
20-DEC-2001;
                                                                                                the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-DEC-2001;
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29-MAY-2002;
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The invention relates to a novel isolated NOVX polypeptide. The polypeptide of the invention demonstrates, antidiabetic, anorectic, acardiant, hyporensive, antiarteriosclerotic, virucide, antibacterial, tungicide, protozoacide, nocorropic, neuroprotective, antiparkinsonian, anticonvulsant, osteopathic, antiarthritic, antiinflammatory, anticonvulsant, osteopathic, antiarthritic, antiinflammatory, continued anticonvulsant, osteopathic, and antilipaemic activities. The polypeptides, nucleic acid molecules and antibodics may be useful for treating or diagnosing diseases including metabolic disorders such as diabetes and obesity, infectious diseases, anorexia, cancer, cardiovascular diseases including hypertension and atherosclerosis, neurodegenerative disorders cuch as Alzheimer's disease, Parkinson's disease and epilepsy, immune disorders e.g. osteoarthritis, haemopoietic disorders, inflammatory skin disorders, asthma and dyslipidaemia.

Churthermore, the nucleic acids and polypeptides may also be used to identify molecules that modulate or inhibit neurogenesis, cell differentiation and proliferation, haemopoiesis, wound healing and angiogenesis, as well as in gene therapy. Finally, the nucleic acids may be used as hybridisation probes, in chromosome mapping, that of preventive medicine and pharmacogenomics. The current sequence is that of
                                       Alsobrook JP, Alvarez E, Anderson DW, Baron M, Boldog FL;
Burgess CE, Caeman SJ, Chapoval A, Dhanabal M, Edinger SR, Eisen A;
Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;
Grosse WM, Guo X, Hackett C, Ji W, Kekuda R, Khramtsov NV;
Lepley DM, Li L, Macdougall JR, Malyankar UM, Mazur A, Mcqueeney K;
Mezes PS, Miller CE, Millet I, Mishra VS, Padigaru M, Patturajan M;
Pena CEA, Peyman JA, Rastelli L, Rieger DK, Shenoy SG, Shimkets RA;
Smithson G, Starling G, Spytek KA, Stone DJ, Tchernev VT, Twomlow N;
Vernet CAM, Zerhusen BD, Zhong M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 YVYEFIYLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQE--IHLECSTSRKSVWLT 122
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                                                                                                                                                                                                                                                                                                                                                    New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 VLMLLAVLIWIGAENLHVKISCSLDWLMVSVIPVAESRNLYIFADELHLGMGCPANRIHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 LMILLTSALSAGSGQSPMTVLCSIDWFMVTVHPFMLNNDVCVHFHELHLGLGCPPNHVQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 6.1e-17;
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y 33.3%; Pred. No. b.r.
''' 33; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                               asthma, or infections.
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Best Local Similarity
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ADM93408
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acquired immunodeficiency syndrome; AIDS; Crohn's disease; infectious disease; anorexia; immune disorder.
                                                                        2001US-00035568.
2001US-0338626P.
2001US-0333072P.
2001US-0348283P.
2001US-0335151P.
2001US-0333912P.
2001US-0333912P.
2001US-0333912P.
2001US-0334300P.
                                                                                                                                                   2002US-0354807P
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2002US-0401479P
                                                           05-NOV-2002; 2002US-00287971
                                                                                                                                                                 2002US-0381043P
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ETTENBERG S.
GANGOLLI E A.
GERLACH V.
                                                                                                                                                                                                                                           ANDERSON D W.
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PATTURAJAN M.
                                                                                                                                                                                                                                                                     CASMAN S J.
CHAPOVAL A.
DHANABAL M.
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MCQUEENEY K.
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MILLER C E.
MILLET I.
MISHRA V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PENA C E A.
PEYMAN J A.
RASTELLI L.
RIEGER D K.
ROTHENBERG M
SHENOY S G.
                                                                                                                                                                                                                                                                                                                                  GORMAN L.
GROSSE W M.
GUO X.
HACKETT C.
                                                                                                                                                                                                                                                         BOLDOG F L.
BURGESS C E.
                                                                                                                                                                                                                                                                                          EDINGER S R
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                                                                                                                                                                                                                                                   BARON M.
                                                                                                                                                                                                                                                                                                  EISEN A.
                                 US2004067882-A1
                                                                                                                                                                                                   07-AUG-2002;
07-AUG-2002;
26-AUG-2002;
                    Homo sapiens
                                                                                                   09-NOV-2001;
                                                                                                                              29-NOV-2001;
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                                                                                                                                                   05-FEB-2002;
                                                                                              NOV-2001;
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                                               38-APR-2004
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(ALVA/)
(ANDE/)
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(MAZU/)
(MCQU/)
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(MILL/)
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(RAST/)
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(ROTH/)
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(BOLD/)
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                                                                                                                                                                                                                                                                                          (EDIN/)
                                                                                                                                                                                                                                                                                                                      (GANG/)
(GERL/)
                                                                                                                                                                                                                                                                                                                                                       (HACK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PADI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PENA/)
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The invention relates to human NOVX polypeptides and the polynucleotides are useful for encoding them. The NOVX polypeptides and polynucleotides are useful for determining the presence of or predisposition to a disease associated with altered levels of the sequences in a mammalian subject, and for treating or preventing a pathology associated with NOVX. The polypeptides, polynucleotides and antibodies that bind immunospecifically to the polypeptides are useful for treating or preventing disorders or syndromes such as congenital heart defects, cardiomyopathy, atherosclerosis, hypertension, pulmonary stenosis, scleroderma, adenocarcinoma, haemophilia, graft-versus-host disease, cancer, neurodegenerative disorders, Alzhaimer's disease, parkinson's disease, multiple sclerosis, diabetes, obesity, bronchial asthma, acquired immunodeficiency syndrome (AIDS), Crohn's disease, infectious disease, anorexia and immune disorders. This sequence represents a human NOVX polypeptide of the invention. Note: The sequence data for this patent is also available from USPTO at seqdata.uspto.gov/sequence.html.
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Burgess CE, Caeman SJ, Chapoval A, Dhanabal M, Edinger SR, Eisen A;
Ellerman K, Ettenberg S, Gangolli EA, Gerlach V, Gorman L;
Grosse WM, Guo X, Hackett C, Ji W, Kekuda R, Khramtson NV;
Lepley DM, Li L, Macdougall JR, Malyankar UM, Mazur A, Moqueeney K;
Mezes PS, Miller CE, Millet I, Mishra V, Padigaru M, Patturajan M;
Pena CEA, Peyman JA, Rastelli L, Rieger DK, Rochenberg ME;
Shenoy SG, Shinkets RA, Smithson G, Spaderna SK, Starling G;
Spytek KA, Stone DJ, Tchernev VT, Twomlow N, Vernet CAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 VLMLLAVLIWIGAENLHVKISCSLDWLMVSVIPVAESRNLYIFADELHLGMGCPANRIHT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated NOVX polypeptide useful treating or preventing disorders or syndromes such as Alzheimer's disease, Parkinson's disease, multiple sclerosis, diabetes, obesity, cancer, bronchial asthma, Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 IMILITSALSAGSGQSPMTVLCSIDWFMVTVHPFMLNNDVCVHFHELHLGLGCPPNHVQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; SEQ ID NO 40; 330pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW73630 standard; protein; 212
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SHIMKETS R A.
SMITHSON G.
SPADERNA S K.
STARLING G.
SPYTEK K A.
STONE D J.
TCHERNEV V T.
TWOMLOW N.
                                                                                                                                                        VERNET C A M.
ZERHUSEN B D.
VOSS E Z.
ZHONG M.
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                                                      (STAR/)
(SPYT/)
(STON/)
(TCHE/)
(TWOM/)
(VERN/)
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                                          SPAD/)
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Secreted protein; human; nutritional supplements; immune stimulant; immune suppressor; haematopoiesis regulator; tissue growth; chemotaxis; activin/inhibin; chemokinesis; haemostasis; thrombolysis; receptor/ligand activity; anti-inflammatory; tumour inhibitor; cadherin/tumour invasion suppressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Racie LA, Treacy M, Spaulding V;
Human secreted protein clone ej265_4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 31; Page 93-94; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lavallie ER,
1, Fechtel K;
                                                                                                                                                                                                                                                                                           97US-00868696.
97US-00868697.
97US-00868898.
97US-00868899.
97US-00868191.
97US-00869192.
97US-00869193.
97US-00869193.
                                                                                                                                                                                                                                                            98WO-US011210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Agostino MJ, Howes SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mccoy JM,
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                                                                                                                                                                                                                                                                                                                  04-JUN-1997;
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9, 2006, 10:15:15 Search completed: May Job time: 106.3 secs

This sequence represents a human secreted protein of the invention. The DNA encoding this sequence was isolated from a human adult placenta CDNA library, and was designated clone ej2654. The DNAs and proteins are predicted to have biological activities which would make them suitable for treating, preventing activities which would make them suitable animals, although no supporting data is given. Suggested activities include nutritional sources or supplements, immune stimulating or suppressing activity, heematopoiseis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, haematory cadherin/tumour invasion suppressor activity, and tumour activity. The DNAs are also stated to be useful for gene therapy. A host cell transfected with the DNA, or its subfragments are also stated to be useful for activity and the DNA, or its subfragments 7 New polynucleotides encoding secreted human proteins - derived from human foetal brain, adult brain, foetal kidney, adult ovary, adult retina, adult placenta or adult uterus cDNA libraries. Gaps 5, 28.0%; Score 223.5; DB 2; Length 212; 33.3%; Pred. No. 1e-16; 1ive 32; Mismatches 43; Indels 5 Query Match 28.0 Best Local Similarity 33.3 Matches 40; Conservative

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7, Appli 7, Appli 7, Appli 61, Appli 81, Appli 13077, A 2, Appli

Appl Appl

12, Appl 84, Appl 2, Appli 5579, Ap

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61 RIHTYVYEFIYLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQEIHLECSTSRKSVW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RIHTYVYBFIYLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQEIHLECSTSRKSVW 120
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                                                                                                                                                                                                                                                                                          Sequence 3903, Application US/09621976
General No. 663063
GENERAL INFORMATION:
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION ESTS and Encoded Human Proteins.
CURRENT APPLICANT ADVENTION USSES. US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SEQ ID NO 3903
LENGTH: 153
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US-09-621-976-5222
; Sequence 5222, Application US/09621976
; Patent No. 663963
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Globert, S.
; APPLICANT: Globert, S.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
US-09-949-016-10862
US-08-453-472-7
US-08-038-948-4
US-08-862-903-7
US-08-862-903-7
US-08-862-903-7
US-09-312-183A-3
US-09-312-183A-2
US-09-312-183A-2
US-08-070-311-14
US-08-070-311-17
US-09-949-016-9905
US-09-949-016-6888
US-09-949-016-6888
US-08-476-515A-84
US-09-393-245-2
US-09-313-245-2
US-09-134-0000C-5579
US-08-469-260A-81
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100.0%; Pred. No. 9.6e-94;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 153; Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
 ; NAME/KEY: SIGNAL
; LOCATION: -17..-1
US-09-621-976-3903
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US-09-621-976-3903
FEATURE:
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         GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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(cgn2_6/ptodata/1/iaa/5_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6_COMB.pep:*

(cgn2_6/ptodata/1/iaa/H_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PETUS COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-10-104-047-3674

US-09-621-976-5223

US-09-949-016-11232

US-09-521-976-6447

US-09-723-806A-8

US-09-723-806A-8

US-09-723-806A-8

US-09-723-806A-8

US-09-723-806A-8

US-09-383-110-3248

US-09-383-110-3248

US-09-383-188-18

US-08-484-9938-18

US-08-484-9938-18

US-08-480-150A-18

US-08-480-150A-18

US-08-453-472-8

US-08-453-472-8

US-08-149-223A-18

US-08-149-223A-18

US-08-149-223A-18

US-08-149-223A-18

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                                                       - protein search, using sw model
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. 6943241e1 full length cDNA;
FILE REFERENCE: H1-A0105
CURRENT PILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
PRIOR PILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3674
LENGTH: 158
                                                                                                                                                                                                                                                             98.7%; Score 789; DB 2; 100.0%; Pred. No. 1.9e-92; ive 0; Mismatches 0;
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99.3%; Pred. No. 6.1e-92;
iive 0; Mismatches 1.
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CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5222
LENGTH: 158
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8-10-104-047-3674
; Sequence 3674, Application US/10104047
; Patent No. 6943241
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 151; Conservative
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Matches 150, Conservative
                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                            ; NAME/KEY: SIGNAL
; LOCATION: -17..-1
US-09-621-976-5222
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US-09-621-976-5223
; Sequence 5223, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.

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Sequence 11232, Application US/09949016

Patent No. 681239
GENERAL INFORMATION:
PAPPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SEQ ID NOS: 207012
SEQ ID NO 11232
FRIEND TILING DATE: PARLED FAREOFFER PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 LMILLTSAFSAGSGQSPMTVLCSIDWFWVTVHPFMLNNDVCVHFHELHLGLGCCPPNHVQP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MALEVLMLLAVLIWTGAENLHVKISCSLDWLMVSVIPVAESRNLYIFADELHLGMGCPAN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENEST. 0.5470/621,976
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5223
LENGTH: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.7%; Score 429; DB 2; L
100.0%; Pred. No. 9e-47;
tive 0; Mismatches 0;
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US-09-621-976-6447
Sequence 6447, Application US/09621976
Parent No. 6639063
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -17..-1
US-09-621-976-5223
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US-09-949-016-11232
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US-09-949-016-11232
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US-09-583-110-3248
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73 RNIILMA-LLHVGALYGITLIPSSKVYTLLWGIFYYLISALGITAGAHRLWSHRTYKARL 131
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                                                                                                                                                                                                                                                                                                Length 56;
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                                                                                                                                                                                                                                                                                                                                                                         111 ECSTSRKSVWLTPVSTENEIKLDPSPFIADFQTTAEELGLL 151
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF THE REPERENCE: GENSET.054 PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/558,823
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                                                                                                                                                                                                                                                                                            Score 211; DB 2;
Pred. No. 2.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19, Application US/08558823
Fatent No. 5876994
GENERAL INFORMATION:
APPLICANT: Rolofs, Wendell L.
APPLICANT: Rolofs, Wendell L.
APPLICANT: Miller, Stuart J.
TITLE OF INVENTION: PHEROMONE DESATURASES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                          Query Match 26.4%; Score 211; DB Best Local Similarity 100.0%; Pred. No. 2.3 Matches 41; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Nixon, Hargrave, Devans & STREET: Clinton Square, P.O. Box 1051
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NAME: ROGALSKY EGG., Peter
REGISTRATION NUMBER: 38 601
REPERENCE/DOCKET NUMBER: 1963/400
TELECOMMUNICATION INFORMATION:
TELEFRONE: (716) 263-1634
TELEFRAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
APPLICANT: Dumas Milne Edwards, J.B APPLICANT: Jobert, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 358 amino acids
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                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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STATE: New York
COUNTRY: U.S.A.
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                                                                                                                                                                         SEQ ID NO 6447
LENGTH: 56
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Sequence 3248 Application US/09583110
Fatent No. 6699703
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
TITLE OF INVENTION: Demoniae for Diagnostics and Therapeutics
CURRENT APPLICATION NUMBER: US 09/107,433
FRIOR FILING DATE: 1998-06-30
FRIOR APPLICATION NUMBER: US 60/085,131
FRIOR APPLICATION NUMBER: US 60/085,131
FRIOR APPLICATION NUMBER: US 60/085,131
FRIOR APPLICATION NUMBER: US 60/081,553
FRIOR FILING DATE: 1997-07-02
79 --RTRVVSEETLLFQTELYFTPRN--IDHDPQEIHLECSTSRKSV-----WLT----PV 124
                                 ||::|||:||
73 RNIILMA-LLHVGALYGITLJFSSKVYTLLWGIFYYLISALGITAGAHRLWSHRTYKARL 131
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                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/09723806A
; Patent No. 6686185
; GENERAL INFORMATION:
; APPLICANT: Gluckemann, Maria Alexandra
; APPLICANT: Logan, Thomas Joseph
; TITLE OF INVENTION: 25934, A NOVEL FATTY ACID DESATURASE AND
; TITLE OF INVENTION: USES THEREFOR
; FILE REFERENCE: 10448-024001
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187,455
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
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25.0%; Pred. No. 0.44;
tive 22; Mismatches 50; Indels
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                                                                                                            125 STENEIKLDPSPFIAD ----FQTTAEELGLLI 152
                                                                                                                                                                   192 VKEKGGKLDMSDLKAEKLVMFORRYYKPGLLL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 STENEIKLDPSPFIAD --- FOTTABELGLLI 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 25.0%
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Sequence 7887, Application US/09328352

Sequence 7887, Application US/09328352

Patent No. 5562987

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 7887
                                                                                                                                                                                                                                                               TITLE OF INVENTION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR APPLICATION NUMBER: US 60/117,747

SEQ ID NO 10162

LENGTH: 323
                                                                                  -----IYLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQEI---HLECSTSRKSV 119
                                                                                                         62 IHTYVYEFIYLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHD--PQEIHLECSTSRKSV 119
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                     18 VYISTSIDYLIILIILFAQLSQNKQKWHIYAGQ-YLGTGLLVGASLVAAYVUNFVPEEWM
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  22 VKISCSLDWLMVSVIPVAE----SRNLYIFADELHLGMG--CPANRIHTYVYEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.4%; Score 75.5; DB 2; Best Local Similarity 25.0%; Pred. No. 0.76; Matches 31; Conservative 16; Mismatches 52;
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US-09-328-352-7887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209 LVTSEGAFSYLARDYGLR---
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Best Local Similarity 24.3%
Matches 34; Conservative
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                                             9
                                                                                                                                                                    70 -----IYLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQEI--HLECSTSRKSV 119
                                                                                                                                                                                                             -----EEEEEIIERLEOSKANOLF 111
                                                                                                                           69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
                                                                                                            22 VKISCSLDWLMVSVIPVAE----SRNLYIFADELHLGMG--CPANRIHTYVYEF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46;
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9.5%; Score 76; DB 2; Length 158; 24.7%; Pred. No. 0.18; tive 27; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                    112 WIVILLIASGGDNLGI-YIPYFASLDWSQTLVALLVF 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                      120 W----LIPVSTENEIKLDPSPFIADFQTTAEELGLLIF 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPAX: (781)893-5007
INFORMATION FOR SEQ ID NO: 3954:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...165
SEQUENCE DESCRIPTION: SEQ ID NO: 3954:
                                                                                                                                                                                                             70 VGLLGLIPİYL----GİRFAIVGEDA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3954, Application US/09107433 Patent No. 6800744 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Massachusetts
COUNTRY: USA
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                             39; Conservative
                         Best Local Similarity
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      Query Match
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                                                                                                                                                                                                                           Sequence 18, Application US/08484158B

Patent No. 5976545

GENERAL INFORMATION:
APPLICANT: Harris Ph.D., Jeffrey D.
APPLICANT: Heu, Kuang T.
APPLICANT: Podolski, Joseph S.
TITLE OF INVENTION: Pharmaceutical Compositions for TITLE OF INVENTION: Immunocontraception
NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,158B
FILING DATE: O'-JUNE-95
CLASSIFICATION NUMBER: US/08/484,158B
FILING DATE: O'-JUNE-95
FILING DATE: 09-NOV-93
PRIOR APPLICATION NUMBER: 08/149,223
FILING DATE: 09-NOV-93
PRIOR APPLICATION NUMBER: 08/012,990
FILING DATE: 29-JAN-93
PRIOR APPLICATION NUMBER: 08/012,990
FILING DATE: 29-JAN-93
PRIOR APPLICATION NUMBER: 07/973,341
FILING DATE: 09-NOV-92
ATTONNEY AGENT: NPORMATION:
ANAME: O'-NOV-92
ATTONNEY AGENT: NPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Illinois
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6653
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 22.64
Matches 42; Conservative
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MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
                                                                              139 ADFQTT 144
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                                                                                              90 FQTELYFTPRNIDHDPQEIHLECSTSRKSV-----WLTPVSTENEIKLDPSPFIADF-QT 143
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                                                                                                                                                                                                                                                                                                                Sequence 18, Application US/08484993B
Patent No. 5837497
GENERAL INFORMATION:
APPLICANT: Harris Ph.D., Jeffrey D.
APPLICANT: Podolski, Joseph S.
TITLE OF INVENTION: Materials and Methods for Immunocontraception NUMBER OF SEQUENCES. 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 9.4%; Score 75.5; DB 1; Length 424; Best Local Similarity 22.6%; Pred. No. 0.88; Matches 42; Conservative 27; Mismatches 50; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CUNTEXT: UNITEG STATES OF AMERICA

ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: ISM

SOFTWARE: PATENTINE PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,993B

FILING DATE: 09-NOV-1993

CLASSIPICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/012,990

FILING DATE: 29-AAN-1993

PRIOR APPLICATION NUMBER: 07/973,341

FILING DATE: 09-NOV-1992

APPLICATION NUMBER: 07/973,341

FILING DATE: 09-NOV-1992

ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, DAVIG W.

REGISTRATION NUMBER: 36,107

REGISTRATION NUMBER: 312/474-6653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 6300 Sears Tower, 233 Sout CITY: Chicago STATE: Illinois COUNTRY: United States of America
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-484-993B-18
                                                                                                                                                            144 TAEE 147
                                                                                                                                                                                                      190 SATE 193
                                                                                                                                                                                                                                                                                                US-08-484-993B-18
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                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-08-484-596A-18
US-08-484-596A-18
; Sequence 18, Application US/08484596A
; Patent No. 598128
; GENERAL INFORMATION:
; APPLICANT: Hauris Ph.D., Jeffrey D.
; APPLICANT: How, Kuang T.;
; APPLICANT: Podolski, Joseph S.
; TITLE OF INVENTION: Materials and Methods for Immunocontraception NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS: 59
; CORRESPONDENCE ADDRESS: 30
; CORRESPENDENCE ADDRESS: 30
; CORRESPONDENCE ADDRESS: 30
; CORRESPONDENCE ADDRESS: 30
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CLASSIFICATION
PRIOR APPLICATION
PRIOR APPLICATION
PRIOR APPLICATION DATA:
PILING DATE:
11-NOV-1993
PRIOR APPLICATION NUMBER:
07/973,341
FILING DATE: 09-NOV-1992
ATORNEY/ABOUT INFORMATION:
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 31745
TELEPHONE: 312/474-6653
TELEPHONE: 312/474-6653
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TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acids
TVPE: amino acid
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MOLECULE TYPE: protein
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Sequence 260, Application US/09876997
Publication No. US20030152921A1
Publication No. US20030152921A1
APPLICANT: Dumas Milne Edwards, Jean Baptiste
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Best Local Similarity 100.
Matches 151; Conservative
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ORGANISM: Homo sapiens
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; NAME/KEY: SIGNAL
; LOCATION: -17..-1
US-09-731-872-260
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Sequence 3674, App
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Sequence 265, App
Sequence 265, App
Sequence 265, App
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Sequence 203, App
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Sequence 4, Appli
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91, Appl
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42407, A
53506, A
53701, A
741, App
151, App
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USIOA_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USIOA_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-377-072-14
US-10-377-072-14
US-10-617-320-3954
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US-10-050-704-113
US-10-665-535-4
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US-10-467-046-3
US-10-472-533-464
US-10-104-047-3674
US-09-731-872-265
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US-09-731-872-265
US-09-745-763-203
US-09-745-763-203
US-10-970-493-91
US-10-970-493-91
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US-10-11-224-91
US-10-450-763-57001
US-10-450-763-57001
US-10-450-763-57701
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Maximum Match 100%
Listing first 45 summaries
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3336, Ap
8692, Ap
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42, Appl
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US-10-306-762-201
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US-10-437-963-166460
US-10-104-047-3492
US-11-097-143-2787
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Sequence 260, Application US/09731872

Sequence 260, Application US/09731872

Patent No. US20020102604A1

SERERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Jobert, Severin

TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78.US3.REG

CURRENT APPLICATION NUMBER: US/09/731,872

CURRENT FILING DATE: 2000-12-07

PRIOR APPLICATION NUMBER: US 60/169,629

PRIOR APPLICATION NUMBER: US 60/187,470

PRIOR PILNG DATE: 2000-03-06

NUMBER OF SEQ ID NOS: 482

SOFTWARE PATENT.

LENGTH: 158
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100.0%; Pred. No. 2.7e-84;
ive 0; Mismatches 0;
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APPLICANT: 1SON, TELLY, Yan
APPLICANT: 1SON, Craig H.; LU, Yan
APPLICANT: WARREN, Eridget A.; ELIOTT, Vicki S.
APPLICANT: WARREN, Eridget A.; ELIOTT, Vicki S.
APPLICANT: BAUGHN, Mariah R.; DING, Li
APPLICANT: TANG, Tom Y.; LAL, Preeti G.
APPLICANT: TANG, Tom Y.; LAL, Preeti G.
APPLICANT: TANG, Tom Y.; LAL, Preeti G.
APPLICANT: TRAN, Uyen K.; KHARE, Reena
APPLICANT: TRAN, Uyen K.; KHARE, Reena
APPLICANT: TRAN, Uyen K.; KHARE, Reena
APPLICANT: TRAN, Uyen K.; KHARE, Reena
APPLICANT: TRAN, Uyen K.; KHARE, Reena
APPLICANT: TRAN, Uyen K.; KHARE, Reena
APPLICANT: TOWENTION: PROTEINS ASSCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
FILE REFERENCE: PC-0903 USN
CURRENT APPLICATION NUMBER: US/10/467,535
CURRENT FILING DATE: 2001-08-08
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
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PRIOR FILING DATE: 2001-03-09
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PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PERL PROGRAM
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98.7%; Score 789; DB
Best Local Similarity 100.0%; Pred. No. 2.7
Matches 151; Conservative 0; Mismatches
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NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 5284076CD1
US-10-467-535-4
                                                                                                                                              121 LTPVSTENEIKLDPSPFIADFQTTAEELGLL
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: YUE, Henry; YAO, Monique G.
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                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/10467535 Publication No. US20040146970A1 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-10-798-512-113
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APPLICANT: JODErt, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78.US4.CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RIHTYVYEFIYLVROGGIRTRVVSEBTLLFQTBLYFTPRNIDHDPQBIHLECSTSRKSVW 120
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98.7%; Score 789; DB 3; I
Best Local Similarity 100.0%; Pred. No. 2.7e-84;
Matches 151; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 2.7e-84;
Matches 151; Conservative 0; Mismatches 0;
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Fublication No. US20030050442A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 62 Human Secreted Proteins
FILE REFERENCE: PZ039F1
CURRENT APPLICATION NUMBER: US/10/050,704
CURRENT FILING DATE: 2002-01-18
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 1090-04-06
PRIOR PRIOR PELICATION NUMBER: 6/128,693
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 344
SOFTWARE: PATCHTIN VOWER: 6/130,991
PRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 344
SOFTWARE: PATCHTIN VOWER: AUGUST OF SEQ ID NOS: 344
SEQ ID NO 113
LENGTH: 158
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                                                                       CURRENT PEDELICATION NUMBER: US/09/876,997
CURRENT FILING DATE: 2001-06-08
PRIOR PEDELICATION NUMBER: US 09/731,872
PRIOR FILING DATE: 2000-12-07
PRIOR FILING DATE: 2000-03-06
PRIOR FILING DATE: 2000-03-06
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 482
SOFTWARE: Patent.pm
SEQ ID NO 260
LENGTH: 158
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; ORGANISM: Homo sapiens
US-10-050-704-113
                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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; LOCATION: -17..-1
US-09-876-997-260
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Sequence 260, Application US/10643836
; Publication No. US200509645841
; GENERAL INFORMATION:
    APPLICANT: Unmas Milne Edwards, Jean Baptiste
; APPLICANT: Dunas Milne Edwards, Jean Baptiste
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE FOF INVENTION: FULL-ENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78 .US.10643, 836
; CURRENT APPLICATION NUMBER: US/10/643, 836
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR PILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 260
; LENGTH: 158
                   61 RIHTYVYEFIYLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQEIHLECSTSRKSVW 120
                                                61 RIHTYVYEFIXLVRDCGIRTRVVSEETLLPQTELYFTPRNIDHDPQEIHLECSTSRKSVW 120
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98.7%; Score 789; DB 5; Length 158;
Best Local Similarity 100.0%; Pred. No. 2.7e-84;
Matches 151; Conservative 0; Mismatches 0; Indels
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Publication No. US20050197285A1
GENERAL INFORMATION:
APLICANT: Human Genome Sciences, Inc.
ITILE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS906CT
CURRENT PAPLICATION NUMBER: US/10/472,533
CURRENT FILING DATE: 2003-09-20
PRIOR APPLICATION NUMBER: US 60/331,287
PRIOR APPLICATION NUMBER: US 60/331,287
PRIOR APPLICATION NUMBER: US 60/371,340
PRIOR APPLICATION NUMBER: US 60/277,340
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 650
                                                                                                                                                         121 LTPVSTENBIKLDPSPFIADFQTTAEELGLL 151
                                                                                                                            121 LTPVSTENEIKLDPSPFIADFQTTAEELGLL 151
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US-10-643-836-260
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Publication No. US20040235709A1

GENERAL INPORMATION:

APPLICANT: Salter-Cid, Luisa

APPLICANT: Chicca, Barbara A.

APPLICANT: Chicca, Dana

APPLICANT: Chicca, Dana

APPLICANT: Chicca, John

APPLICANT: Chicca, John

TITLE OF INVENTION: GSSP3 Polynucleotides and Polypeptides and Uses Thereof

TITLE OF INVENTION: GSSP3 Polynucleotides and Polypeptides and Uses Thereof

CURRENT APPLICATION NUMBER: US/10/467,046

CURRENT FILING DATE: 2003-08-01

PRIOR APPLICATION NUMBER: US 60/266,156

PRIOR FILING DATE: 2001-02-02

NUMBER OF SEQ ID NOS: 3

SOFFWARE PATENTING DATE: Patentin version 3.0
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Best Local Similarity 100.0%; Pred. No. 2.7e-84;
Matches 151; Conservative 0; Mismatches 0;
FILE REFERENCE: PZ039P1
CURRENT APPLICATION NUMBER: US/10/798,512
CURRENT APPLICATION NUMBER: US/10/798,512
CURRENT FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US/09/684,524
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 1999-04-09
PRIOR PILING DATE: 1999-04-09
PRIOR PILING DATE: 1999-04-06
PRIOR PILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 344
SOFTWARE: PATENTIN VET: 2.0
SOFTWARE: PATENTIN VET: 2.0
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US-10-798-512-113
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ORGANISM: Homo sapiens
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US-10-467-046-3
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NAME/KEY: SIGNAL
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LENGTH: 158
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Sequence 265, Application US/09876997
Publication No. US20030152921A1
GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT:
GOBER, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REPERENCE: 78.US4.CIP
CURRENT FILING DATE: 2001-06-08
RICH APPLICATION NUMBER: US 09/731,872
PRIOR APPLICATION NUMBER: US 09/731,872
PRIOR PILING DATE: 2000-012-07
RICH APPLICATION NUMBER: US 60/187,470
PRIOR FILING DATE: 2000-03-06
RICH APPLICATION NUMBER: US 60/169,629
PRIOR FILING DATE: 1999-12-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 429; DB 3; Pred. No. 3.6e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.7%; Scor.
100.0%; Pred. No. 5...
0; Mismatches
                                        60/187,470
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Publication No. US20050096458A1
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PRIOR FILING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: US 60,
NUMBER OF SEQ ID NOS: 482
SOFTWARE: Patent.pm
SEQ ID NO 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 53.7
Best Local Similarity 100.
Matches 82; Conservative
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                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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Matches 82; Conserv
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SEQ ID NO 265
                                                                                                                                                                                                                                                                                                                                                                                             -17...-1
                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: -17
US-09-731-872-265
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                                                                                                                                                                                                                    LENGTH: 106
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Batent No. US2002012604A1

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Bougueleret, Lydie
APPLICANT: Jobert, Severin
TITLE OF INVERTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78.US3.REG
CURRENT APPLICATION NUMBER: US/09/731,872
CURRENT PILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,629
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                                                                                                                                                                                                             Query Match 98.7%; Score 789; DB 5; I
Best Local Similarity 100.0%; Pred. No. 2.7e-84;
Matches 151; Conservative 0; Mismatches 0;
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98.2%; Score 785; DB 4;
Best Local Similarity 99.3%; Pred. No. 8.1e-84;
Matches 150; Conservative 0; Mismatches 1;
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; Publication No. US20030236392A1
; GENERAL INFORMATION:
   APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1e1
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR PILING DATE:
   NUMBER: PRIOR FILING DATE:
   NUMBER: PRIOR FILING DATE:
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                                                                 TYPE: PRT; ORGANISM: Homo sapiens
US-10-472-533-464
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US-10-104-047-3674
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SEQ ID NO 464
LENGTH: 158
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65 YVYEFIYLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQE--IHLECSTSRKSVWLT 122
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                                                                                                                                                                                        9 TMITLTSALSAGSGGSPWTVLCSIDWFWVTVHPFMLNNDVCVHFHBLHLGLGCPPNHVQP 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
Best Local Similarity 33.3%; Pred. No. 7.9e-18;
Matches 40; Conservative 33; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/745,763
FILING DATE: 18-5un-2000
CLASSIFICATION: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MCDITUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 203:
US-09-745-763-203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jacobs, Kenneth
MCCOY, John M.
LaVallie, Edward R.
Collins-Racie, Liea A.
Evans, Cheryl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 203, Application US/09745763
Patent No. US20020065394A1
GENERAL INFORMATION:
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TELEFAX: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Merberg, David
Treacy, Maurice
Spaulding, Vikki
TITLE OF INVENTION: SECRETED
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STRANDEDNESS: <Unknown>
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Cambridge
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                                                                                                                                                                                                     임
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PRIOR PELING DATE: 2002-11-05

PRIOR FILING DATE: 2001-11-05

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PRIOR FILING DATE: 2001-11-06

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PRIOR PELING DATE: 2001-11-09
                                                              APPLICANT: Bougueleret, Lydde APPLICANT: Bougueleret, Lydde APPLICANT: Dobert, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAB ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78.US3 REG
CURRENT APPLICATION NUMBER: US/10/643,836
CURRENT APPLICATION NUMBER: US/09/731,872
PRIOR PELING DATE: 2000-12-07
PRIOR PELING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR APPLICATION NUMBER: US 60/169,470
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR PILING DATE: 1999-12-08
PRIOR PILING DATE: 1999-12-08
PRIOR PILING DATE: 1990-13-06
PRIOR FILING DATE: 1900-03-06
PRIOR FILING DATE: PRIOR DATE: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.7%; Score 429; DB 5; I
100.0%; Pred. No. 3.6e-42;
ive 0; Mismatches 0;
                               APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Bougueleret, Lydie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.2%; Score 225.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 40, Application US/10287971
Publication No. US20040067882A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
....hes 82; Conservative
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ORGANISM: Homo sapiens
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; LOCATION: -17..-1
US-10-643-836-265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 IMILITSAFSAGSGQSPMTVLCSIDWFMVTVHPFMLNNDVCVHFHELHIGLGCPPNHVQP 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 VLMLLAVLIWTGAENLHVKISCSLDWLMVSVIPVAESRNLYIFADELHLGMGCPANRIHT 64
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                                                        US-10-09-7-021-91

US-10-09-7-021-91

Publication No. US20040002591A1

GENERAL INFORMATION:

APPLICANT: ROSEN et al.

TITLE OF INVENTION: 50 Human Secreted Proteins
FILE REFERENCE: P2016P2

CURRENT APPLICATION NUMBER: US 60/262,066

PRIOR PRIOR APPLICATION NUMBER: US 60/262,066

PRIOR PRIOR APPLICATION NUMBER: US 60/262,066

PRIOR APPLICATION NUMBER: US 60/262,066

PRIOR PILING DATE: 2000-01-128

PRIOR PILING DATE: 1999-03-04

PRIOR PILING DATE: 1999-03-04

PRIOR PILING DATE: 1999-03-04

PRIOR PILING DATE: 1997-09-05

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; LOCATION: (180)
; OTHER INFORMATION: Xaa equals any amino acid US-10-047-021-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
RESULT 15
US-10-047-021-91
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9, 2006, 10:17:00 Search completed: May Job time: 67.6 secs

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(without alignments)
357.655 Million cell updates/sec
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                                                                                                      May 9, 2006, 10:15:47; Search time 19.8 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 5.1.8
Copyright (c) 1993 - 2006. Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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                                                                   OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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799
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                        Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		Sequence 3674, Ap	Sequence 788, App	Sequence 787, App	m	773,	771,	777,	Sequence 774, App	Sequence 779, App	Sequence 775, App	e 8621	Sequence 8620, Ap		Sequence 7840, Ap	Sequence 3492, Ap	Sequence 11630, A	Sequence 10915, A	Sequence 8166, Ap	Sequence 81, Appl	153	Sequence 11, Appl
SUMMARIES	ID		US-11-072-512-3674	US-10-475-075-788	US-10-475-075-787	US-10-821-234-1033	US-10-995-561-773	US-10-995-561-771	US-10-995-561-777	US-10-995-561-774	US-10-995-561-779	US-10-995-561-775	US-11-096-568A-8621	US-11-096-568A-8620	US-11-096-568A-8619	US-11-188-298-7840	US-11-072-512-3492	US-11-188-298-11630	US-11-098-686-10915	US-11-079-463-8166	US-11-045-004-81	US-11-188-298-15337	US-10-835-475-11
	DB	-	7	σ	Φ	σ	Φ	σ	σ	σ	σ	0	11	11	11	11	11	11	11	11	11	11	σ
	Query Match Length DB		158	148	143	216	3803	3960	5335	5406	5415	5464	242	394	398	460	649	393	477	269	440	497	489
dł	Query Match		78.5	97.0	94.1	28.0	10.7	10.7	10.7	10.7	10.7	10.7	9.6	9.6	9.6	9.1	8.9	8.4	8.4	8.4	8.3	8.3	8.2
	Score		08/	775	752	223.5	85.5	85.5	85.5	85.5	85.5	85.5	76.5	76.5	76.5	73	71.5	67.5	67.5	67	66.5	99	65.5
	Result No.		-	7	m	4	ഹ	9	7	ω	6	10	11	12	13	14	15	16	17	18	19	20	21

Sequence 2, Appli Sequence 1, Appli	22	Seguence 552, App	Sequence 552, App	Sequence 552, App	Sequence 1, Appli	Sequence 2, Appli	Sequence 28984, A	Sequence 28983, A	8	Sequence 8, Appli	Ξ	Sequence 5581, Ap	Sequence 8122, Ap	Sequence 3472, Ap	Sequence 5580, Ap	Sequence 5579, Ap	Sequence 11, Appl	Sequence 11, Appl	Sequence 998, App	5147	Sequence 5925, Ap	Sequence 34086, A
US-10-835-475-2 US-10-835-475-1	US-10-194-487-552	US-10-195-883-552	US-10-195-888-552	US-10-195-889-552	US-11-014-367-1	US-11-185-567-2	US-11-096-568A-28984	US-11-096-568A-28983	US-11-096-568A-28982	US-11-288-493-8	US-11-098-686-11063	US-11-096-568A-5581	US-10-467-657-8122	US-11-188-298-3472	US-11-096-568A-5580	US-11-096-568A-5579	US-11-031-737A-11	US-11-031-482-11	US-11-087-099-998	US-11-087-099-5147	US-11-188-298-5925	US-11-096-568A-34086
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514	1032	1032	1032	1032	1032	1032	150	174	252	476	315	497	524	524	604	624	838	838	1111	1111	359	396
8 8	8.5	8.2	8.2	8.2	8.2	8.2	8.1	8.1	8.1	8.1	8.0	8.0	8.0	8.0	0	8.0	8.0	8.0	8.0	8.0	7.9	7.9
65.5 65.5	65.5	65.5	65.5	65.5	65.5	65.5	65	65	65	65	64	64	64	64	64	64	64	64	64	64	63.5	63.5
22	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Length 158; Query Match 98.2%; Score 785; DB 11; Length 15 Best Local Similarity 99.3%; Pred. No. 3.6e-82; Matches 150; Conservative 0; Mismatches 1; Indels APPLICANT: TAMBCHIKA, ICHIRO
APPLICANT: SEKI, NACHIKO
APPLICANT: SEKI, NACHIKO
APPLICANT: SCHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOTUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGHARI, KENJI
APPLICANT: NAGHARI, KENJI
TILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072, 512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350, 978
PRIOR PILING DATE: 2002-01-25
PRIOR PRILING DATE: 2002-01-25
PRIOR PRILING DATE: 2001-05
NUMBER OF SEQ ID NOS: 4096 ; Sequence 3674, Application US/11072512; Publication No. US20060029945A1; GENERAL INFORMATION: APPLICANT: 1SOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISONO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YUKI
APPLICANT: OTSUKA, KAORU SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 3674 NAGAI, KEIICHI IRIE, RYOTARO ; ORGANISM: Homo sapiens US-11-072-512-3674 APPLICANT

1 MALEVLMILLAVLIWTGAENLHVKISCSLDWLMVSVIPVAESRNLYIFADELHLGMGCPAN 60

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Sequence 1033, Application US/10821234

Sequence 1033, Application US/10821234

BULICACTION NO. US20050255114A1

GENERAL INFORMATION:

APPLICANT: Labat, Liabst, District

APPLICANT: Stache-Crain, Birgit

APPLICANT: Andarmani, Susan

APPLICANT: Andarmani, Susan

APPLICANT: Andarmani, Susan

APPLICANT: Andarmani, Susan

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APPLICANT: Andarmani, Susan

APPLICANT: With Struct APPLICATION NUMBER: US/10/820,047

PRIOR FILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SOFTWARE: PLE SEQ_Genes Version 1.0

SEQ ID NO 1033

LENGTH: 216
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Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIHTYVYEFIYLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQEIHLECSTSRKSVW 120
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                                                                                                                                                                                                                                                                                                                        94.1%; Score 752; DB 9; Length 14
100.0%; Pred. No. 1.9e-78;
Live 0; Mismatches 0; Indels
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33.3%; Pred. No. 6.8e-18;
tive 32; Mismatches 43
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Best Local Similarity 100.0
Matches 143; Conservative
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; ORGANISM: Homo sapiens
US-10-821-234-1033
                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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   SOFTWARE: Patent.pm
SEQ ID NO 787
LENGTH: 143
                                                                                                                                                               ; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -17..-1
US-10-475-075-787
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US-10-821-234-1033
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Sequence 788, Application US/10475075

Publication No. US2066053498A1

GENERAL INFORMATION:

APPLICANT: Bejanin, Stephane

APPLICANT: Dumas Milne Edwards, Jean-Baptiste

APPLICANT: Jobert, Severin

APPLICANT: Jobert, Severin

APPLICANT: Jobert, Severin

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APPLICANT: Jobert, Severin

APPLICANT: Jobert, Jobert
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APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Jobert, Severin
APPLICANT: Glordano, Jean-Yves
TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins
PILE REFERENCE: G-081US03PCT
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                                                                                                   61 RIHTYVYEFIYLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQEIHLECSTSRKSVW 120
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1 MALEVLMLLAVLIWIGAENLHVKISCSLDWLMVSVIPVAESRNLYIFADELHLGMGCPAN
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thes 0; Indels
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CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: PCT/IB01/00914
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 918
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Publication No. US20060053498A1
GENERAL INFORMATION:
APPLICANT: Bejanin, Stephane
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Best Local Similarity 100.0
Matches 148; Conservative
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; NAME/KEY: SIGNAL
; LOCATION: -17..-1
US-10-475-075-788
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118 ---SVWLTPVS--TENEIKLDP 134
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             FILE REFERENCE: CL001559
                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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US-10-995-561-774
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US-10-995-561-779
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CAEDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION WIMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 771
LENGTH: 3960
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LELLLQIANKIQNGALNCEEKLTLAKNTLQ-------ADAAHLESGQPVQCE 470
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                                                                                                                                                                                                                                                                                                                                                                    471 SDVIMYIQECEGLIRQLQVDLQILRDENYYQLEELAFRVMRLQDELVTLRLECTNLYRKG 530
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GENETIC POLYMORPHISMS ASSOCIATED WITH
CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
DETECTION AND USES THEREOF
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                                                                                                                                                                                           10.7%; Score 85.5; DB 9; Length 3803; 25.4%; Pred. No. 1.5;
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25.4%; Pred. No. 1.6;
Live 23; Mismatches 58; Indels 25
                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                  58;
                                                                                                                                                                                                                              23; Mismatches
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 773
LENGTH: 3803
                                                                                                                                                                                                                                                                                                                                                                                                                      ---SVWLTPVS--TENEIKLDP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                         531 HFTSLELVPPSTLTTTHLKAEP 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 ---SVWLTPVS--TENEIXLDP 134
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Publication No. US20050272054A1
GENERAL INFORMATION:
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Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORP;
TITLE OF INVENTION: DETECTION AND US
TITLE OF INVENTION:
                                                                                                                                                                                                                                Conservative
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Best Local Similarity 25.43
Matches 36; Conservative
                                                                                                                                     ; ORGANISM: Homo sapiens
US-10-995-561-773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-10-995-561-771
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Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PELING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 NRIHTYVYEFIYLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQEIHLECST-SRK- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            379 SDVIMYIQECEGLIRQLQVDLQILRDENYYQLEELAFRVMRLQDELVTLRLECTNLYRKG 438
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                                                                                                                                                                                                                                                                                                                                                               58; Indels
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                                                                                                                                                                                                                                                                                            ch 10.7%; Score 85.5; DE Similarity 25.4%; Pred. No. 2.3; 36; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.7%; Score 85.5; D 25.4%; Pred. No. 2.3; ive 23; Mismatches
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 777
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Best Local Similarity 21.5
Matches 40; Conservative
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                                                                                                                               TYPE: PRT
ORGANISM: Glycine max
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LENGTH: 394
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US-11-096-568A-8621
US-11-096-568A
Sequence 8621, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
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Publication No. US20050272054A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT FALING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                3 LEVLMLLAVLIWTGAENLHVKISCSLDWLMVSVIPVAESRNLYIFADELHLGMGCPA---
                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                            Length 5415;
                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                              58;
                                                                                                                                                                                                                            DB 9;
TITLE OF INVENTION: DETECTION AND USES THEREOF FILE REFERENCE: CLOO1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7:9
LENGTH: 5415
                                                                                                                                                                                                                          10.7%; Score 85.5; D
25.4%; Pred. No. 2.3;
:ive 23; Mismatches
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                                                                                                                                                                                                                                         Best Local Similarity 25.4% Matches 36, Conservative
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CORGANISM: Homo sapiens
US-10-995-561-775
                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-10-995-561-779
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Sequence 8620, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REPERBING: 2750-15922US2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 287 QVVHFYCWKGSALLNNMSNIDSRVLKVTBVQREKISGLNSVLLNDNDFASKVFCNMPSEE 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 GCPANRIHTYVYEFIYLVRDCGIRT------RVVSEETLLFQTELYFTPRNIDHDP 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QEIHLEC-----STSRKSVWLTPVSTE----NEIKLDPSPFIADF--QTTAEE 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 GCPANRIHTYVYEFIYLVRDCGIRT-----RVVSEETLLFQTELYFTPRNIDHDP 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 NISWARLHVLGYD-IYISQDSSCESDVFELLVKPVRLVRDNELLDQEFV-----NIMHAL 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       47;
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                                                                                                                                                                                                                                                                                                                                                                                                          Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 LAVLIWTGAENLH---VKISCSLDWLMV-----SVIPVAESRNLYIF
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21.5%; Pred. No. 0.48;
tive 29; Mismatches 70;
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LOCATION: (1). (242)
OTHER INFORMATION: Ceres Seq. ID no. 15169117
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OTHER INFORMATION: Ceres Seq. ID no. 15169116
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
LENGTH: 242
TURNER 242
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------1NO 150
                                                                     92 TELYFTPRNIDHDPQEIHLEC-----STSRKSV-----WLTPVSTE---NEIKLD- 133
                                                                                                  151 QSSYHSPCAIDYNNQNSIEQCEIADLPDLATGSETVKKVLANDWISWLYTEYSFDGIRIDT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 LAVLIWTGAENLHVKISCSLDWLMVS----VIPVAE-----SRNLYIFADE 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 LHLGMG---CPANRIHTYVYE-----FIYLVRDCGIRTRVVSEETLLFQ--TELYFTP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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8.9%; Score 71.5; DB 11; Length 649;
Best Local Similarity 23.3%; Pred. No. 6.2;
Matches 38; Conservative 27; Mismatches 63; Indels 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 FGHGSNQSVRHLKCSLFKKSL-LGSVSDNGIVTLMDVNSQSPY 198
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APPLICANT: NAGALERI, KENJI
APPLICANT: MAGALERI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVAL FULL length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR APPLICATION NUMBER: US 2001-379298
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR APPLICATION NUMBER: JP 2001-379298
NUMBER OF SEQ ID NOS: 4096
NUMBER OF SEQ ID NOS: 4096
                                                                                                                                                                                                                                                                                                                         ; Sequence 3492, Application US/11072512; Publication No. US20060029945A1; GENERAL INFORMATION:
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Job time : 19.8 secs
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: 150GAI, TAKAO
APPLICANT: 5UGIYAMA, TOMOXASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISONO, YUUKO
APPLICANT: ISONO, YUUKO
                                                                                                                                                                134 ----PSPFIADFQTTA 145
                                                                                                                                                                                                           211 VKHVEKSFWPDFÓKAÁ 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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TAMECHIKA, ICHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTSUKA, KAORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEKI, NAOHIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CORGANISM: Homo sapiens
US-11-072-512-3492
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HIO, YURI
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                                                                                                                                                  US-11-096-568A-8619
Sequence 8619, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION UNMER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 GCPANRIHTYVYEFIYLVRDCGIRT------RVVSEETLLFQTELYFTPRNIDHDP 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 QEIHLEC-----STSRKSVWLTPVSTE-----NEIKLDPSPFIADF--QTTAEE 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 LAVLIWIGAENLH---VKISCSLDWLMV----SVIPVAESRNLYIF----ADELHLGM 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 SVIPVAESRNLYIFADEL--HLGMGCPANRIHTYVYEFIYLVRDCGIRTRVVSEETLLFQ 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 9.6%; Score 76.5; DB 11; Length 398; Best Local Similarity 21.5%; Pred. No. 0.9; Matches 40; Conservative 29; Mismatches 70; Indels 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.1%; Score 73; DB 11; Length 460;
22.8%; Pred. No. 2.7;
tive 21; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-11-188-298-7840

| Sequence 7840, Application US/11188298
| Publication No. US20060075522A1
| GENERAL INFORMATION:
| APPLICANT: Abad, Mark S. et al.
| TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT FILE REFREENCE: 38-21(53452)B
| CURRENT APPLICATION NUMBER: US/11/188,298
| CURRENT FILING DATE: 2005-07-22
| PRIOR APPLICATION NUMBER: 60/592,978
| PRIOR PLILING DATE: 2004-07-31
| NUMBER OF SEQ ID NOS: 22569
| SEQ ID NO 7840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
i LOCATTON: (1)..(198)
i TTER INFORMATION: Ceres Seq. ID no. 15169115
US-11-096-568A-8619
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US-11-188-298-7840
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                   148 LGLLIF 153
                                               347 KGCICF 352
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Best Local Similarity
Matches 31; Conserv
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GenCore version 5.1.8 Copyright (c) 1993 - 2006 Biocceleration Ltd.	OM protein - protein search, using sw model	May 9, 2006, 10:13:22 ; Search time 17.1 Seconds (without alignments) 860.887 Million cell updates/sec	
Copyric	protein sea	Мау 9,	
	OM protein -	Run on:	

Title:	US-10-664-025-3903
Sequence:	1993 1 MALEVLMLLAVLIWTGAENLPSPFIADFQTTAEELGLLIF 153
Scoring table: BLOSUM62 Gapop 10	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	283416 seqs, 96216763 residues
Total number of	Total number of hits satisfying chosen parameters: 283416

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Total number of hits satisfying chosen parameters:		
chosen	0	
atistying	seq length: 0 seq length: 2000000000	
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0% 100% 45 summaries	
Match Match first	* * * * *
Minimum Maximum Listing	PIR 80:* 1: pir1: 2: pir2: 3: pir3: 4: pir4:
Post-processing:	Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ription	sperm-binding glyc		binding	ō	, 0	stearoy1-CoA 9-des	->-	probable bacteriop	cadmium resistance	hypothetical prote			യ	LIM protein kinase	DNA repair protein	sperm-binding glyc	probable family 31	hypothetical prote	hypothetical prote	probable resistanc	pantoate-beta-alan	conserved hypothet	hypothetical prote		0	peptidyldlycine mo	peptidylglycine mo	hypothetical prote	Līm protein kinase	
SUMMARIES	ΩI	A60503	T42725	T30847	T30849	G70519	A24699	A82094	AE0152	H95188	A98055	T45895	T33152	S70399	I58353	H84028	A30334	T38598	T23302	T18995	C71436	A84953	H64155	B64384	S50434	A36000	URBOAP	URRTAP	T25331	148737	
	DB	-	~	~	~	~	П	N	~	N	~	~	~	~	Н	N	Н	~	~	7	~	7	7	Н	N	ч	-	Н	~	1	
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RESULT 2
T42725
actin binding protein ACF7, neural isoform 1 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 03-Nov-2000
C;Accession: T42725
S;Perniar, G; Mathieu, M.; De Repentigny, Y.; Vidal, S.M.; Kothary, R.
Genomics 38, 19-29, 1996
A;Title: Cloning and characterization of mouse ACF7, a novel member of the dystonin sub-A;Reference number: Z20900; MUID:97124842; PMID:8954775

long-chain-fatty-a	hypothetical prote	probable resistanc	probable invasion	probable invasion	hypothetical prote	cobyrinic acid a,c	probable transport	hypothetical prote	conserved hypothet	nifr3/smm1 family	stearoyl-CoA 9-des	glutamate synthase	aromatic-L-amino-a	aromatic-L-amino-a	aromatic-L-amino-a
F90488	T25888	D71437	E91092	A85938	T21628	AG2297	S78172	D71436	2763	A97544	A32115	E69123	DCFFD2	DCFFA	OCFFD1
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2 F9	2 T25	2 D71	2 E9		_	2 A		2 07	2 AB	2 A9	2 A3	2 E6	1 00	1	2
513 2 F9	2098 2 T2	~	458 2 E9		~	·	7	7	0	336 2 A9	7	7	н	-	-
8.7 513 2 F9	~	~	6 458 2	6 458 2	6 464 2	6 514 2	5 262 2	5 273 2	5 336 2	7	5 355 2	5 499 2	5 503 1	5 510 1	5 511 1 1
69.5 8.7 513 2 F9	~	~	8.6 458 2	6 458 2	8.6 464 2	8.6 514 2	5 262 2	8.5 273 2	5 336 2	8.5 336 2	8.5 355 2	5 499 2	5 503 1	5 510 1	5 511 1 1

ALIGNMENTS

RESULT 1 A60503 Specime binding glycoprotein ZP3 precursor - golden hamster N.Alternate names: sperm receptor; zona pellucida glycoprotein ZP3 C,Species: Mesocricetus auratus (golden hamster) C,Species: Ho.Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C,Accession: A60503 R;Kinloch, R.A.; Ruiz-Seiler, B.; Wassarman, P.M. Dev. Biol. 142, 414-421, 1990 A,Title: Genomic organization and polypeptide primary structure of zona pellucida glyco A,Title: Genomic organization and polypeptide primary structure of zona pellucida glyco A,Reference number: A60503, MUID: 91078540; PMID: 2257975 A,Accession: A60503 A,Molecule type: DNA A,Residues: 1-422 <kin> A,Coss-references: UNIPARC: UPI00001744E3; GB:M63629 A,Molecule type: Lanslated the codon CAA for residue 251 as Glu, and AGG for residu C,Comment: This sulfated glycoprotein in the zona pellucida of the oocyte is a receptor C;Superfamily: sperm-binding glycoprotein zP3; ZP domain homology C,Keywords: glycoprotein; oocyte F;45-300/Domain: ZP domain homology <zph></zph></kin>
 Query Match 11.6%; Score 92.5; DB 1; Length 422; Best Local Similarity 23.4%; Pred. No. 0.089; Matches 51; Conservative Astches 66; Indels Astches 71; Gaps Astches 71; G

09:24:03 2006

Wed May 10

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A; Molecule type: mRNA
A; Residues: 1-2033 <BER>
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                                                                                                                                                            A; Map position: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                          622
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        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1825 <BER>
A;Residues: 1-1825 <BER>
A;Residues: 1-1825 <BER>
A;Cross-references: UNIPARC:UPI000016D118; EMBL:U67203; NID:g1675221; PID:g1675222; PIDN C;Genetics:
A;Genetics: ACF7
A;Map position: 4
C;Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein G;Keywoxds: actin binding
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C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C;Accession: T30849 #sequence_revision 21-Oct-1999 #text_change 22-Oct-1999
R;Bernier, G.; Mathieu, M.; De Repentigny, Y.; Vidal, S.M.; Kothary, R.
Genomics 38, 19-29, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     actin binding protein ACF7, neural isoform 2 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 03-Nov-2000
C;Accession: T30847
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                                                                                                                                                                                                                    10.6%; Score 84.5; DB 2; Length 1825; 25.4%; Pred. No. 3.6; tive 23; Mismatches 58; Indels 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         474 HFSSLELVPPSTLTTTHLKAEP 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 ---SVWLTPVS--TENEIKLDP 134
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Best Local Similarity 25.4%;
Matches 36; Conservative
A; Accession: T42725
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A; Map position
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A;Title: Cloning and characterization of mouse ACF7, a novel member of the dystonin sub A;Reference number: Z20900; MUID:97124842; PMID:8954775
A;Accession: T30849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.Cole. S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Salandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A; Authors: Squres, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Fitle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference mumber: A70500; MUID:98295987; PMID:9634230
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A;Cross-references: UNIPROT:007719; UNIPARC:UPI0000D1020; GB:Z97193; GB:AL123456; NID:g
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stearoyl-CoA 9-desaturase (EC 1.14.19.1) [similarity] - rat
NyAlternate names: acyl-CoA desaturase; Delta9 fatty acid desaturase
NyAlternate names: acyl-CoA desaturase; Delta9 fatty acid desaturase
C;Species: Rattus norvegicus (Norway rat)
C;Species: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 05-Oct-2004
C;Accession: A24699; JX0150; Ī58133
T$FTNiede, M.A.; Ozols, J.; Stritumatter, P.
J. Biol. Chem. 261, 13230-13235, 1986
A;Title: Construction and sequence of cDNA for rat liver stearyl coenzyme a desaturase.
A;Reference number: A24699; MUID:87008535; PMID:2428815
A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Species: Mycobacterium tuberculosis
C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----ADAAHLESGQPVQCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LEVIMILIAVLIWIGAENLHVKISCSLDWLMVSVIPVAESRNLYIFADELHLGMGCPA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein Rv1914c - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Superfamily: Mycobacterium tuberculosis hypothetical protein Rv1914c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
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                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.8%; Score 78.5; DB 2; Length 135; 34.7%; Pred. No. 0.66; tive 9; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 IWTGAENLHVKISCSLDWLMVSVIPV----AESRNLYIFADELHLGMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58;
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 10.6%; Score 84.5; DB 2;
Best Local Similarity 25.4%; Pred. No. 4.1;
Matches 36; Conservative 23; Mismatches 58;
                                                                                                              A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      577 LELLLQIANKIQNGALNCEEKLTLAKNTLQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |: | | | : | : | : | HFSLELVPPSTLTTTHLKAEP 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 ---SVWLTPVS--TENEIKLDP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Conservative
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probable bacteriophage protein YPO1246 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Species: Versinia pestis
C;Species: O2-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE0152
B;Parkhill, J:; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G., Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, A.Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; WUID:21470413; PMID:11586360
A;Accession: AE0152
A;Accession: Preliminary
A;Residues: 1-468 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q8ZGP1; UNIPARC:UPI0000DCD86; GB:AL590842; PIDN:CAC90080.1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cipecies: Streptococcus pneumoniae (Species: Streptococcus pneumoniae) (Species: Streptococcus pneumoniae) (Species: Streptococcus pneumoniae) (Species: Streptococcus pneumoniae) (Species: Streptococcus pneumoniae) (Species: Oliver) (Species: Streptococcus pneumoniae) (Species: Oliver) (Species: Oli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cadmium resistance transporter, probable SP1625 [imported] - Streptococcus pneumoniae
                  ---IDRLLEEVNDQMSTYRKDSE 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 LVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQEIHLECSTSRKSVWLTPVSTENEIK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 WIGAENLHVKISCSLDWLMVSVIPVAESRNLYIFADELHLGMGCPANR--IHTYVYEFIY 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 9.6%; Score 76.5; DB 2; Similarity 20.4%; Pred. No. 4.8; 31; Conservative 20; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                  ---OPGIADSKTL--OTE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.5%; Score 76; DB 24.7%; Pred. No. 2; ive 27; Mismatches
                                                                                                    LTPVS--TENEIKLDPSPFIADFOT 143
                                                                                                                                                                                           --PFAVSTOT 126
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Best Local Similarity 24.7%
Matches 39; Conservative
                  64 MGTTYNIKYIQ---
                                                                                                                                                                |: | : |
LSRFNQHTSSE-
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                                                                                                    121
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Best Local &
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                                                                                                                                                           Arities Structure and regulation of rat liver microsomal stearoyl-CoA desaturase gene.

Arritle: Structure and regulation of rat liver microsomal stearoyl-CoA desaturase gene.

Arcession: JX0150, MUID: 91210202; PMID: 1982442

ArAccession: JX0150

Araccession: JX0150

Arcession: J290, Ar. 292-358 (MIH)

Arcession: J290, Ar. 292-358 (MIH)

Arcession: J290, Ar. 292-358 (MIH)

Arcession: J290, Ar. 292-358 (MIH)

Article: Identification of novel mRNAs expressed in oligodendrocytes.

Article: Identification of novel mRNAs expressed in oligodendrocytes.

Arcession: J58133

Arcession: J58133

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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: A82094
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardson, D.; Erwolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.
I, R.R.; Makalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: A82094
A;Status: prediminary
A;Molecule type: DNA
A;Readidues: 1-367 *HEIA
A;Cross-references: UNIPROT:Q9XFS3; UNIPARC:UPI0000002362; GB:AE004300; GB:AE003852; NID
A;Experimental source: serogroup O1; strain N16961; biotype E1 Tor
C;Genetics:
A;Gene: VC2289
A;Map position: 1
C;Superfamily: hypothetical protein H10172
A;Residues: 1-358 <THI>
A;Cross-references: UNIPROT:P07308; UNIPARC:UPI000004210A; GB:J02585; NID:g206859; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thiamin biosynthesis lipoprotein ApbE VC2289 [imported] - Vibrio cholerae (strain N16961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---TYVYEFIYLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQEIHLECSTSRKSVW 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.6%; Score 77; DB 1; Length 358 25.0%; Pred. No. 3.1; vative 22; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 RNLYIFADELHLG-----MGCPANRIHTYVYE-FIYLVRDCGI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 STENEIKLDPSPFIAD----FOTTAEELGLLI 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
9.6%; Score 76.5; DB
Best Local Similarity 26.9%; Pred. No. 3.6;
Matches 39; Conservative 21; Mismatches
                                                                                                                                Biochem. 108, 1022-1029, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 25.0*
Matches 38; Conservative
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6

OY 70IYLVRDCGIRTRVVSEETLLFQFELYFTPRNIDHDPQEIHLECSTSRKSV 119	:: :
A98055 A98055 Hypothetical protein cadD [imported] - Streptococcus pneumoniae (strain R6) C;Species: Streptococcus pneumoniae C;Bpecies: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004 C;Accession: A98055 C;Accession: A98055 B;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; F. e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M. y. P.; Sun, P.M.; Winkler, M.B. J. Bacteriol. 183, 5709-5717, 2001 J. Bacteriol. 183, 5709-5717, 2001 J. Bacteriol. 183, 5709-5717, 2001 J. Althores: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;tle: Genome of the Bacterium Streptococcus pneumoniae Strain R6. J.;Authores: A97872; MUID:21429245; PMID:11544234 A;Accession: A98055 A;Accession: A98055 A;Accession: A98055 A;Accession: A98055 A;Accession: A98055 A;Accession: Appendix ANA A;Accession: Appendix AVIRA A;Accession: Appendix AVIRA A;Accession: Appendix AVIRA A;Cross-references: UNIPROT:097PJ0; UNIPROT:08DNY0; UNIPARC:UPI0000051908; GB:AE007317; C;Genetics: A;Gene: cadD	RESULT 12 T33152 hypothetical protein T04D1.4 - Caenorhabditis elegans C;5pecies: Caenorhabditis elegans C;5pecies: Caenorhabditis elegans C;5pecies: Caenorhabditis elegans C;bate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004 C;Accession: T33152 R;Davidson, S.; Wohldmann, P. Submitted to the EMBL Data Library, May 1998 A;Description: The sequence of C. elegans cosmid T04D1. A;Reference number: Z21292 A;Accession: T33152 A;Actus: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-2957 < ADAV> A;Cross-references: UNIPROT:061845; UNIPARC:UP1000007A573; EMBL:AF067617; PIDN:AAC17559 A;Experimental source: strain Bristol N2; clone T04D1 C;Genetics: A;Man postifion: 1
••	Aintrons: 122/3; 293/3; 515/3; 1205/2; 1577/1; 2221/3; 2776/1; 2864/3 Quent Match Best Local Similarity 24.7%; Pred. No. 50; Matches 23; Conservative 17; Mismatches 35; Indels 18; Gaps 3;
	Qy 62 IHTYVYEFIXLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQE 107
OY 120 WLIPVSTENEIKLDPSPFIADFQTTAEELGLLIF 153 DD 112 WIVTLLTIASGGDNLGI-YIPYFASLDWSQTLVALLVF 148	Db 2116 QLMCVLAMCQRAQGSNDLKPIDLKRAMSIDPMP 2148
PRESULT 11 T45895 hypothetical protein F4P12.250 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004 C;Accession: T45895 R;Bloecker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat, M. submitted to the Protein Sequence Database, January 2000 A;Reference number: 223016 A;Reference number: 223016 A;Residues: preliminary A;Molecule type: DNA A;Residues: 1-256 <blo> A;Residues: 1-256 <blo> A;Cross-references: UNIPROT:Q9LFG4; UNIPARC:UP100000A485C; EMBL:AL132966 A;Experimental source: cultivar Columbia; BAC clone F4P12</blo></blo>	llucida glycoprotein C - cat res: Felis silvestris catus (domestic catus Felis silvestris catus (domestic catus 128-Oct-1996 #sequence_revision 27-Feb-1810
A;Map position: 3 A;Introns: 2/3; 53/1; 122/3; 152/3 A;Note: F4P12.250	Query Match 9.4%; Score 75.5; DB 2; Length 424; Best Local Similarity 22.6%; Pred. No. 5.4; Matches 42; Conservative 27; Mismatches 50; Indels 67; Gaps 11;
Query Match 9.5%; Score 76; DB 2; Length 256; Best Local Similarity 20.8%; Pred. No. 2.6; Matches 36; Conservative 18; Mismatches 51; Indels 68; Gaps 5; Qy 1 MALEVLMLIAVLIWTGAENLHVKISCSLDWL	Qy 1 MALEVLMILAVLIWTGAENLHVKISCSLDWLMVSVIPVAESR 42

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A;Status: translated from GB/EMBL/DDBJ
A;Abloacus: translated from GB/EMBL/DDBJ
A;Abloacus: translated from GB/EMBL/DDBJ
A;Abloacus: mRNA
A;Residues: 1-647 <RES-
A;Cross-references: UNIPROT:P53669; UNIPARC:UPI000012E690; GB:D31873; NID:g1684611; PIDN
A;Experimental source: strain Wistar; tissue brain
C;Genetics:
A;Genetics:
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R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Reference number: A83650; MuID:20512582; PMID:11058132
A; Accession: H84028
A; Accession: H84028
A; Accession: H84028
A; Accession: H84028
A; Holecule type: DNA
A; Residues: 1-232 <STO>
A; Cross-references: UNIPROT:09K8H4; UNIPARC:UPI00001330B1; GB:AP001517; GB:BA000004; NID
A; Experimental source: strain C-125
C; Genetics:
A; Gene: BH3032
C; Superfamily: DNA repair protein radc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: IS8353
K; Obano, I.; Mizuno, K.
Oncogene 11, 701-710, 1995
A; Title: Likk-1 and Likk-2, two members of a LIM motif-containing protein kinase family.
A; Reference number: IS8353; MUID:95380177; PMID:7651734
                                                                                                                             85 EETLLFQTELYFTPRNIDH-----DPQEIHLECSTSRKSVWLTPVSTENEIKLDPSPFI 138
                                                                                                                                                                                     129 HSKLYCGOCYYOTVVTPVIEQILPDSPGSHLPHTVTLVSIPASAHGKRGLSVSIDPPHGP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----SRNLYIFADELHLG 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIM protein kinase (EC 2.7.1.-) 1 [similarity] - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA repair protein BH3032 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 PGCGTEHSHTVRVQGVDPGCMSPDVKNSIHIGDRILEINGTPIRNVPLDEIDLLIQETSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIPRNIDHDPQEIHLECSTSRKSVWLTPVSTENEIKLDPSPFIADFQTTAEELG 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 HVKISCSLDWLMVSVIPVAE --
                                                                                                                                                                                                                                                                                                              139 ADFQTT 144
                                                                                                                                                                                                                                                                                                                                                                                                       VPFRŤŤ 161
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10;
                                                                                                                                                                                       47 FADELHLGMGCPANRIHTYVYEFIYLVRDCGIRTRVVSEETLLFQTE----LYFTPRN-- 100
                                                                                                                                                                                                                  -----IDHDPQEIHLECSTSRKSVWLTPVSTENEIKLDPSPFIADFQTT-- 144
                                                                                                                                                                                                                                                                                                             142 LHKQTVFIGSLNASIVH-PREVPKE--ALRRSA-ASLICLHNHPSGDPTPSREDIEVTHR 197
                                                                                          2 ALEVLMLLAVLIWIGAEN-----LHVKISCSLDWL-------MVSVIPVAESRNLYI 46
                                                                                                                        28 ALSNQEIVAIMLRTGTKNESVLQLAQHVLCHFDGLRLLREATVEELTSIHGIGEAKAIE-
                                                 Gaps
                                                 47;
  Length 232;
                                                 69; Indels
9.3%; Score 74.5; DB 2;
23.9%; Pred. No. 3.3;
tive 27; Mismatches 69;
Query Match
Best Local Similarity 23.9%
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             ::| ||
198 LAQVGKLI 205
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Search completed: May 9, 2006, 10:15:40 Job time : 18.1 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

May Run on:

9, 2006, 10:11:54 ; Search time 264.6 Seconds (without alignments) 407.959 Million cell updates/sec

Title: Perfect

US-10-664-025-3903 799 1 MALEVLMLLAVLIWTGAENL......PSPFIADFQTTAEELGLLIF 153 score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2166443 seqs, 705528306 residues Searched:

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	
SUMMARIES			ΙD	
			DB	
			Score Match Length DB	
	dip	Query	Match	
			Score	
		Result	No.	

	Description	Q86ws3 homo sapien	homo	mus m	Q9ji83 mus musculu	Q80ww3 mus musculu	Q9hbj0 homo sapien		Q925u0 mus musculu	Q8k4n9 mus musculu	P23491 mesocricetu	Q4t0a6 tetraodon n	Q6zsd7 homo sapien	Q9upn3 homo sapien	Q5vw20 homo sapien	_		_	Q63em2 bacillus ce	Q5dtz2 mus musculu	Q9qxz0 mus musculu				Q81twl bacillus an	Q8qlnl mamestra co	Q71ak8 mamestra co	Q804d8 bufo arenar	Q72b14 desulfovibr	Q4rq55 tetraodon n	Q8k405 lagurus lag	Q91191 white spot
SUMMARIES	ΙD	Q86WS3 HUMAN	Q8N9U6_HUMAN	Q4FZG8 MOUSE	Q9JI83_MOUSE	Q80WW3 MOUSE	Q9HBJ0_HUMAN	Q4V7E2_RAT	Q925U0_MOUSE	Q8K4N9_MOUSE	ZP3 MESAU	Q4TOA6_TETNG	Q6ZSD7_HUMAN	MACF1 HUMAN	QSVW20 HUMAN	Q95YL0_CIOSA	Q81GP9_BACCR	Q6HM43_BACHK	Q63EM2_BACCZ	QSDTZ2_MOUSE	MACF1 MOUSE	O4PLLS_MOUSE	Q6FLR6_CANGA	Q73C23_BACC1	Q81TW1_BACAN	QBQLN1_NPVMC	Q71AK8 9NUCL	Q804D8_BUFAR	Q72B14_DESVH	Q4RQ55 TETNG	Q8K405_9RODE	Q91L91_wssv
	DB	2	~	7	~	~	~	7	7	7	-	~	~	М	N	7	7	~	~	~	Н	7	~	0	7	~	~	~	7	~	~	7
	Query Match Length DB	158	158	164	173	173	212	173	202	92	422	408	1062	5430	5430	1003	1241	1241	1241	1900	5327	7354	526	1241	1241	272	272	486	442	2502		433
de	Query	98.7	98.2	54.0	29.3	28.8	28.0	27.5		12.9	•	10.8	10.7	10.7	10.7	10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.5	10.5	10.5	10.3	10.3	10.3	10.3	•	ο. ο.	•
	Score	789	785	431.5	234	230	223.5	219.5	142	103	92.5	86.5	85.5	85.5		85	85	82	æ	84.5	84.5	84.5	84	84	84	82.5	82.5	82.5	82	80.5	79.5	79.5
	Result No.	п	7	е	4	2	9	7	8	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	59	30	31

	Q7tza9 mycobacteri 007719 mycobacteri Q4t2w2 tetraodon n	Q9bidO anopheles g Q7pep3 anopheles g	Q8jmey mamestra co P07308 rattus norv Q60xp7 caenorhabdi	7 -	Q6c4m0 yarrowia li Q8zgpl yersinia pe
Q4MPH4_BACCE Q5CYH3_CRYPV	Q7TZA9_MYCBO O07719_MYCTU Q4T2W2_TETNG	Q9BIDO ANOGA Q7PEP3 ANOGA	QBUMES SNUCE ACODI RAT Q60XP7_CAEBR	Q6NRU2_XENLA Q9KPS3_VIBCH	Q6C4MO_YARLI Q8ZGP1_YERPE
77 77	0 0 0	000	7 11 7	0 0	0 0
1241 2223	135 135 361	501	358 3032	253 367	390 468
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79	78.5 78.5 78.5	78	c:// 77	76.5 76.5	76.5 76.5
32	9.8 4.0 9.0 9.0	38	4 4 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	4 4 8	4 4 7

ALIGNMENTS

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Atlansaer R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Alausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
R.A. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hasteh F.,
B. Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
R. Brapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
R. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raba S.S., McKernan P.J., McKernan R.J., Malke J.A., Gunzarane P.H.,
R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
R. Halton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
R. Halton B.K., Kereman M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
R. Schein J.E., Jones S.J.M., Marra M.A.;
R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Director MGC Project;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 158 AA; 17971 MW; EEB43D6FBBABB1FF CRC64;
                                                                                                                                        01-UNN-2003 (TrEMBLrel. 24, Created)
01-UNN-2003 (TrEMBLrel. 24, Last sequence update)
13.SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein FLJ36198.
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                                                                        158 AA.
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EMBL, BC036256; AA436256.1; -; mRNA.
Ensembl; ENSG00000149507; Homo sapiens.
                                                                        PRT;
                                                                    QB6WS3 HUMAN PRELIMINARY;
Q86WS3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [3]
NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo.
NCBI_TaxID=9606;
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Attaubherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunazatne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Villalon D.K., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Mhiting M., Madan A., Young A.C., Schwutz J., Myers R.M.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
C. Grimwood J. Schmutz J.M., Marra M.A.,
Cheneration and initial analysis of more than 15,000 full-length human
                                                                                                                                                      RIHTYVYEFIYLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQEIHLECSTSRKSVW 120
                                                                                                                                                                                                RIHTYVYEFIYLVRDCGIRTRVVSEETLLEQTELYFTPRNIDHDPQEIHLECSTSRKSVW 120
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       MALEVLMLLAVLIWTGAENLHVKISCSLDWLMVSVIPVAESRNLYIFADELHLGMGCPAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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EMBL; BC099498; AAH99498.1; -; mRNA.
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SEQUENCE 164 AA; 18849 MW; 49ADE19216BE8606 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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55.9%; Pred. No. 2.2e-36;
ive 25; Mismatches 41
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Q4FZG8;
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NIH MGC Project;
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R. T. Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

R. Wakamateu A., Hayaahi K., Saro H., Nagai K., Kimura K., Makita H.,

R. Wakamateu A., Hayaahi K., Saro H., Nagai K., Kimura K., Makita H.,

R. Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

R. Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

R. Agahari K., Murakami K., Yasuda T., Iwayamagi T., Magamura Y.,

R. Mirata M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,

R. Dunra Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,

R. A Tanasaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,

R. Tahida S., Ono Y., Takahashi-Fujii A., Hara H., Hotuta T.,

R. Musano J., Kanehori K., Takahashi-Fujii A., Hara H., Artuaka S.,

R. Nomura Y., Takayauchi S., Watanabe M., Hiraoka S., Yosida M.,

R. Nomura Y., Takayauchi S., Watanabe M., Sano S.,

R. Musashino K., Yuuki H., Oshima A., Saashi N., Sano S.,

M. Nomiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,

R. Makagawa S., Senoh A., Mizoguchi H., Goto Y., Shimiau F., Wakebe H.,

R. Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,

R. Pujimori Y., Komiyama H., Tashiro H., Tanagami A., Pujiwara T.,

R. Pujimori Y., Komiyama M., Tashiro H., Takama Y., Okamoto S.,

R. Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,

R. Matsumura K., Bakaima Y., Matanabe M., Komatsu T.,

R. Matsuhama Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,

R. Matsuhama Sugano J., Satoh T., Shirai Y., Takahashi Y., Wamashita R.,

R. Makai K., Yada T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,

R. Makai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,

R. Mompa M., Hata H., Watanabe O., Isogai T., Sugano S.,

R. Makai K., Yada T., Nakamura N., Ohara O., Isogai T., Sugano S.,

R. Mompa M., Hata H., Watanabe O., Isogai T., Sugano S.,

R. Makai K., Yada T., Ohara O., Isogai T., Sugano S.,

R. Makai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugani R.,

R. Makai K., Yada T.
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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       Length 158;
                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AK093517; BAC04191.1; -; mRNA.
Ensembl; ENSG00000149507; Homo sapiens.
SEQUENCE 158 AA; 17942 MW; EEB43D70ABA391E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ36198.
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98.7%; Score 789; DB 2; I 100.0%; Pred. No. 2.1e-73;
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Best Local Similarity 99.3
Matches 150; Conservative
                                                                             151; Conservative
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                              Best Local Similarity
Matches 151; Conserv
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       Query Match
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Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konoo H., Adachi J., Fukuda S., Alaxawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Richell P., Lewis S., Matsuo Y., Nikaido I., Fesole G., Quackenbush J., Schriml L.M., Staubli F., Suuki R., Magner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamico N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Winshaw-Bonis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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STRAIN=C57BL/6J; TISSUE=Placenta;
STRAIN=C57BL/6J; TISSUE=Placenta;
MEDLINE=9927953; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y., Hayashizaki Y., Hayashizaki Carninci P., Hayashizaki Carninci P., Hayashizaki Y., H
                                                                                                                                                          01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-FBB-2005 (TrEMBLrel. 29, Last annotation update)
EPCSSG (FLACI) (Mus musculus adult female placenta cDNA, RIKEN full-length enriched library, clone:1600019P04 product:placental specific protein 1, full insert sequence).
                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20453190; PubMed=10995572; DOI=10.1006/geno.2000.6302; Cocchia M., Huber R., Pantano S., Chen B.Y., Ma P., Forabosco A., Ko M.S., Schlessinger D.; "PLACI, an Xq26 gene With placenta-specific expression."; Genomics 68:305-312(2000).
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
121 WLMPLSTEEDPKPVKSPFMTDFEATPEELGLL 152
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                                                                                                                       173
                                                                                                                  Q9J183 MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                            Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
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RC STRAIN-CSTBL/63; TISSUE=Placenta;
RA Adachi J., Aizawa K., Akahira S., Pukuda S., Fukunishi Y., Puruno M., Arawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Puruno M., Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Puruno M., Rahangaki T., Hara A., Hayateu N., Hiramoto K., Hiraoka T., Hori F., Imotami K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H., Rawai J., Kojima Y., Konimo H., Kouda M., Koya S., Kurihara C., Rawai J., Kojima Y., Nomura K., Numazaki R., Ohno M., Asakai T., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Ishahashi F., Tanaka T., Yasunishi A., Yoshida K., Yoshino M., Mayashizaki Y., Yasunishi A., Yoshida K., Yoshino M., Mayashizaki Y., Imoka M., Hayashizaki Y., Musamateu W., Hayashizaki Y., Musamateu W., Hayashizaki Y., Musu Musculus.

BMBL, AF250838; AAF81275.1; -; mRNA.

Ensembl: ENSMUSGO000061082; Mus musculus.

RO; Go:0005615; C:extracellular space; TAS.

SEQUENCE 173 AA; 19626 MW; 674AEF2B68181162 CRC64;
Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gutsincholdi M., Gissi C., Godzik A., Gough J., Grimmond S., Gutsincholdi M., Gissi C., Godzik R., King B.L., Kanaji H., Kawasawa Y., Kadzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maltais L., Marchionni L., McKenzte L., Miki H., Nagachima T., Numata K., Okido T., Pavan W.J., Pertea G. Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Arvasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Sultana R., Manner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Winning L.G., Wynshaww Boris A., Yanagisawa M., Yang I., Yang I., Yang I., Yang I., Yang I., And Hinning L.G., Wynshaww Boris A., Yanagisawa M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Alzawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Riniaki A., Yoshinow W., Waterston R., Lander E.S., Rogers J., Rinner R. Harashishia A., Yoshinow W., Waterston R., Lander E.S., Rogers J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birney E., Hayashizaki Y.;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Muramatsu M., Esperaki Y.; pubtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Mateumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara B., Watshiwagi K.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RIKEN integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
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Matches 42; Conservative 3
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X STRAIN-C57BL/6J; TISSEE=Embryo;

X Straueberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Straueberg R.L., Zeeberg B., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahesley J., Heltone E., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

Bronnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"" "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                67 YEFIYLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQEIHLECSTSRKSVWLT-PVS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YEFIYLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQEIHLECSTSRKSVWLT-PVS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70
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7 MLLAVLIWIGAENLHVKISCSLDWLMVSVIPVAESRNLYIFADELHLGMGCPANRIHTYV 66
                                                                    11 VLVAFMLFSYSEQNQVNVLCSTDWFMVTVHPFLLNNDVYVHFYEVHLGLGCPPNHVHPHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 VLVAFMLFSYSEONOVNVLCSTDWFMVTVHPFLLNNDVYVHFYEVHLGLGCPPNHVHPRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
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MGI; MGI:1926287; Placi.
GO; GO:0005615; C:extracellular space; TAS.
SEQUENCE 173 AA; 19573 MW; 79DDC0179BD730B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Placental specific protein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.8%; Score 230; DB 2; 34.4%; Pred. No. 1.7e-15; ive 32; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 28.8%
Best Local Similarity 34.4%
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q80WW3_MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                 126 TE 127
                                                                                                                                                                                                                                                                                                                                                     130 AK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Plac1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67
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MOUSE
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A STEAGUE PLACENTE.

REDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;

REDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Fearingold E.A., Grouber L.H., Derge J.G.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altechul S.F., Jordan H., Moore T., Max S. I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M.,

Butkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Signal Sequence and Keyword Trap in silico for Selection of Full-
Length Human cDNAs Encoding Secretion or Membrane Proteins from Oligo-
Capped cDNA Libraries.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Placenta;
Otsuki I., Ota I., Nishikawa I., Hayashi K., Suzuki Y., Yamamoto J., Wakamatsu A., Kimura K., Sakamoto K., Hatano N., Kawai Y., Ishii S., Saito K., Kojima S., Sugiyama I., Ono I., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Nagai K., Sugano S.,
                                                                                                                                                                                                                                                                                                                                            WCLEOTIDE SEQUENCE.
MEDLINE=20453190; PubMed=10995572; DOI=10.1006/geno.2000.6302; Cocchia M., Huber R., Pantano S., Chen E.Y., Ma P., Forabosco i Ko M.S., Schlessinger D.; "PLACI, an Xq26 gene with placenta-specific expression."; Genomics 68:305-312(2000).
                                                                                                                                                   R-2001 (TrEMBLrel. 16, Last sequence update)
P-2005 (TrEMBLrel. 31, Last annotation update)
(Hypothetical protein FLJ90605) (Placenta-specific 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH MGC Project;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AF234654; AAG22596.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sci. U.S.A. 99:16899-16903(2002).
                                                                                             212 AA.
                                                                                             PRT;
                                                                                                                                   Created)
                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Res. 12:117-126(2005).
                                                                                           Q9HBJO HUMAN PRELIMINARY;
Q9HBJO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mouse cDNA sequences.
                                                                                                                                                                                                                                Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (FEB-2002)
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                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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AK 131
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alteshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Alteshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Ward J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Rableton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKwam P.J., McKernan K.J., Malak J.A., Gunarane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A. Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rachards S., Worley K.C., Hale S., Garchenko Y., Bouffard G.G.,
M. Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodiiguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>ب</u>
                                                                                                                                                                                                                                                                                               65 YVYEFIYLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQE--IHLECSTSRKSVWLT 122
                                                                                                                                                                                                                        9 LMILLTSAFSAGSGQSPMTVLCSIDWFMVTVHPFMLNNDVCVHFHELHLGLGCGPPNHVQP 68
                                                                                                                                                                                                   5 VLMLLAVLIWIGAENLHVKISCSLDWLMVSVIPVAESRNLYIFADELHLGMGCPANRIHT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 LIWTG-AENLHVKISCSLDWLMVSVIPVAESRNLYIFADELHLGMGCPANRIHTYVYEFI 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                     Gaps
                                                                                                                                                                 2:
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m
                                                                                                                             Length 212;
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                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                       212 AA; 23616 MW; D449300A597DD023 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EC097979; AAH97979.1; -; mRNA.
NCE 173 AA; 19546 MW; 9CB11878F671CEEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                 43;
                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.5%; Score 219.5; DB 2 35.6%; Pred. No. 2.1e-14;
                                                                                                                         28.0%; Score 223.5; DB 33.3%; Pred. No. 1e-14; ative 32; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                         173 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30; Mismatches
                 EMBL; BC022335; AAH22335.1; -; mRNA.
EMBL; BC066327; AAH66327.1; -; mRNA.
Ensembl; ENSG0000170965; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
EMBL; AK075086; BAC11392.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                            Best Local Similarity 33.39
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                       Q4V7E2 RAT PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                        HGNC; HGNC: 9044; PLAC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Placenta-specific 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH MGC Project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Plac1;
                                                                                                                                                                                                                                                                                                            69
                                                                                       SEQUENCE
                                                                                                                             Query Match
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NUCLECTIDE SEQUENCE.

STRAIN=C57BL/6J; TISSUB=In vitro fertilized eggs;

NUCLEOTIDE SEQUENCE.

STRAIN=C57BL/6J; TISSUB=In vitro fertilized eggs;

NEMAIJ J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arawaw T., Hara A., Shibata K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojbori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H., Nathorner M., Pesole G., Quackenbush J.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Rohim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Baka J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Lyons P., Marchlouni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whihttaker C., Wilming L.,

Nordone P., Marchall V., Weitz C., Whihtenker C., Wilming L.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Nandone P., Marchall V., Weitz C., Whittaker C., Wilming L.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Nandone P., Marchall V., Weitz C., Whittaker C., Wilming L.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Whithataker C., Wilming L.,

Suzuki H., Sato K., Schoenbach C., Walland V., Weitz C., Whittaker C., Wilming L.,

Suzuki H., Sato K., Schoenbach C., Walland V., Weitz C., Wilming L.,

Suzuki H., Sato K., Schoenbach C., Walland V., Weitz C., Wilming L.,

Suzuki H., Sato K., Schoenbach C., Walland V., Weitz C., Wilming L.,

Suzuki H., Sato K., Schoenbach C., Walland V., Weitz C., Wilming L.,

Suzuki H., Sato K., Schoenbach C., Walland V., Weitz C., Wilming L.,

Suzuki H., Sato K., Schoenbach
                                YLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQEIHLECSTSRKSVWLT-PVSTE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=2222142; PubMed=12237121; DOI=10.1016/S0006-291X(02)02194-0; Mano H., Nakatani S., Aoyagi R., Ishii R., Iwai Y., Shimoda N., Jincho Y., Hiura H., Hirose M., Mochizuki C., Yuri M., Im R-H., Funada-Wada U., Wada M.;

"IF3, a novel cell-differentiation factor, highly expressed in the murine liver and ovary.";
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STRAIN=C57BL/6J; TISSUB=In vitro fertilized eggs;
MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21610718; PubMed=11747200; DOI=10.1002/gene.10010; Yan C., Fendola F.L., Jacob R., Lau A.L., Eppig J.J., Matzuk M.M.; "Ospl encodes a novel mouse oocyte-secreted protein."; Genesis 31:105-110(2001)
                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Initiate factor 3 (Occyte-secreted protein 1 precursor) (In vitro
fertilized eggs CDNA, RIKEN full-length enriched library,
clone:7420700J01 product:INITIATE FACTOR 3, full insert
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MEDLINE=22334683; PubMed=12466851; DOI=10.1038/nature01266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem. Biophys. Res. Commun. 297:323-328(2002).
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01-DEC-2001 (TrEMBLrel. 19,
10-MAY-2005 (TrEMBLrel. 30,
                                                                                                                                                                                                 Q925U0 MOUSE PRELIMINARY;
Q925U0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=Oospl; Synonyms=if3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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AN Mistade T., Conton M., Saitor R., Sunkid H., Yomannaka I., Kiyomawa H.,

Mistade C., Conton M., Saitor R., Sunkid H., Yomannaka I., Kiyomawa H.,

Radik Y., Tomato M., Saitor R., Sunkid H., Yomannaka I., Kiyomawa H.,

Baldarill E., Pasada D., Brusis C., Horchia C., Corbani L.E., Cousins S.,

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Blake J., Saitor B., Saitor R., Saitor M., Saitor R., Saitor B.,

Roman L., Kamapin M., Mateuda M., N., Soitor R., Frezer K. K.,

Roman L., Kamapin M., Mateuda M., N., Soitor R., King B.L.,

Roman L., Radit D., Brusis C., Chordik M., Gough J.,

Roman L., Radit D., Brusis C., Hickara M., Jackson I.J., Jarvis E.D.,

Roman L., Radit D., Brusis C., Hickara M., Jackson I.J., Jarvis E.D.,

Roman L., Radit S., Patechen C., Porces R., King B.L.,

Roman R., Radit M., Marchiad M., Marchiad M., Rayan M., Pertra G., Pesole G.,

Ravasi T., Reed J.C., Reed D.J., Reid J., Rijng B.L.,

Ravasi T., Reden M., Pertra G., Serou M., Shinada K.,

Sandellin A., Schnieder C., Sepule G., Many Y., Wals B.C.,

Sultona R., Takennka Y., Taylor W.S., Tesadale R.D., Tomita M.,

Ravasi T., Saiton M., Rath.

Miyaraki M., Sandar M., Materston M., Matana K., Andraba V.,

Shirker M., Saiton M., Materston M., Matana K., Shinada R.,

Shirker M., Sakai K., Sasaki D., Shibata K., Shimada R., Takenaka Y.,

R. Miyaraki A., Sakai K., Sasaki D., Shibata K., Shimada R.,

R. Miyaraki M., Shaki K., Sasaki D., Shibata K., Shimada R.,

R. Miyaraki M., Shibata W., Hayabulaki Y.,

R. Miyaraki M., Sakai K., Sasaki D., Shibata K., Shimada R., Inton M.,

R. Miyaraki M., Shibata W., Hayabulaki Y.,

R. Miyaraki M., Shibata W., Hayabulaki Y.,

R. Miyaraki M., Shibata W., Hayabulaki Y.,

R. Mannic P., Shibata W., Hayabulaki Y., Shibata R., Mahawa M.,

R. Miyaraki M., Shibata W., Hayabulaki Y., Shibata W., Hayabulaki M.,

R. Miyaraki M., Ishikawa W., Mathura T., Rashiro H., Itoh M.,

R. Miyaraki M., Shibata W., Hayabulaki Y., Shahaka W., Hayabulaki W.,

R. Miyaraki M., Ishikawa W., Mathura T., Rashama W., H

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62 PVTI--TWPNDTYEFIYRTYSCGIANKVLCDVTLL-KTQLTYISKNASLQ-AEMSLSCVM 117
                                                                                                                                                                                                                                                                                                                                                                  58 PANRIHTY --- VYEFIYLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQEIHLECST 114
                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                               3 LEVIALLAVL----IWTGAENLHVKISCSLDWLMVSVIPVAESRNLYIFADELHLGMGC
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22222142; PubMed=12237121; DOI=10.1016/S0006-291X(02)02194-0; Mano H., Nakatani S., Aoyagi R., Ishii R., Iwai Y., Shimoda N., Jincho Y., Hiura H., Hirose M., Mochizuki C., Yuri M., Im R-H., Funada-Wada U., Wada M.;
                                                                                                                                                                               Gaps
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01-FEB-1996 (Rel. 33, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Zona pellucida sperm-binding protein 3 precursor (Zona pellucida glycoprotein ZP3) (Sperm receptor) (Zona pellucida protein C).
Name=ZP3; Synonyms=ZPC;
                                                                                                                                                                            18;
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                                                                                                               Length 202;
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Pred. No. 0.011;
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                            21 Potential.
23013 MW, 6CD040EF26BB95FB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                               17.8%; Score 142; DB 2; L. 26.8%; Pred. No. 2.6e-06; Live 29; Mismatches 65;
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Biochem. Biophys. Res. Commun. 297:323-328(2002).
Biochem. Biophys. Res. Commun. 297:323-328(2002).
BMBL, ABO86437; BAC11848.1; -; mRNA.
Ensembl; ENSWIGSO000041857; Mus musculus.
MGI: MGI:2149230; Ocoppl.
GO; GO:0005615; C:extracellular space; TAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 SRKSVWLTPVSTENEIKLDPSPFIADFQTTAEE 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 HNQSPHFCEAESRGDFTGDPPGWTEDMRARRDE 150
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Best Local Similarity 30.5%
Matches 29; Conservative
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NUCLEOTIDE SEQUENCE
                                                      202 AA;
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P23491;
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45827 MW; D0F95BE7FF8E7E01 CRC64;
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  422 AA;
                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=99883;
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  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                     The pellucida glycoprotein hZP3, the hamster sperm receptor.";

The pellucida glycoprotein hZP3, the hamster sperm receptor.";

Dev. Biol. 142:414-421(1990).

The pellucida glycoprotein hZP3, the hamster sperm receptor.";

Dev. Biol. 142:414-421(1990).

The pellucida glycoprotein binding, induction of the acrosome reaction and prevents post-fertilization polyspermy, is composed of three to four glycoproteins, ZP1, ZP2, ZP3, and ZP4. ZP3 is essential for sperm binding and zona marrix formation.

The SUBGINIT: Polymers of ZP2 and ZP3 organized into long filaments cross-linked by ZP1 homodimers (By similarity).

The SUBGINIT: Polymers of ZP2 and ZP3 organized into long filaments cross-linked by ZP1 homodimers (By similarity).

The SUBGINIT: Polymers of ZP2 and ZP3 organized into long filaments cross-linked by ZP1 homodimers (By similarity).

The SUBGINIT: Occapies.

The SUBGINIT: Polymers of ZP2 and ZP3 organized into long filaments cross-linked by ZP3 occapies.

The DWARN The ZP domain is involved in the polymerization of the ZP3 proteins to form the zona pellucida.

The PPM: Proteolytically cleaved before the transmembrane segment to promain and processing in the condition of the ZP3 proteins to form the zona pellucida.

The PPM: Proteolytically cleaved before the transmembrane segment to promain and processing the secreted ectodomain incorporated in the zona pellucida.
            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea; Cricetidae, Cricetinae, Mesocricetus.
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similarity).
similarity).
similarity).
similarity).
                                                                                                                                                                                                                                                                                                                                                                        PTM: N-glycosylated (By similarity).

PTM: O-glycosylated; removal of O-linked glycans may play an important role in the postfertilization block to polyspermy (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00682, ZP_1; 1.
PROSITE; PS51034; ZP_2; 1.
Cleavage on pair of Easic residues; Extracellular matrix;
Fertilization; Glycoprotein; Pyrrolidone carboxylic acid; Receptor;
Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     By similarity.
Zona pellucida sperm-binding protein 3.
Removed in mature form (By similarity).
Extracellular (Potential).
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                                                                                                                  Kinloch R.A., Ruiz-Seller B., Wassarman P.M.; "Genomic organization and polypeptide primary structure of zona
                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
SIMILARITY: Belongs to the ZP domain family. ZPC subfamily.
SIMILARITY: Contains 1 ZP domain.
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Similarity.
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 Mesocricetus auratus (Golden hamster)
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InterPro; IPR001507; Endoglin/CD105.
Pfam; PF00100; Zona pellucida; 1.
PRINYS: PR00023; ZPELUCIDA.
SWART; SM00241; ZP; 1.
                                                                                         TISSUE=Ovary;
MEDLINE=91078540; PubMed=2257975;
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422
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                                                                             NUCLEOTIDE SEQUENCE.
                                                    NCBI_TaxID=10036;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGLSYQLLLCGLLCGGA-----KQCCSQPLWLLPGGTPTPGKLTSSVEVECLEAELVVTV 55
                                                                                                                                                                                                                                                                    SRNLY----IFADELHLGM-GC-PANRIHTYVYEFIYLVRDCGIRTRVVSEETLLFQTE 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 VYSDELRLGV---EQRDHCRAHASSEGGEEEYIILVGLADCGTK-HWVSEDALIYINLLI
                                                                  Gaps
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Neopterygii; Neopterygii; Acanthomorpha; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontoidea; Tetraodontidae; Tetraodon.
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NUCLEOTIDE SEQUENCE.
Genoscope; Whitehead Institute Centre for Genome Research;
Gubmitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                              71,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35;
   Length 422;
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                                                              66; Indels
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47840 MW; CABA9142A7302BD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-SEP-2005 (TrEMBLrel.. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel.. 31, Last annotation update)
Chromosome 3 SCAF11271, whole genome shotgun sequence.
ORFNames=GSTENG00009437001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 -----KLDPSPFIADFQ-----TTAEELGLLIF 153
   Score 92.5; DB 1;
Pred. No. 0.82;
                                                                                                                                    1 MALEVLMLLAVLIWTGAENLHVKISCSLD-WLMVSVIP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 IMEENWNTEKLSPTSHLGEVAYLQAEVQTGSHLPLLLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              408 AA
ch 11.6%; Score 92.5; Dl
1 Similarity 23.4%; Pred. No. 0.82
51; Conservative 30; Mismatches
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Nature 431:946-957(2004).
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Q4T0A6;
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Name=MACF1; Synonyms=ABP620, ACF7, KIAA0465, KIAA1251;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K., Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., Octsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Marsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y., Sugiano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
FTPR----NIDHDPQEIHLECSTSRK----SVWLTPVSTENEIKLDPSPFIAD---FQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LEVIMLLAVLIWTGAENLHVKISCSLDWLMVSVIPVAESRNLYIFADELHLGMGCPA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 NRIHTYVYEFIYLVRDCGIRTRVVSEETLLFQTELYFTPRNIDHDPQEIHLECST-SRK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (620)
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Q9URN3; O75053; Q8WXY2; Q9H540; Q9UKP0; Q9ULG9;
16-OCT-2001 (Rel. 40, Created)
01-FEB-2005 (Rel. 46, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2015 (Rel. 48, Last annotation update)
13-SEP-2015 (Rel. 48, Last annotation update)
13-SEP-2015 (Rel. 48, Last annotation update)
13-SEP-2015 (Rel. 48, Last annotation update)
13-SEP-2015 (Rel. 48, Last annotation update)
13-SEP-2015 (Rel. 48, Last annotation update)
13-SEP-2015 (Rel. 48, Last annotation update)
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13-SEP-2015 (Rel. 48, Last annotation update)
13-SEP-2015 (Rel. 48, Last annotation update)
13-SEP-2015 (Rel. 48, Last annotation update)
13-SEP-2015 (Rel. 48, Last annotation update)
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                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ45612.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                      1062 AA
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GO; GO:0003779; F:actin binding; IEA.
InterPro; IPR001715; Calponin-like.
InterPro; IPR002017; Spectrin.
                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                 QEZSD7_HUMAN PRELIMINARY;
QEZSD7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00033; CH; 1.
SMART; SM00150; SPEC; 2.
PROSITE; PS50021; CH; 1.
SEQUENCE 1062 AA; 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; LENGT, CH; 1. Pfam; PF00307; CH; 1.
                                                                                                                           | :| |:
115 LAFDLRLV 122
                                                                                             144 TAEELGLL 151
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Q6ZSD7; 341-461.
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Best Local Similarity
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96
                                               64
                                                                                                                                                                                                                      12
HUMAN
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NUCLEOTIDE SEQUENCE (ISOFORM 2).
MEDLINE=20001959; PubMed=10529403; DOI=10.1006/bbrc.1999.1538;
Okuda T., Matsuda S., Nakatsugawa S., Ichigotani Y., Iwahashi N.,
Takahashi M., Ishigaki T., Hamaguchi M.;
"Molecular cloning of macrophin, a human homologue of Drosophila
kakapo with a close structural similarity to plectin and dystrophin.";
Biochem. Biophys. Res. Commun. 264:568-574(1999).
                homo saptens (Humman).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE OF 182-4812 (ISOFORM 2), AND ALTERNATIVE SPLICING.
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Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: F-actin-binding protein which may play a role in cross-linking actin to other cytoskeletal proteins. Also binds to microtubules (By similarity).
-!- SUBCELLUIAR LOCATION: Cytoplasmic.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O., Nagase T.;
genes: manual
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Nakajima D., Nomura N., Ohara O.;
"Characterization of cDNA clones in size-fractionated cDNA libraries
from human brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Prediction of the coding sequences of unidentified human genes. XV. The complete sequences of 100 new cDNA clones from brain which code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20026884; PubMed=10559237; DOI=10.1074/jbc.274.47.33522; Sun Y., Zhang J., Kraeft S.-K., Auclair D., Chang M.-S., Liu Y., Sutherland R., Salgia R., Griffin J.D., Ferland L.H., Chen L.B.; "Molecular cloning and characterization of human trabeculin-alpha, giant protein defining a new family of actin-binding proteins", J. Biol. Chem. 274:33522-33530(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21833812; PubMed=11845288; DOI=10.1007/800335-001-3037-3; Gong T.-W.L., Besirli C.G., Lomax M.I.; MACF1 gene structure: a hybrid of plectin and dystrophin."; Mamm. Genome 12.852-861(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [4]
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 868-2350 (ISOFORM 2)
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Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 868-5430 (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22158633; PubMed=12168954;
Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara "Construction of expression-ready cDNA clones for KIAA curation of 330 KIAA cDNA clones.";
DNA Res. 9:99-106(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=1;
IsoId=Q9UPN3-1; Sequence=VSP_007341, VSP_012090;
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NUCLEOTIDE SEQUENCE OF 1544-5057 (ISOFORM 2).
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MEDLINE=98116662; PubMed=9455484;
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DNA Res. 6:337-345(1999).
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sapiens (Human)
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                                                                                                                                                    NCBI_TaxID=9606;
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Pred. No. 89;
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OI-FEB-2005 (TrEMBLrel. 29, Created)

OI-FEB-2005 (TrEMBLrel. 29, Last sequence update)

OI-FEB-2005 (TrEMBLrel. 31, Last annotation update)

Microtubule-actin crosslinking factor 1.

Name=WACF1; ORFNames=RP11-69E11.1-001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.7%; Scor.
25.4%; Pred. No. e.,
... 23; Mismatches
                                                                                                                          Spectrin 5.
Spectrin 6.
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Spectrin 14.
Spectrin 15.
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2 (Potential)
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Spectrin 19.
Spectrin 20.
Spectrin 21.
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Spectrin 26.
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Spectrin 31.
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Spectrin 36.
Spectrin 37.
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Spectrin 23
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Spectrin 25
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Spectrin 29
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EF-hand 2.
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Matches
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R GO; GO:0005737; C:cytoplasm; IDA.

R GO; GO:00051015; F:calcium ion binding; NAS.

GO; GO:00051015; F:calcium ion binding; NAS.

R GO; GO:00051017; F:microtubule binding; NAS.

R GO; GO:00017; F:microtubule binding; NAS.

R InterPro; IPR001399; RF-Hand_type.

R InterPro; IPR001399; RF-Hand_type.

R InterPro; IPR001308; GAS2.

R InterPro; IPR001308; GAS2.

R InterPro; IPR001309; FF-Hand_type.

R InterPro; IPR001309; EF-Hand_type.

R Pfam; PF00187; GAS2; 1.

R Pfam; PF00187; GAS2; 1.

R Pfam; PF00187; GAS2; 1.

R PMART; SM00012; EF-hand; 1.

R SMART; SM00120; ACTININ_1; 1.

R RNOSITE; PS00019; ACTININ_1; 1.

R RROSITE; PS00019; ACTININ_2; 1.

R RROSITE; PS00019; EF-HAND_1; 2.

R RROSITE; PS00019; EF-HAND_1; 2.

R RROSITE; PS00019; EF-HAND_1; 2.

R RROSITE; PS00019; FF-HAND_1; 2.

R RROSITE; PS00019; ACTININ_1; 1.

R ROSITE; PS00019; ACTININ_2; 1.

R ROSITE; PS00019; ACTININ_2; 1.

R ROSITE; PS00019; ACTININ_1; 1.

R ROSITE; PS00019; ACTININ_2; 1.

R ROSITE; PS00019; ACTININ_1; 1.

R ROSITE; PS00019; ACTININ_2; 1.

R ROSITE; PS00019; ACTININ_2; 1.

R ROSITE; PS00019; ACTININ_2; 1.

R ROSITE; PS00019; ACTININ_2; 1.

R ROSITE; PS00019; ACTININ_2; 1.

R ROSITE; PS00019; ACTININ_2; 1.

R ROSITE; PS00019; ACTININ_2; 1.

R ROSITE; PS00019; ACTININ_2; 1.

R ROSITE; PS00019; ACTININ_2; 1.

R ROSITE; PS00019; ACTININ_2; 1.

R ROSITE; PS00019; ACTININ_2; 1.

R ROSITE; PS00019; ACTININ_2; 1.

R ROSITE; PS00019; ACTININ_2; 1.

R ROSITE; PS00019; ACTININ_2; 1.

R ROSITE; PS00019; ACTININ_2; 1.

R ROSITE; PS00019; ACTININ_2; 1.
                                                                                         Incla_QUDN13-4; Sequence=VSP_012090, VSP_012091;
Note=No experimental confirmation available;
-! TISSUE SPECIFICITY: Ubliquitously expressed.
-!- SIMILARITY: Belongs to the plakin or cytolinker family.
-!- SIMILARITY: Contains 1 actin-binding domain.
-!- SIMILARITY: Contains 2 CH (calponin-homology) domains.
-!- SIMILARITY: Contains 1 SH3 domain.
-!- SIMILARITY: Contains 1 SH3 domain.
-!- SIMILARITY: Contains 37 spectrin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EWBL; AF029290; BAA83821.1; -; mRNA.

EWBL; AF141968; AAF06360.1; -; mRNA.

EWBL; AF322330; AAL39000.1; -; Genomic_DNA.

EWBL; AF325330; AAL39000.1; -; Genomic_DNA.

EWBL; AF325331; AAL39000.1; JOINED; Genomic_DNA.

EWBL; AF32533; AAL39000.1; JOINED; Genomic_DNA.

EWBL; AF32533; AAL39000.1; JOINED; Genomic_DNA.

EWBL; AF32533; AAL39000.1; JOINED; Genomic_DNA.

EWBL; AF325336; AAL39000.1; JOINED; Genomic_DNA.

EWBL; AF325336; AAL39000.1; JOINED; Genomic_DNA.

EWBL; AF325336; AAL39000.1; JOINED; Genomic_DNA.

EWBL; AF325339; AAL39000.1; JOINED; Genomic_DNA.

EWBL; AR325340; AAL39000.1; JOINED; Genomic_DNA.

EWBL; AB007934; AAL39000.1; JOINED; Genomic_DNA.

EWBL; AB007934; BAA86565.1; -; mRNA.

EWBL; AB007934; AAL39000.1; -; Genomic_DNA.

EWBL; AL1375334; AAL39000.1; -; Genomic_DNA.

EWBL; AB007934; BAA86565.1; -; mRNA.

FUR; TO0079; TO0079.

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FUR; TO0079; TO0079.

FUR; TO0079; TO0079.
IsoId=Q9UPN3-3; Sequence=Not described;
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CH 1.
CH 2.
                     Name=4;
IsoId=Q96PK2-1; Sequence=External;
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531 HFTSLELVPPSTLTTTHLKAEP 552

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sapiens (Human).

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61 RIHTYVYEFIYLVRDCGIRTRVVS-EETLLFQTELYFTPRNIDHDPQEIHLECSTSRKSV 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Merazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R GO; GO:001609; C:membrane; IEA.

R GO; GO:001609; E:membrane; IEA.

GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0004713; F:proctein receptor activity; IEA.

GO; GO:0004713; F:proctein revosine kinase activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:00048872; F:receptor activity; IEA.

GO; GO:0006488; P:proctein amino acid phosphorylation; IEA.

R InterPro; IPR001099; BGF like.

R InterPro; IPR001099; BFF like.

R InterPro; IPR001099; Prot_kinase.

R InterPro; IPR001245; FV Dkinase.

R InterPro; IPR001245; TYr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R Pfam; PF001404; Ephrin_lbd; 1.

R Pfam; PF001404; Ephrin_lbd; 1.

R Pfam; PF001404; Ephrin_lbd; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1003 AA; 112737 MW; FFDA7C7CD9A99077 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              Satou Y., Imai K.S., Satoh N.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO57735; BAB68344.1; -; mRNA.
HSSP, P54763; 1JPA.
                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                  PRT; 1003 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00104; FNTYPEII.
PRINTS; PR00109; TYRKINASE.
SWART; SW006615; EPH_1bd; 1.
SWART; SW006615; EPH_1bd; 1.
SWART; SW00219; TYRKC; 1.
PROSITE; PS01186; EGF 2; UNKNOWN 1.
PROSITE; PS00109; PROTEIN KINASE ATP; 1.
PROSITE; PS500109; PROTEIN KINASE DOM; 1.
PROSITE; PS500109; PROTEIN KINASE TYR; 1.
PROSITE; PS50109; PROTEIN KINASE TYR; 1.
PROSITE; PS50109; PROTEIN KINASE TYR; 1.
KINASE; RECEPLON; SAM_DOMĀIN; 1.
KINASE; RECEPLON; SAM_LOMĀIN; 1.
KINASE; RECEPLON; SAM_LOMĀIN; 1.
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                                                                                                                                                                                                                                      EPH receptor tyrosine kinase.
                                                              RESULT 15

O95YLO CIOSA PRELIMINARY;
AC O95YLO;
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426 IELLLQIANKIQNGALNCEEKLTLAKNTLQ-------ADAAHLESGQPVQCE 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 LEVLMLLAVLIWIGAENLHVKISCSLDWLMVSVIPVAESRNLYIFADELHLGMGCPA--- 59
                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                  Corby N.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                    EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                       Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.7%; Score 85.5; DB 2; 1
25.4%; Pred. No. 89;
ive 23; Mismatches 58;
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AL37853; CAI21814.1; -; Genomic_DNA.
AL365277; CAL16417.1; -; Genomic_DNA.
AL37853; CAH70156.1; -; Genomic_DNA.
AL37853; CAH73668.1; JOINED; Genomic_DNA.
AL35277; CAH73668.1; JOINED; Genomic_DNA.
AL365277; CAH73668.1; JOINED; Genomic_DNA.
AL355477; CAH73668.1; JOINED; Genomic_DNA.
AL355477; CAH71814.1; JOINED; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0003779; F:actin binding; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0007050; P:calcium ion binding; IEA.
INCEPPO: IPR001715; Calponin actin bd.
INCEPPO: IPR001715; Calponin act bd.
INCEPPO: IPR001049; EF hand Ca bd.
INCEPPO: IPR001049; EF hand Ca bd.
INCEPPO: IPR001054; Glyco hydro 5.
INCEPPO: IPR002017; Spectrin.
Pfam; PF00036; efhand; 2.
Pfam; PF00185; GAS21.
Pfam; PF00185; Spectrin; 27.
ProDom; PD000012; EF-hand; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AL365277, CAIZ1814.1, JOINED; Ge
R EMBL, AL442071; CAIZ1814.1, JOINED; Ge
R EMBL, AL137853; CAI16417.1, JOINED; Ge
R EMBL, AL4326477; CAI16417.1, JOINED; Ge
EMBL, AL442071; CAI16417.1, JOINED; Ge
EMBL, AL432071; CAI70156.1, JOINED; Gen
EMBL, AL442071; CAH70156.1, JOINED; Gen
EMBL, AL442071; CAH70156.1, JOINED; Gen
EMBL, QSVW20; 68-301.
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SWART; SM00054; EFb; 2.
SWART; SM00243; GAS2; 1.
SWART; SM00150; SPEC; 33.
PROSITE; PS00019; ACTININ_1; 1.
PROSITE; PS00020; ACTININ_2; 1.
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Best Local Similarity 25,4%
Local Similarity 25,4%
These 36; Conservative
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                                                                                                                                        NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
                                                                                    NCBI_TaxID=9606;
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임
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Gaps

58;

Job time : 266.6 secs

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